

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 116716

TO: Vanessa L Ford

Location: REM/3B25/3C18

Art Unit: 1645

Friday, March 12, 2004

Case Serial Number: 09/543407

From: Barb O'Bryen

Location: Biotech-Chem Library

Remsen E01A69

Phone: 571-272-2518

PoB

barbara.obryen@uspto.gov

Search Notes

RUSH



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STIC-Biotech/ChemLib

116716

From:

Chan, Christina

Sent:

Thursday, March 11, 2004 12:51 PM

To: Subject: Ford, Vanessa; STIC-Biotech/ChemLib RE: In re: 09543407 sequence search

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841

Remsen, 3E89



----Original Message-----

From: Sent: Ford, Vanessa

T .

Thursday, March 11, 2004 11:40 AM Chan, Christina

Subject:

In re: 09543407 sequence search

Please search SEQ ID NO: 12, 14, 16, 18, 20, 22, 24, 26, 28 and 30. Please include interference searches. Please

rush.

Vanessa L. Ford

Biotechnology Patent Examiner

Office: REM 3B25 Mailbox: REM 3C18 Phone: 571.272.0857 Art Unit: 1645



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Searcher:
Phone:
Location:
Date Picked Up:
Date Completed:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where	applic.)
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DRLink:	
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1: genesecr1980s.*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKLLKVAAFAAIVVSGSALA......VTRVVTHEMAHANNATANQY 151
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	:
92	92	92	92	92	92	93	94.5	94.5	95	98	98.5	98.5	100.5	109	109	109	113	115	
11.8	11.8	11.8	11.8	11.8	11.8	11.9	12.1	12.1	12.2	12.6	12.6	12.6	12.9	14.0	14.0	14.0	14.5	14.8	1
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AAY44402	AAU79539	AAY44404	AAU79538	AAY44403	AAB36331	AAE36890	ABP74039	ABU36649	ABR82647	ABR82645	ABB62708	ABB65764	AAB36342	AAB36319	AAB36324	AAB36340	ABR82644	AAB36320	
Aay44402	Aau79539	Aay44404	Aau79538	Aay44403	Aab36331	Aae36890	Abp74039	Abu36649	Abr82647	Abr82645	Abb62708	Abb65764	Aab36342	Aab36319	Aab36324	Aab36340	Abr82644	Aab36320	
Human tar	Truncated	Human tru	Truncated	Human tru	Escherich	Plectreur	Candida a	Protein e	E. coli c	E. coli o	Drosophil	Drosophil	Salmonell	Salmonel	Salmonell	Salmonel:	E. coli	Salmonel.	

ALIGNMENTS

RESULT 1 AAB36346 UX22XEXEXEXX8888XEXEXEXEXEXEXEXEXEXEXSOOOOOO WPI; 2000-672631/65. N-PSDB; AAC64622. Salmonella enteritidis. Escherichia coli. White AP, Doran JL, 05-APR-2000; 2000WO-CA000356 WO200060102-A2 Synthetic. vaccine; immune response; immunogen Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; 26-FEB-2001 AAB36346; AAB36346 standard; protein; 151 05-APR-1999; 12-OCT-2000. AgfA::PT3#1 amino acid sequence SEQ ID NO:12 (UYVI-) UNIV VICTORIA: (first entry) 99US-0127888P Collison SK, ₿ Kay WW;

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 135; 139pp; English.

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CspA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native

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RESULT 2
AAB36347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA comprising sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or compose into the animal in conjunction with a carrier or diluent. (1) is comply that the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for comply an immune response in an animal. In a fimbrial presentation compose in an animal in a fimbrial protein which the compose in an eliciting an immune response in an eliciting an immune response in an animal. In a fimbrial protein to immunogenicity and adhesion properties are presented in high numbers (up to immunogenicity and adhesion properties relevant for an efficient live compose in an animal in a subunit proteins are usually strong communogens, which may be important for directing an immune response composed in a subunit proteins are usually strong composed in the inserted epitope, and hybrid fimbriae are easy and conservation of the present invention
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Best Local :
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant. AgfA protein useful for eliciting immune response in animal.
                                                                                                     N-PSDB; AAC64623.
                                                                                                                                                     White AP, Doran JL,
                                                                                                                     WPI; 2000-672631/65.
                                                                                                                                                                                                                                       05-APR-1999;
                                                                                                                                                                                               (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                    05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                     12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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Disclosure; Page 136; 139pp; English.

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RESULT 3
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Best Local (
                                                        26-APR-1993;
     (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP. (KING/) KING J.
                                                                                         26-APR-1994;
                                                                                                                       10-NOV-1994.
                                                                                                                                                        WO9425598-A2
                                                                                                                                                                                          Salmonella
                                                                                                                                                                                                                      Salmonella; AgfA; vaccine
                                                                                                                                                                                                                                                      AgfA sequence.
                                                                                                                                                                                                                                                                                         25-MAR-2003
26-JUN-1995
                                                                                                                                                                                                                                                                                                                                        AAR74625;
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41; Conservative
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Pred. No. 1.7e-58;
0; Mismatches 0;
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RESULT 4
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Best Local Similarity 90.3
Matches 136; Conservative
The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described
                                                                                                                                                                 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-APR-1999;
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                                                                                                          Disclosure; Page 135; 139pp; English
                                                                                                                                                                                                                                                                                                                                                               White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-OCT-2000
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N-PSDB; AAQ87467.
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DB; AAC64617.
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                                                                                                                                                                                                                                                                                                                                                               Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agfA; chromosomal gene replacement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fig 7B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.2%;
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                                                                                                                                                                                                                                                                                                                                                               Collison SK,
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Pred. No. 2.2e-58;
4; Mismatches 11
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(Updated
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Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant Agfa; CsgA and Agfa-homologue finbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
Collinson SK,
                                                                                                             26-APR-1994;
                                                                                                                                                03-JUN-1997
                                                                                                                                                                                                                                                                                                Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                   Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
                                                                                                                                                                                                                                                                                                                                                                         Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW23570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW23570 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 151 AA;
                                                                        26-APR-1993;
                                                                                                                                                                                   US5635617-A
                                                                                                                                                                                                                                            Misc-difference
                                   (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                                                                                                                                                                                                         enteritidis 27655-3b agfA
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                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
Kay
                                                                          93US-00054452
                                                                                                           94US-00233788
                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                        /note= "Encoded by GCC"
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90.1%;
Doran JL
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Pred. No. 2.2e-5
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
.2e-58;
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AAB36352
ID AAB3
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Best Local !
Recombinant agfA gene which encodes foreign
                                                                                     N-PSDB; AAC64628.
                                                                                                        WPI; 2000-672631/65
                                                                                                                                                                                                                                                                       05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella enteritidis
                                                                                                                                                                 White AP,
                                                                                                                                                                                                                    (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                          05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella; agfA; chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AgfA::PT3#7 amino acid sequence SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifical hybridise to nucleic acid molecules from greater than 99% of Salmonell strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from greater than 90% of Salmonell strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated 25-MAR-2003 to correct pf field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example
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135; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune response;
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                                                                                                                                                           Doran JL,
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                                                                                                                                                                                                                                                                    99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.6%;
                                                                                                                                                           Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 690; DB 2;
Pred. No. 6.5e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene replacement; fimbrin; epitope;
                                                                                                                                                           SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                         Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151
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(Updated or
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having a segment replaced by a foreign DNA sequence epitope or antigen, expresses recombinant AgfA

05-APR-2000; 2000WO-CA000356

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agfa, CsgA and Agfa-homologue fimbrin subunits, respectively, (2)
CC directing recombination of a recombinant gene into the chromosome of the CC homologous species, (3) directing recombination of a recombination of the chromosome of the homologous species, replacing the native CC copy of that gene, and (4) eliciting an immune response in an animal, cC comprising separating an amino acid polymer comprising a recombinant Agfa CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the cC polymer into the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant Agfa protein which is useful for celiciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong composed, which may be important for directing an immune response constitute the inserted epitope, and hybrid fimbriae are usually strong inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                       12-OCT-2000
                                                                                                                                              Escherichia
                                                                                                                                                                  Salmonella enteritidis.
                                                                                                                                                                                                vaccine; immune response; immunogen
                                                                                                                                                                                                                        Salmonella;
                                                                                                                                                                                                                                                                                                                                       AAB36353;
                                                                                         WO200060102-A2
                                                                                                                                                                                                                                                              AgfA::PT3#8
                                                                                                                                                                                                                                                                                                   26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                         AAB36353 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF1/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein useful for eliciting immune response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNAAL VNYDQLVTRVVTHEMAHA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAK---
                                                                                                                                                                                                                    agfA; chromosomal gene replacement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                              COLI
                                                                                                                                                                                                                                                        amino acid sequence SEQ ID NO:26.
                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 138; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                --NYDOLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNÁTÁNQY
                                                                                                                                                                                                                                                                                                                                                                       protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Pred. No. 1.4e-54;
D; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----NNATANQY 151
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                                                                                                                                                                                                                    fimbrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 151;
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RESULT 8
AAB36349
ID AAB3
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AC AAB3
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DT 26-F
XX
DE AgfA
XX
KW Salm
KW Vacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the accompliation of the present sequence is given in the accompliation of the present sequence is given in the accompliation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant AgfA, CegA and AgfA-homologue fimbria subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                     Salmonella;
                                                            AgfA::PT3#4 amino acid sequence SEQ ID NO:18
                                                                                                       26-FEB-2001
                                                                                                                                                                                    AAB36349 standard; protein; 151 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122;
                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLLKVÄAFÄÄIVVSGSÄLÄGVVPQWGGGCNHNGGGNSSGPDSTLSIYQYGSÄNÄÄLÄLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                 SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 AA
immune response;
                                                                                                                                                                                                                                                                                       NNAALVNQTASDSSVMVRQVGFGNNATANQX
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Doran JL,
                     agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 614; DB 3; I
Pred. No. 1.2e-50;
6; Mismatches 23;
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                                                                                                                                                                                                                                                                                          151
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                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-672631/65.
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  121
                                               121 NNAALVNYDQLVTRVVTHEMAHANNATANQY
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                                                                                                                                                                                                                                           1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGHHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                              Similarity
NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                            MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                      SDARKSETTITQSGYGNGAD
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                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                           78.7%;
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                                                                                                                                                                                                                                                                                                                   Score 613; DB 3;
Pred. No. 1.5e-50;
7; Mismatches 22
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                                                    151
                                                                                                                                                                                                                                                                                                                                                                  Length 151
                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                     Gaps
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120

120

60 60

AAB36350 standard; protein; 151

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AAB36350;

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CC segment invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC AgfA, CsgA and AgfA, homologue fimbria subunits, respectively, (2) CC homologous species; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immune response in an animal, CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for copy of the expression of recombinant agfA protein which is useful for conjuncting an immune response in an animal. In a fimbrial presentation conjunction with a carrier or diluent. (1) is conjuncting an immune response in an expression of recombinant AgfA protein which is useful for conjuncting an immune response in an expression of recombinant agfA protein which is useful for conjuncting an immune response in an expression of recombinant agfA protein which is useful for system the heterologous antigens are presented in high numbers (up to immunogens, which may be important for directing an immune response conjunction, the protein protein segment is conjunction, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response conjunction, the carrier fimbrial presentation of the exemplification of the present invention. The present sequence is given in the exemplification of the present invention.
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                                                 S
                                                                                                    Query Match
Best Local (
                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AgfA::PT3#5 amino acid sequence SEQ ID NO:20
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                                                                                 122;
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                                                                                                  Similarity
                    MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
151
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                                                                                            78.4%;
80.8%;
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                                                                        Score 611; DB 3; 1
Pred. No. 2.3e-50;
7; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kay WW;
                                                                                                          Length 151;
                                                                         Indels
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RESULT 10
AAB36354
ID AAB36354
AC AAB36534
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                                                           CC Regment of the gene has been replaced by a segment of a foreign DNA CC segmenc which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) CC homologues species; (3) directing recombinant gene into the chromosome of the homologues species, (3) directing a recombinant gene into the chromosome of the back into the chromosome of the homologues species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, CC protein containing a replacement segment or segments of foreign amino CC Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is CC eliciting an immune response in an interoducing the cuseful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit protein are usually strong cimmunogens. which may be immortant for directing an usually strong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               片
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immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Escherichia coli.
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Best Local Similarity
The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or
                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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N-PSDB; AAC64627.
                                                                                                                                                                                                                            Disclosure;
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80.1%;
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Best Local Similarity
Matches 122; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the accomplisher of the present invention.
                                                                                                                                                WPI; 2000-672631/65.
N-PSDB; AAC64631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                     05-APR-1999;
                                                                                                                                                                                                                                                                                 05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AgfA::PT3#10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 151
                                                                                                                                                                                                                                                                                                                12-OCT-2000
                                                                                                                                                                                                                                                                                                                                            WO200060102-A2
                                                                                                                                                                                                                         (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the present invention
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                                                                                                                                                                                           ΑP,
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                                                                                                                                                                                           Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                     99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.5%;
                                                                                                                                                                                             Collison
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Pred. No. 1.1e-49;
6; Mismatches 23
                                                                                                                                                                                           SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:30
                                                                                                                                                                                           Kay WW
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described

Recombinant agfA gene having a segment replaced by a foreign which encodes foreign epitope or antigen, expresses recombina protein useful for eliciting immune response in animal.

expresses recombinant use in animal.

DNA sequence AgfA

Disclosure; Page 139; 139pp; English.

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

N-PSDB; AAC64624.

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RESULT 13
AAB36348
ID AAB36
XX AAB36
XX AAB36
XX AAB36
XX 26-FE
XX 26-FE
XX Salmo
XW vacci
XX Salmo
OS Esche
OS Esche
OS Esche
XX Synth
XX 12-OC
XX 12-OC
XX 05-AP
XX 05-AP
XX 05-AP
XX UYVI
XX WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC Agfa, CsgA and Agfa-homologue fimbrin submits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the chromosome of the chromosome of the homologous species; (3) directing recombination of a recombinant gene into the chromosome of the comprision species; and (4) eliciting recombination of a recombinant gene cc copy of that gene; and (4) eliciting an immune response in an animal, cc comprision separating an amino acid polymer comprising a recombinant Agfa carid sequence or sequences grown on a Salmonella, E. coli or carid sequence host cell, from the host cell and introducing the cuseful for the expression of recombinant Agfa protein which is useful for the expression of recombinant Agfa protein which is useful for system the heterologous antigens are presented in high numbers (up to immunogens, which may be important for directing an immune response in an animal. In a fimbrial presentation communogens, which may be important for directing an immune response important for directing an immune response communogens, which may be important for directing an immune response companies the inserted epitope, and hybrid fimbriae are usually strong companies to purify in large amount. The present sequence is given in the exemplification of the present invention
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WPI; 2000-672631/65
                                                                                                      05-APR-1999;
                                                                                                                                    05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                 Synthetic.
                                                                   (UYVI-) UNIV VICTORIA
                                                                                                                                                                              12-OCT-2000
                                                                                                                                                                                                             WO200060102-A2
                                                                                                                                                                                                                                                                Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                    Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                              AgfA::PT3#3 amino acid sequence SEQ ID NO:16
                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB36348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB36348 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKLLKVAAFAAIVVSGSALAGVVFOWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDARKSETTITOSGYGNGADVGQGADNSTIELTONGFRNNATYDOLVTRVVTHEMAHAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                 Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                   99US-0127888P
                                                                                                                                                                                                                                                                                                               response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.4%;
                               Collison
                                                                                                                                                                                                                                                                                                               immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 603; DB 3;
Pred. No. 1.3e-49;
                             SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                             Kay WW,
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RESULT 14 AAR62761 ID AAR62

121

NNAALVNOTASDSSVMVROVGFGNNATANOY

151

AAR62761 standard; protein; 120 AA

AgfA sequence.

10-NOV-1994 WO9425598-A2 Salmonella enteritidis. Salmonella; AgfA; vaccine 27-AUG-2003 25-MAR-2003 26-JUN-1995

(revised)
(revised)
(first entry)

AAR62761;

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                                                                                                                                                                                                                                                                                                                                                                   CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene cc back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA acid sequence or sequences grown on a Salmonella, E. coli or composition of the animal in conjunction with a carrier or diluent. (I) is coliver into the animal in conjunction with a carrier or diluent. (I) is cusful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant agfA protein which is useful for coliver into the heterologous antigens are presented in high numbers (up to 500,000 copiese/cell), the hybrid fimbrin protein possesses both the carrier fimbrial subunit proteins are usually strong communogens, which may be important for directing an immune response conjunction with the inserted epitope, and hybrid fimbriae are easy and conjunct the expressive to purify in large amount. The present sequence is given in the expressive to purify in large amount. The present sequence is given in the expressive to purify in large amount. The present sequence is given in the expressive to purify in large amount.
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Matches
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                                                                                                                                                                                                                                                                                                                                                 Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 136; 139pp; English.
                                                                                                                                                                                                                                                                          Local
121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                      121;
                                                                 61
                                                                                                            61
                                                                                                                                                                                                                                                                          Similarity
                                                  SDARKSETTÍTÓSGYGNGADVGÓGADNSTÍELTÓNGFRNNATIDÓWNAKNSDÍTVGÓYGG
                                                                                SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                          MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                        74.5%;
80.1%;
                                                                                                                                                                                                                                                                   Score 580; DB 3;
Pred. No. 2.1e-47;
                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                          Length 151;
                                                                                                                                                                                                                                          Indels
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                                                    120
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RESULT 15
AAW23569
ID AAW23
X P P X R R X P X P X P X P X P X X E X P T X R X X P X P X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X 
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Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents the Salmonella enteritis 27655-3b TnphoA mutant strain AgfA protein. The encoding DNA and isolated AgfA protein are used in genetic immunization and vaccine compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                    WPI; 1997-309886/28.
N-PSDB; AAT74141.
                                                                                                                                                                                                                                                                                                                                                                                                               03-JUN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enteropathogenic bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella enteritidis 27655-3b TnphoA mutant agfA fragment.
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29-SEP-1997
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                    Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                        Collinson SK,
                                                                                                                                                                                                                                           (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
                                                                                                                                                                                                                                                                                                  26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                         26-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
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(first entry)
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                                                                                                                                                                                        Doran JL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enterobacteria; S.enteritidis; antibody.
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Pred. No. 1.2e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORP.
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Best Local Sim:
Matches 106;
                                                                                                                                                                                                                                                                       strain. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                      Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents an agfA fragment encoded by an agfA gene
fragment derived from Salmonella enteritidis 27655-3b TnphoA mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Fig 7; 85pp; English
43
                        82 GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 127
                                                                          -
                                                                                                     22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
                                                                                                                                                                             Similarity
GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN
                                                                              VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
                                                                                                                                                            Conservative
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                                                                                                                                                          Score 560; DB; Pred. No. 1.2.0; Mismatches
                                                                                                                                                                             1.2e-45;
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Search completed: March 11, 2004, 18:33:36
Job time : 46.9 secs

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Maximum DB
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Maximum Match
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Perfect score:
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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US-09-841-835-2
US-09-866-038A-3
US-09-36-156-1204
US-09-072-96-129
US-09-072-967-204
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US-09-543-681A-6966
US-09-543-681A-6966
US-09-543-681A-6966
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US-09-336-478-61
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US-08-233-788A-57
US-09-196-387-8
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Sequence 59, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 3, Appli
Sequence 204, App
Sequence 199, App
Sequence 191, Appli
Sequence 204, App
Sequence 3, Appli
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75.5	76.5	76.5	76.5	77	77	77	77	77.5	77.5	77.5	78	78	78	78	78	78.5	79
9.7	9.8	9.8	9.8	9.9	9.9	9.9	9.9	9.9	9.9	9.9	10.0	10.0	10.0	10.0	10.0	10.1	10.1
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Sequence 7, Appli	Sequence 13002, A	Sequence 2, Appli	Sequence 2, Appli	Sequence 5434, Ap	Sequence 39, Appl	Sequence 8, Appli	Sequence 280, App	Sequence 3401, Ap	Sequence 4, Appli	Sequence 22119, A	Sequence 2, Appli	Sequence 1, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 10, Appl	Sequence 9, Appli

ALIGNMENTS

RESULT 1 US-08-233-788A-59

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION : 435
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua: 35,570
REFERENCE/DOCKET NUMBER: 920043.403C2
REFERENCE/DOCKET NUMBER: 920043.403C2
TELEFAX: (206) 622-4900
TELEFAX: (206) 622-4900
TELEFAX: 13723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-233-788A-59
                                                          Query Match
Best Local S
Matches 135
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
NUMBER OF SEQUENCES: 61
CORRESPONDEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 6300 C
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ZIP: 98104-7092
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                              Similarity
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                                                            Conservative
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                                                          Score 690; DB 1; Length 151; Pred. No. 7.1e-62; Mismatches 12; Indels
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US-08-233-788A-57 RESULT 2

Sequence 57,

tent No.

GENERAL INFORMATION:

ITLE OF INVENTION:

Seattle

Washington

U.S.Ā.

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; LENGTH: 120 mino acids
; TYPE: amino acid
; TOPDLOGY: linear
; MOLECULE TYPE: protein
US-08-233-788A-57
            Sequence 8, Application US/09196387 Patent No. 6277613 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 3723836 SEEDANBERRY INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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                                                                                                                                                                        GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 127
                                                                                                                                                                                                                                                   VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
                                                                                                                                           GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 106
                                                                                                                                                                                                                    VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
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                                                                                                                                                                                                                                                                                             71.9%; Score 560; DB 1; Length 120; ilarity 100.0%; Pred. No. 6e-49; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Doran, James L.
Kay, William W.
Collinson, Karen S.
Clouthier, Sharon C.
CHOUTHIER, SHARON C.
VENTION: METHODS AND COMPOSITIONS FOR DETECTION
VENTION: OF SALMONELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seed and Berry
00 Columbia Center,
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                                                                                                                                                                                                                                                                                                                  tent No.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                      TITLE OF INVENTION: A PROTE TITLE OF INVENTION: OF USE NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/0
FILING DATE: June 10, 19
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., Davi
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                               CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                     STREET:
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TOPOLOGY: linear
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CITY: Hackensack
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Smith, Susan
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61 82 Matches 106; Query Match Best Local Similarity

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TELEFAX:

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US-09-196-387-8 RESULT 3

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Best Local (
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                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/0
FILING DATE: June 10, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: de Lange, Titia
APPLICANT: Smith, Susar
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
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LENGTH: 673 amino acida
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
RELECOMMUNICATION INFORMATION:
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REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 600-1-230 CIP1
                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                    APPLICATION NUMBER: US/09/196,387 FILING DATE:
                                                                                                                                                                                                                                                                                                                     COUNTRY: U
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STATE: New Jersey
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Pred. No. 0.6;
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TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-841-835-10
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              Query Match
Best Local Similarity
 Matches
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GENERAL INFORMATION:
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Best Local (
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 949 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER: DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT
TITLE OF INVENTION: OF USE THEREOF
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                                                                                                                                                                                                                                                   NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
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CITY: Hackensack
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
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Similarity 30.4%;
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; Pred. No. 0.94
15; Mismatches
                Score 92;
Pred. No.
Mismatches
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                DB 4;
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 57;
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                              Length 949
 Indels
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Gaps
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US-09-841-835-2
; Sequence 2, Application US/09841835
; Patent No. 6506587
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                                                                    RESULT 8
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US-09-196-387-2
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US-09-196-387-2
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SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amin-
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Best Local !
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GENERAL INFORMATION:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/09:
PILING DATE: June 10, 1999
ATTORNEY/AGENT INFORMATION:
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APPLICANT: de Lan
APPLICANT: Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 201-1
201-343-1684
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Smith, Susan
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APPLICANT: Gregg, Morin B.

APPLICANT: Walter, Funk D.

APPLICANT: Walter, Funk D.

APPLICANT: Mieczyslaw, Piatyszek A.

TITLE OF INVENTION: A Second Mammalian Telomerase FILE REFERENCE: 080/003C

CURRENT APPLICATION NUMBER: US/09/972,115A

CURRENT FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: US 60/128,577

PRIOR FILING DATE: 2000-04-10

PRIOR FILING DATE: 1909-04-13

PRIOR FILING DATE: 1999-04-13

NUMBER OF SEQ ID NOS: 64
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US-09-972-115A-8
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
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MOLECULE TYPE:
HYPOTHETICAL:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
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RESULT 11
US-08-864-038A-3
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US-09-336-115C-6
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Best Local Similarity
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SEQ ID NO 8
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APPLICANT: Guy, Bruno
TITLE OF INVENTION: LT and CT in Parenteral Immunization
TITLE OF INVENTION: Methods Against Helicobacter Infection
FILE REFERENCE: 06132/055002
CURRENT APPLICATION NUMBER: US/09/336,115C
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: US 09/100,258
PRIOR APPLICATION NUMBER: US 09/100,258
PRIOR PILING DATE: 1998-06-19
NUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: VARIANT LOCATION: 721
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                                                                                                                                                                                                                                                                                                                   AYQAVFLAINAAVGL---WNTIGYAVMCGNGNGTESGPGSVIFNDQPGQDSTQITCNRFE 158
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                                                                                                                                                                        GVYQFCKAKNGS-SSSSNGGNGSSTQTTATTTQDGVTITTTYNNNKATVKFD--
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                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                           28;
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Pred. No. 0.97;
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RESULT 12
US-09-056-556-204
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                                           Sequence 204, Application US/0905, Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/864
FILING DATE: May 28, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-1844
FILING DATE: 15-July-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
REFERENCE/DOCKET NUMBER: F-56
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)986-23340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Kunio
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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              TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
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TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: peptide
LOCATION: from 1 to 738
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Mie-prefecture
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35.4%;
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CONTAINING SAID CDNA, HOST CELES TRANSFORMED WITH SAID
VECTOR, POLYPEPTIDE PRODUCED THERBBY, METHOD OF PRODUCING
SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epithelial cell
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Pred. No. 1
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Patent No. 645836
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              ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                         NUMBER OF SEQUENCES: 3
                                                                                                                                                                    TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
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LENGTH: 943 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                           STREET:
                                                               COUNTRY:
                                                                                                                          ADDRESSEE:
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TOPOLOGY: 1:
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                                                                                              Seattle
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                                                                           Washington
                                                                                                          6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington
                                                                                                                                                                                                                                                                                                                                                             Application US/09072596
                                                                                                                                                                                     Lodes, Michael J.
Hendrickson, Ronald C.
                                                                                                                                                                                                                               Houghton, Raymond
Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   943 amino acids
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Dillon, Davin C.
                                                                                                                                                                                                                                                                                                               Reed, Steven G.
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                                                                                                                                                                                                                    Twardzik, Daniel R.
                                                                                                                                                                                                                                                                  Campos-Neto, Antonia
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IBM PC compatible
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                                                                                                          701 Fifth Avenue
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US-09-477-135A-131
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CURRENT FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 0899823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR PILING DATE: 1996-06-14
PRIOR PILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
PRIOR FILING DATE: 1995-06-15
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SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
                                                                                                                                                                                                                        LENGTH: 943
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELECHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 05-MAY CLASSIFICATION:
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                                                      266 İGLTĞSGLLĞF-----ĞĞLNSĞTĞN-----IĞLFNSĞTĞNVGIĞNSĞTĞNWĞIĞNSĞ 312
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69 TITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD---ITVGQY-----
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                                                                                           12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR----KSET 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR---KSET 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
33; Conserva
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                                                                                                                                    Conservative
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25.6%;
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                                                                                                                                    15;
                                                                                                                              Score 89; DB 4
Pred. No. 1.9;
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Mismatches
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Pred. No. 1.9;
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                                                                                                                                                                     DB 4;
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                                                                                                                                  Indels
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; TOPOLOGY: 11
US-09-072-967-204
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US-09-072-967-204
                                                                                                                                                                                                                                      Query Match 11.4%;
Best Local Similarity 25.6%;
Matches 33; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206) 682-6031
(INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lodes, Mic
APPLICANT: Hendricks
TITLE OP INVENTION: UTITLE OP INVENTION: UTITLE OP INVENTION: UNIMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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266 GNYNTGLAN 274
                                       119 GGNNAALVN 127
                                                                               206 NSYNTGFGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSNTGGFNMGQYNTGYLNS 265
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                                                                                                                                                           159 IGLTGSGLLGF-----GGLNSGTGN-----IGLFNSGTGNVGIGNSGTGNWGIGNSG 205
                                                                                                                   69 TITQSGYGNGADVGQGADNSTIBLTQNGFRNNATIDQWNAKNSD---ITVGQY----- 118
                                                                                                                                                                                                   12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR---KSET 68
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5. 6592877
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Todes, Michael J.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Ronald C.
VENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
VENTION: AND DIAGNOSIS OF TUBERCULOSIS
EQUENCES: 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skeiky, Yasir A.W.
Dillon, Davin C.
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; Pred. No. 1.9;
15; Mismatches 5
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Search completed: March 11, 2004, 18:44:23

Job time : 13.4 secs

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Minimum DB
Maximum DB
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No.
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
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seq length: 2000000000
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1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*

11: /cgn2_6/prodata/1/pubpaa/US09E_PUBCOMB.pep:*

12: /cgn2_6/prodata/1/pubpaa/US09E_PUBCOMB.pep:*

13: /cgn2_6/prodata/1/pubpaa/US09E_PUBCOMB.pep:*

14: /cgn2_6/prodata/1/pubpaa/US09E_PUBCOMB.pep:*

15: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*

16: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*

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18: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
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Gapop 10.0 , Gapext 0.5
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779
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     10 US-09-972-115A-8
14 US-10-199-937-4
18 US-08-934-666A-6
18 US-10-238-075-749
15 US-10-369-493-20619
18 US-99-99-6-634-131
10 US-09-997-182-131
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US-09-841-835-10
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US-10-032-585-7876
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Sequence 20638, A
Sequence 7776, Ap
Sequence 8, Appli
Sequence 10, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 79, Appli
Sequence 79, App
Sequence 131, App
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45	44	43	42	41	40	39	38	37	36	<u>ა</u>	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
80	80		•	•	•	80.5	•	81	81	81	81	81.5	81.5	82	82	82	82.5	83	83	83	w	83.5	Δ	85	85	85	87.	87.5	88
10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.4	10.4	10.4			•	•	10.5	10.5	10.6	10.7	10.7	10.7	10.7	10.7	10.8	10.9	10.9	10.9	11.2	11.2	11.3
255	255	527	527	350	251	251	247	812	408	134	65	730	438	386	254	253	873	562	254	254	597	253	271	956	956	257	482	892	354
10	10	14	9			10						9	14	14	10	10	10	14	10	10	9	5	14	14	Ц	5	14	10	10
US-09-880-748-1281	US-09-880-748-1153	US-10-080-170-348	US-09-712-363-156	US-10-156-761-13168	US-09-880-748-1554	US-09-880-748-1122	US-10-322-673-48	US-10-369-493-9134	US-10-156-761-11222	US-10-394-575-61	US-09-996-194-16	US-09-801-368-126	US-10-156-761-9343	US-10-050-704-100) US-09-880-748-1226	US-09-880-748-2098	US-09-952-267-13	US-10-156-761-13039	US-09-880-748-1165	US-09-880-748-1136	US-09-793-306-146	US-09-880-748-1850	US-10-156-761-11721		US-10-121-032-63	US-09-880-748-1494	-10-156	US-09-952-267-5	US-09-820-843A-21
1281,	115	Sequence 348, App	156,	131	1554,	112	Sequence 48, Appl		Sequence 11222, A	æ	Sequence 16, Appl	126, Ar	9343,	100,		2098	13,	1303		1136	146, Ar				Sequence 63, Appl				Sequence 21, Appl

ALIGNMENTS

US-10-369-493-20638

Sequence 20638, Application US/10369493 Publication No. US20030233675A1

GENERAL INFORMATION:

```
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Greyen C.
APPLICANT: Galdman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/03-02-28
CURRENT ETLING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ. ID NOS: 47374
SEQ ID NO 20638
LENGTH: 445
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                                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                       NAME/KEY: unsure
LOCATION: (1)..(445)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Rhodopseudomonas palustris FEATURE:
19 AAFAADSNTVYLNOTGNDQQANITQSGNGNSVGAFNGNSGFLQENGTLSGA-NLLTVKQS
                                                                                                                               7 AAFAA-----IVVSGSALAGVVPQWGGGG-----NHNGG-----GNSSGPDSTLSIYQY
                                                                                                                                                                                                          Similarity
                                                                                                                                                                                  Conservative
                                                                                                                                                                             12.8%; Score 100; DB 15; Length 445; 26.6%; Pred. No. 0.11; :ive 20; Mismatches 56; Indels 5
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78

GENERAL INFORMATION:

APPLICANT: Terry,

Bo, Jiang

Roemer D.

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Sequence 7876, Application US/10032585
Publication No. US20030180953A1
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APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                                                                                                                                                                                     ITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          532 TGLTNN---NNSKSPAKSKKKSNFD----NNSNSALNNLDKSKLKINTNEITNISETTSN 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 IELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNYDQLVTRVVTHEMAHANNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30. GNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNST 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNNNGSGNSSGTTNNSNNYNN------KSISKKNE-----IDDGDDLNPTSITNN 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNSNSV-----GRDIQGKQSGAGNSAAIFQEGTGSDVELQQTGTSNGAVPSGWNWTN 129
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                                                                                                                                                                                                                                                                                                                                                                 411 Hackensack Avenue, 4th Floor
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                                                         US-09-841-835-10
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Query Match
Best Local Similarity
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GENERAL INFORMATION
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Patent No. US20020076795A1
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                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
                                                                                                                                                                                                                       NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
FILING DATE:
                                                                                                                                                                        TELEFAX: 201
TELEFAX: 133521
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MEDIUM TYPE: Floppy
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                                                         TOPOLOGY: Illeat
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                          TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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Smith, Susan
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 11.8%;
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Score
Pred.
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92;
No.
DB 9;
1.8;
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             Length 949;
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US-09-841-835-8

Sequence 8, Application US/09841835 Patent No. US20020076795A1 GENERAL INFORMATION:

APPLICANT:

de Lange, Titia Smith, Susan

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

09/196,387

FILING DATE:

MEDIUM TYPE: Floppy

Floppy disk

07601

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

STREET: 411
STREET: 411
CITY: Hackensack
Jersey

New Jersey

USA

NUMBER OF SEQUENCES: 1

ADDRESSEE:

Klauber & Jackson

ATTORNEY/AGENT INFORMATION

NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742

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; ORGANISM: Candida albicans US-10-032-585-7876

TYPE: PRT

ID NO 7876 ENGTH: 688

SOFTWARE: PatentIn version 3.1

Query Match

Conservative

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US-09-972-115A-8
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                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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PRIOR APPLICATION DATA:
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APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS
TITLE OF INVENTION: OF USE THEREOF
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                                                                                                                                                                                                                                                                                                                                    TYPE: amino a
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                 158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                 65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                    99 VAAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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                                                                                                                                                                    6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR
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linear
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NO
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SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Applicat
Publication No. US20
GENERAL INFORMATION:
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SEQ ID NO 8
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Best Local :
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APPLICANT: Geron Corporation
APPLICANT: Gregg, Morin B.
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                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/199,937
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/606,035
PRIOR FILING DATE: 2000-06-28
PRIOR PELICATION NUMBER: 60/141,582
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Christenson, Erik
APPLICANT: DeMaggio, Anthony J.
APPLICANT: Goldman, Phyllis S.
APPLICANT: MCElligott, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/128,577
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 1999-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gregg, Morin B.
APPLICANT: Walter, Funk D.
APPLICANT: Mieczysław, Piatyszek A.
TITLE OF INVENTION: A Second Mammalian Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 27866/36559
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CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT FILING DATE: 2001-10-05
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                                                                                                                                                                                                                                                                                                              LENGTH: 1327
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158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
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                                    65 KSETTIT----OSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                  35;
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                                                                                                                      6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR
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                                                                                                                                                                                     Similarity
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No. US20030190739A1
                                                                                                                                                                  Conservative
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Pred. No.
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT: Al-Garawi
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,175
REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,666A
FILING DATE: 01-APR-1997
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617-428-7045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
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271 NNAEQLLNQAAN 282
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                                                                                                                                                                                                                                                  l Similarity
40; Conserv
                                                    GVYQFCKAKNGS-SSSSNGGNGSSTQTTATTTQDGVTITTTYNNNKATVKFD-----IT 270
                                                                               G-----ADNSTIELTONGFRNNATIDQWNAKNSDITVGQYGGNNAALVNYDQLVTRVVT 137
                                                                                                              STGPGKSMSIDEFKKLNEAYQIIQQALKNQSGFPELG-GNGTKVSVNYNYECRQTADING 217
                                                                                                                                             SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNG------ADVGQ 83
                                                                                                                                                                                                            AFAAIVVSGSALAGVVPQW------GGGGNHNGGGN-----
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20.8%; Pred. No. 1
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                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20619
LENGTH: 486
                                                                                           Matches
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                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
                                                                                                                                                                                FEATURE:
NAME/KEY: unsure
LOCATION: (1)...(486)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 0003145
PRIOR FILING DATE: 2000-03-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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86 SVVVAGTDYRDIVÁGVLÞSLGGVKKAYAIGDGSGÞFAPFKDLASDTPFSAPEFGAADGFV 145
                                    11 AIVVSGS----ALAGVVPQWGGGGNHNGGGNSSGP-----DSTLSIYQYGSANAAL 57
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                                                                                       l Similarity
35; Conserv
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                                                                                       Conservative
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o. US20030148324A1
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                                                                                                        11.5%;
                                                                                                     Score 89.5;
Pred. No. 1.
                                                                                  Mismatches
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                                                                                                                      Length 486;
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US-09-996-634-131
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CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILLING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILLING DATE: 1997-12-15
PRIOR FILLING DATE: 1997-12-15
PRIOR FILLING DATE: 1996-06-14
PRIOR FILLING DATE: 1996-06-15
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILLING DATE: 1995-06-15
                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
                                                                                                                                                                                                                                                                                    Sequence 131, Application US/09997182 Publication No. US20030049263A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. SEQ ID NO 131
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                                                                                                          FILE REFERENCE: 61258
CURRENT APPLICATION NUMBER: US/09/997,182
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
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TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences
TITLE OF INVENTION: immunostimulatory Peptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR---KSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITQSGYGNGADVGQGADNSTIBLTQNGFRNNATIDQWNAKNSD---ITVGQY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPLFHVTGLGLMLTLQQAGGASVIAAKFDPAQAARDIEAHKV 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -QYGGNNAALVNYD--QLVTRVVTHEM 140
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Pred. No. 3
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3.5;
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US-09-997-181-131
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 Sequence 199, Appropriate Publication No.
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Publication No.
                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 131
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TYPE: PRT
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 Application US/10193002
5. US20030135026A1
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; ORGANISM: Mycobacterium tuberculosis US-09-997-182-131
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CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 169
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
FILE REFERENCE: 61257
                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mycobacterium tuberculosis
                                            119 GGNNAALVN 127
                                                                                                313 NSYNTGFGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSNTGGFNMGQYNTGYLNS
                                                                                                                                                                                                 266 IGLTGSGLLGF----
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                                                                                                                                                69 TITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD---ITVGQY-----
                                                                                                                                                                                                                                                   12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR----KSET 68
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Similarity 25.6%;
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GNYNTGLAN 381
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Pred. No. 3.5;
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RESULT 15
US-10-084-843-204
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                                                     Sequence 204, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
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Best Local S
Matches 33
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SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/10/193,002

FILING DATE: 10-Jul-2002

CLASSIFICATION: «UNKnown»

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/072,596

FILING DATE: 05-MAY-199

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 11.4%; Score 89; DB Local Similarity 25.6%; Pred. No. 3.5; Mismatches 33; Conservative 15; Mismatches
                                     APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98104-7992
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                               266 GNYNTGLAN 274
                                                                                                                                                                                                                                                               206 NSYNTGFGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSNTGGFNNGQYNTGYLNS 265
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ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indes, Michael J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TUBERGULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 350
                                                                                                                                                                                                                                                                                                                     69
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                                                                                                                                                                                                                                       GGNNAALVN 127
                                                                                                                                                                                                                                                                                                    TITQSGYGNGADVGQGADNSTIBLTQNGFRNNATIDQWNAKNSD---ITVGQY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 943 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
Skeiky, Yasir A.W.
Dillon, Davin C.
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Vedvick, Thomas S.
Twardzik, Daniel R.
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Dillon, Davin C.
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Search completed: March 11, 2004, 19:18:34 Job time : 25.6 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: 
    Vuknown>

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Houghton, Raymond
Vedrick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                             119 GGNNAALVN 127
                                                                                                                                                              206 NSYNTGFGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSNTGGFNMGQYNTGYLNS 265
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        69 TITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD---ITVGQY-----
                                                                                                                                                                                                                                                                                           12 IVVSG$ALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR----KSET 68
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                                                                                   GNYNTGLAN
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TYPE: amino acid
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STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                          11.4%; Score 89; DB 14; Length 943; ilarity 25.6%; Pred. No. 3.5; Conservative 15; Mismatches 55; Indels
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Title:
Perfect score:
Sequence:
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                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                   Database
                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein search, using sw model
PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
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779
1 MKILKVAAFAAIVVSGSALA......VTRVVTHEMAHANNATANQY 151
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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520 501.5 501.5 106 106 101.5 100.5 98.5 98.5

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91 91 90.5 90.5 90 90 90.5 89.5

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Description A;Collinson, S, 20011nson, S, 2
Description A;Collinson, S, 20011nson, S, 2
R;Collinson, S J. Bacteriol. J. Bacteriol. A;Title: Purif. A;Accession: A A;Contents: 27 A;Accession: A A;Accession
rein ag ein csg l prote l prot
R;Collinson, S.K. J. Bacteriol, 173 A;Title: purifica A;Reference numbe A;Contents: 27655 A;Accession: A448 A;Accession: A486 A;Status: prelimi A;Molecule type: A;Residues: 21-33 A;Note: sequence C;Genetics: A;Gene: agfA C;Function: A;Description: ma A;Note: fimbriae C;Keywords: fimbriae C;Keywords: fimbriae F;1-20/Domain: si F;21-151/Product: Query Match Best Local Sim: Matches 136; Qy 1 1 MK Db 1 MK Oy 61 SD Oy 61 SD

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Length 151; ; 1; Indels 0; Gaps 0;	ch 89.2%; Score 695; DB 2; 1 Similarity 90.1%; Pred. No. 1.8e-50; 136; Conservative 4; Mismatches 11;	Query Match Best Local S Matches 136	
d <sig> experimental <mat></mat></sig>	lmbria : signal sequence #status predicted <sl ict: fimbrin protein agfA #status exper</sl 	Keywords: fir 1-20/Domain: 21-151/Produ	a a C
imbriae Lissue plasminogen activator	major component of thin aggregative flae bind to fibronectin, plasminogen, t	Function: Description: Note: fimbri	P P O
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ay, w.w.	K.; Emody, L.; Muller, K.H.; Trust, T 173, 4773-4781, 1991	Collinson, S. Bacteriol. 1	٠ ٣ ١
idue 44 as Ile	source: strain 27655-3b thors translated the codon ACG for residue	Experimental	P P :
	-52 <co2></co2>	Accession: PC Molecule type Residues: 21-	2
C43599.1; PID:g1184714	151 <col/>	Residues: 1-1 Cross-referen	PP :
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ng thin, aggregative fimbriae. 497	178, 662-667, 1996 nella enteritidis agfBAC operon encodi: mber: JC6039; MUID:96146512; PMID:8550	Bacteriol. 1 Title: Salmon Reference num	D D G
ser, P.A.; Kay, W.W.	C6039; PC6015; A44898 .K.; Clouthier, S.C.; Doran, J.L.; Banı	Accession: JC Collinson, S.	۲. ان کا
text_change 08-Oct-1999	monella enteritidis -1996 #sequence_revision 31-Dec-1996 #1	Species: Salm Date: 31-Dec-	CC.
dis	RESULT 1 JC6019 fimhrin nrotein acfA precursor - Salmonella enteritidis	SULT 1 8039 mbrin protein	JCC
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probable sugar ABC probable PPE prote	2 440 2 AD153		
hypothetical prote class 3 outer memb	2 945 2 T2199		
protein F39D8.1b (2 615 2 E7066 2 940 2 D8972		
hypothetical glyci	3 434 2 E7076		
hypothetical prote probable PPE prote	3 301 2 B8453		
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probable PPs proce hypothetical prote	4 3300 2 D7057 4 407 2 T2195		
merozoite 45K surf	4 347 2 B3911		

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121

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A;Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62282.1; PID:g1147564
A;Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Augune, Bilattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; R.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G64846
                                                                                                               A; Molecule type: DNA
A; Residues: 1-151 <BLAT>
                                                                                                                                                      A;Status: nucleic acid sequence not shown; translation not
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A;Title: Expression of two csg operons is required for production A;Reference number: S70783; MUID:96414468; PMID:8817489
A;Accession: S70788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: csgA protein; major curlin protein
C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change
C;Accession: S70798; G64846; S31202; S34560; S34559
R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.
Mol. Microbiol. 18, 661-670, 1995
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A; Residues: 1-151 <HAM>
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S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Title: Complete genome sequence of a multiple drug resistant
A;Title: Complete genome sequence of a multiple drug resistant
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A;Title: Complete genome sequence of a multiple drug resistant
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A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AI0635
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       Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74126.1; Experimental source: strain K-12, substrain Mg1655; Olsen, A.; Arnqvist, A.; Hammar, M.; Sukupolvi, S.; Normark, S. 21. Microbiol. 7, 523-536, 1993
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90.1%;
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Pred. No. 1.8e-50;
4; Mismatches 11
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Davis, P.; Davies, R.
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A;Title: The RpoS sigma factor rel
A;Reference number: S31202; MUID:9
A;Accession: S31202
A;Molecule type: DNA
A;Residues: 1-6,'V',8-151 <OLS1>
A;Cross-references: EMBL:L04979
                                                                                                                                                                                       A;Status: Pickers DNA
A;Molecule type: DNA
A;Residues: 1-152 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34843.1;
A;Cross-references: strain O157:H7, substrain;
                                                                                                                                                                                                                                                                                                   A;Title: Complete genome sequence of enterohemorrhagic E
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D90806
                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change C;Accession: D90806 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
D90806
                                                                                                                                                                    A;Gene:
                                                                                                                                                                                                                                                                                                                                                                  gasawara, N.; Yasunaga,
DNA Res. 8, 11-22, 2001
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                                                                                                                                                                                                                                                                                  A; Status: preliminary
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A;Residues: 1-133,'RQRDSGWLW' <OLS3>
A;Cross-references: EMBL:LO4979; NID:g290424;
A;Experimental source: strain K-12, substrain
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R;Olsen, A.N.; Arnqvist, A.M.
submitted to the EMBL Data Libb
A;Reference number: S34559
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                                                                                                                                                                                                                                                                                                                                                                                 Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii,
Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori,
                                                                                    Conservative
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                                                                                                     64.4%;
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                                                                                  21;
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                                                                           Score 501.5; DB 2
Pred. No. 1.6e-34;
1; Mismatches 30
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No. 4.7e-36;
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W3110
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RIMD 0509952
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                                                                                                                    152;
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Shinagawa,
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QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG

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A;Molecule type: DNA
A,Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-A;Cross-references: EMBL:L03710
R;Martindale, D.W.; Taylor, F.M.
Nucleic Acids Res. 16, 2189-2201, 1988
A;Title: Multiple introns in a conjugation-specific gene from Tetrahymena thermophila.
A;Title: Multiple introns in a conjugation-specific gene from Tetrahymena thermophila.
A;Reference number: S03650; MUID:88189811; PMID:3357771
A;Accession: S03650
A;Molecule type: DNA
A;Residues: 236-250,'I',252-255,'N',257-773 <MAR>
                                                                                                                                                                                                                                                  RESULT 6
S42136
                                                                                                                                                                     R;Taylor, F.M.; Martindale, D.W.
Nucleic Acids Res. 21, 4610-4614, 1993
A;Title: Retroviral-type zinc fingers and glycine-rich repeats A;Reference number: S42135; MUID:94051569; PMID:8233798
A;Accession: S42135
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, October 1992
A;Reference number: S42136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iller, L.; Grotbeck, E.J.; Davis, Nature 409, 529-533, 2001
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hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cnjB protein - Tetrahymena thermophila
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                                                                                                                                                                                                                                                                                                                                                                                                   Species: Tetrahymena thermophila; Date: 19-Mar-1997 #sequence revisi; Accession: S42136; S42135; S03650; Taylor, F.M.; Martindale, D.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Residues: 1-152 <STO>
;Cross-references: GB:AE005174; NID:gl2514574; PIDN:AAG55788.1;
;Experimental source: strain O157:H7, substrain EDL933
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Best Local :
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65.8%; Pred. No. 1.6e-34;
cive 21; Mismatches 30
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                                                                                                                                                                                                                                                                                                                                                                           A;Experimental source: strain 1021, megaplasmid pSymB R;Gallbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Amp pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D. A;Title: The composite genome of the legume symbiont Sinorhizobium A;Reference number: A96039; MUID:21368234; PMID:11474104
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A;Introns: 85/3;
C;Keywords: zinc
                                                                                                                                                                                                                                                                                                                          A; Gene: SMb21548
                                                                                                                                                                                                                                                                                                                                                             A; Contents: annotation
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A; Residues: 1-2174 < KUR>
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A;Gene: cnj
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                                                                           738 ----GGYANTANVGFKGLTLTTQGSHAAGIVAQSVGGGGGTGGTASSYSAGIGFTASVAV
                                                                                                                                                                                11 AIVVSGSALAGVVPQ--WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET
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 GGTGGNGGA
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Mismatches

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QGADNSTI -- ELTQNGFRNNATIDQWNAK---NSDITV

115

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793

-GGNATGGDAGFGSFQIGGGGGG----

Score 104; Pred. No. 1

.9 DB

2

Length 2174;

E.; Komp, C.; Lelaure D.H.; Wong, K.; Yeh, K m meliloti.

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F;1451-1464/Region: zinc finger CC
F;1478-1491/Region: zinc finger CC
F;1591-1514/Region: zinc finger CC
F;1590-1543/Region: zinc finger CC
F;1555-1568/Region: zinc finger CC
F;1579-1592/Region: zinc finger CC
F;1579-15615/Region: zinc finger CC
F;1602-1615/Region: glycine-rich
                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A,Title: The complete sequence of the 1,683-kb pSymB megaplasmid
A,Reference number: A95842; MUID:21396508; PMID:11481431
A,Accession: B95965
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C;Genetice:
                                                                                                                                                                                                                                            C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                                                                 hypothetical glycine-rich protein [imported] - C;Species: Sinorhizobium meliloti
                                                    Cross-references: GB:AL591985; PIDN:CAC49389.1; PID:g15140875; GSPDB:GN00167
                                                                                                                                                                                                                                                                                                                                                                                 1686 QTGGGWGSNDN-----QQQQNENTGGGGWGSSNSNQTNNESSWGSNNQA 1729
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                                                                                                                                                                                                                                                                                     Sinorhizobium meliloti (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33;
Abola, P.; Ampe, S.; Federspiel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                         P.; Vorholter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                       from
N.A.; Fisher, R.F.
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                                                                                                                                                                     the N2-fixing
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                                                                                                                                                                                                           F.J.; Herna
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JC6040

fimbrin protein agfB precursor - Salmonella enteritidis

C;Species: Salmonella enteritidis

C;Species: Salmonella enteritidis

C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999

C;Accession: JC6040

C;Accession: JC6040

R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.

J. Bacteriol. 178, 662-667, 1996

J. Bacteriol. 178, 662-667, 1996
                                                                                                                                                      В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Function:
A;Description: minor component of thin aggregative
A;Note: fimbriae bind to fibronectin, plasminogen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: agfB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43598.1; A;Experimental source: strain 276755-3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-151 <C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Salmonella enteritidis agfBAC operon encoding thin, A;Reference number: JC6039; MUID:96146512; PMID:8550497 A;Accession: JC6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
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A; Residues: 1-151 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleation component of curlin monomers [imported] - Salmonella enterica subsp. c;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AH0635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Atthors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K. A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero: A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AH0635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 413,
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                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                     22-151/Product:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-21/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Keywords: fimbria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S.; Moule,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                  107 NAKNSDITVGQYGGNNAALVNYDQLVTRVVTHEMAH 142
       108 AYGNSAAIIQKGSGNKANITQYGTQKTAVVVQKQSH 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49
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                                                                                                                                                                                                                                                                                                 29;
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                                                                                                                                       IGQVGTDNSA-RVRQEGSKLLSVISQEGGNNRAKVDQAGNYNFAYIEQTGNANDASISQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IYQYGSANAALALQSDARKSETTITQSGYGNGADYGQGADNSTIELTQNGFRNNATIDQW 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGQVGTDNSA-RVRQEGSKLLSVISQEGENNRAKVDQAGNYNFAYIEQTGNANDASISQS 107
                                                                                                                                                                                                                                                                                                                                                                                                                   signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                       12.9%;
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; Pred. No. 0.15;
17; Mismatches
                                                                                                                                                                                                                                                                                   Score 100.5; D
Pred. No. 0.18;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIDN:CAD08267.1; PID:g16502314; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aggregative fimbriae
plasminogen, tissue plasminogen
                                                                                                                                                                                                                                                                                                                                                        DB 2;
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                                                                                                                                                                                                                                                                                      49;
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                                                                                                                                                                                                                                                                                                                                                     Length 151;
                                                                                                                                                                                                                                                                                   Indels
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RyMevel.Ninio, M.; Terracoi, K.; Remun, ...
RyMevel.Ninio, M.; Terracoi, K.; Remun, ...
EMBO J. 10, 2259-2266, 1991
A,Title: The ovo gene of Drosophila encodes a zinc finger protein required for female
A,Title: The ovo gene of Drosophila encodes a zinc finger protein required for female
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
S16356
                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-1213 < MEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ovo protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
C;Accession: S16356
                                                                                                                                                                                                                                                                                                 A;Gene: FlyBase:ovo
                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X59772
                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
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C;Species: Drosophila melanogaster
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
A56038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-1028 <GAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Multiple products from the shavenbaby-ovo gene A;Reference number: A56038; MUID:95021209; PMID:7935398 A;Accession: A56038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: FlyBase:FBgn0003028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Garfinkel, M.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: A56038
                                                                                                                                                                       Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                         Cross-references: FlyBase:FBgn0003028
Introns: 931/3; 1152/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 ARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 12.6%;
Similarity 24.5%;
                                     ARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDI-----
                                                                                                                  LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD 62
                                                                                        LONAAAAYIMSAGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TVGQ------YGGNNAAL------VNYDQ-----LVTRVVTHEMAHA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GGNGYINCGGVG-GPNNS---LDGNNLLNFASVSNYNESNSKFHNHHHHHOH 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQNAAAAAYIMSAGSG-----GGGCTGNGGGGASGPGGGPSANSGGGGGGG-----
                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .; Wang, J.; Liang, 1
14, 6809-6818, 1994
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-GGNGYINCGGVG-GPNNS---LDGNNLLNFASVSNYNESNSKFHNHHHHHQH
                                                                                                                                                                                           12.6%;
                                                                                                                                                                       15;
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                                                                                                                                                                   Score 98.5; DB
Pred. No. 2.8;
15; Mismatches
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Pred. No. 2
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                                                                                 GGGCTGNGGGGASGPGGGPSANSGGGGGGG-----
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R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldra, E.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                  hypothetical protein AGR_L_228 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002 C;Accession: H98144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: AD3143
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, erage, G.; Gillet, W.; Grant, C.; Guenthner, F.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung,
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A; Residues: 1-145 < KUR>
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Best Local S
Matches 38
                                                                                                                                                        Residues: 1-145 < KUR>
                                                                                                                                                                                               Status: preliminary
                                                                                                                                                                                                               Accession: H98144
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                                         Query Match
                                                                                                  Gene:
                                                                                                                                       Cross-references:
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th 12.3%; Score 96; DB Similarity 27.1%; Pred. No. 0.4 38; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          μ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVGHQYGRHNLS-AVGQEGHDNYGSTTQNGNRNVAGIGQFGSNHTTILTQDGNGNIAAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATID 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIRKSFIASALVALVGLSAAAPAMANDVRIEQYGWSNSAGGAQEGYGNRIRTYQNGGYNR
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                                                                                linear
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                                                                                                                                     GB:AE007870; PIDN:AAK88682.1;
                                                                                chromosome
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27.1%;
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Pred. No. 0.41;
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                    DB 2;
0.41;
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                                                                                                                                   PID:g15158413;
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    59;
                                    Length 145;
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  20;
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                                                                                                                                     GSPDB:GN00170
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probable PPB
C;Species: My
C;Date: 17-Ju
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C;Accession: A70762

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: A70762
                                                                                           Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague A;Title: Genome sequence, MUID:21470413; PMID:11586360
                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1238 <KUR>
                                                                                                                                                                                R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barr
                                                                                                                                                                                                                                 C; Accession: AHC R; Parkhill, J.;
                                                                                                                                                                                                                                                                           probable exported protein YPO0309 [imported] - Yersinia pestis (strain CO92 C;Species: Yersinia pestis C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
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A; Cross-references:
                                                                                      A; Accession: AH0038
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;Species: Mycobacterium tuberculosis
;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003
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39; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGYGNGADVGQGADNS-----TIELTQNGFRNNATIDQ--WNAKNSDITVGQYGGNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ--SDARKSETTITQ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q-VGRGCSANVSQGGNDNVA 138
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  GB:AL590842;
  PIDN:CAC89171.1;
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PID:g15978410;
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  GSPDB:GN00175
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; Holroyd, S
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409 SĀFSĀĪTATĞHLTĀEWĞQĞAMLQTHSSLĞDATTLIHENDITAMSSGISLINEANQG 464 42 DSTLSIYOYGSANAALALQSDARKSETTITQSGYGN 77	409 SAFSAİTATĞHLTAEWĞQĞAMLQTHSSLĞDATTLIHFNDITAMSSĞISLINEANQG 46 42 DSTLSIYQYGSANAA
Query Match 12.0%; Score 93.5; DB 2; Length 1238; Best Local Similarity 25.1%; Pred. No. 7.3; Matches 45; Conservative 19; Mismatches 48; Indels 67; Gaps 9; 7 AAFAAIVVSGSALAGVVPQWGGGGNHANGGGNSG	Query Match Best Local Similarity Matches 45; Conser 7 AAFAAIVVS(

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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Perfect score:
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Result No.

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ALIGNMENTS

STANDARD; PRT; 151 AA. (Rel. 34, Created) (Rel. 42, Last sequence update) (Rel. 42, Last annotation update)		RN [2] RP SEQUENCE RC SPECIES=S RX MEDLINE=2: RA MCClellann RA Courtney RA Leonard S RA Ryan E., (2) RA Waterston RT "Complete RT "Complete RT LT2."; RL Nature 41: RN [3] RP SEQUENCE RP SEQUENCE RP SEQUENCE RA Parkhill : RA Parkhill : RA Churcher (4)		RESULT 1 CSGA_SALTY ID CSGA_SALTY AC P55225; DT 01-OCT-1990 DT 01-OCT-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Doran J.L., Collinson S.K., Burian J., Sarlos G., Munro C.K., Kay C.M., Banner P.A., Peterkin P.I., "DNA-based diagnostic tests for Salmonella speciet the structural gene for thin, aggregative fimbriae J., Clin. Microbiol. 31:2263-2273(1993).
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Collinson S.K., Clouthier S.
"Salmonella enteritidis agff
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MEDLINE=94013373; PubM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriol. 173:4773-4781 (1991).
- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY ASTEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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1, aggregative fimbriae
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SEQUENCE FROM N.A.
STRAIN=K12 / MC1655;
STRAINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMett G. III, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Pavis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enteritidis.";

J. Bacteriol. 173:4773-4781(1991).

-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND T FIBRONECTIN.
                                                                                                                      MEDLINE=91310586; PubMed=1677357;
Collinson S.K., Emoedy L., Trust T.J.,
"Purification and characterization of
                                                                                                                                                                                                                                Arnqvist A., Olsen A., Pfeifer J., "The Cr1 protein activates cryptic fibronectin binding in Escherichia Mol. Microbiol. 6:2443-2452(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Kashimoto K.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                   STRAIN=K12 / YMEL;
MEDLINE=93023873; PubMed=1357528;
                                                                                                                                                                                                                                                                                                                                                                                                                             "A 718-kb DNA sequence of the I corresponding to the 12.7-28.0
                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 21-40.
STRAIN=K12 / YMEL;
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Escherichia coli.
Mol. Microbiol. 7
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Olsen A., Arnqvist
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RpoS sigma factor relieves H-NS-mediated transcriptional
Rssion of csgA, the subunit gene of fibronectin-binding c
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EcoGene; EGG11489; cegA.
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28-FEB-2003
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Appl. Environ. Microbiol. 67:2367-2370(2001).
[2]
SEQUENCE FROM N.A.
STRAIN=0157:H7 / EDL933 / ATCC 700927;
STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharzaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-0157:H7 / ATCC 43895;
MEDLINE-21218556; PubMed=11319125;
MEDLINE-21218556; PubMed=11319125;
Uhlich G.A., Keen J.E., Elder R.O.;
"Mutations in the cegD promoter associated with variations expression in certain strains of Escherichia coli 0157:H7."
Appl. Environ. Microbiol. 67:2367-2370(2001).
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CSGA OR Z1676 OR ECS1420.
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ONA Res. 8:11-22(2001).

-I-FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURCULED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GREEN FROM TO TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
MEDLINE=21534947; PubMed=11677608; Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wai Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
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SEQUENCE FROM N.A.
STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
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an email to license@isb-sib.ch).
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           SPECIES=S.typhimurium; STRAIN=SR-11;
MEDLINE=98117058; PubMed=9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
Rourli fibers are highly conserved between Salmonella typhimurium a:
Escherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEF17
CSGB OR AGFB OR STM1143.
                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                     Salmonella typhimurium, Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                  CSGB
                                                                                                       SEQUENCE FROM N.A.
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-i- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.

-COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AVIEWPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONE.
                                                                                                                                                       Enterobacteriaceae; Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.,
"Comparative genomics of Salmonella enterica serovar Typhi st.
and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL627269; CAD08267.1; -. EMBL; AE016840; AAO69400.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=Ty2 / ATCC 700931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of a multiple drug enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Krogh A., Larsen T.S., Leat Quail M.A., Rutherford K., Whitehead S., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    imbria; Signal; Complete proteome
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SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                  SALTY
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                                                                                                                                                                                                                                                                                                                                                                                                                         NAKNSDITVGQYGGNNAALVNYDQLVTRVVTHEMAH 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQW 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
180:722-731(1998).
                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16254 MW;
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30.2%;
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Leather S., Moule S., O'Gaora
K., Simmonds M., Skelton J.,
                                                                                                                                                                                                    and
                                                                                                                                                                   Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.077; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 101.5;
Pred. No. 0.
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MINOR CURLIN SUBUNIT
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                                                                                                                                                                    Enterobacteriales;
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DT 10-0C
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Matches 29
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Fimbria; Signal; Complete proteome
Porter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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SEQUENCE FROM N.A.
SPECIES=S.typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720;
SPECIES=3.typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=S.enteritidis; STRAIN=27655-3B;
MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A.,
"Salmonella enteritidis agfBAC operon encoding thin, aggr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., La
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S.
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mul
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan
Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eimbriae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriol. 178:662-667(1996).
FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.
COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERRNTIALLY AFTEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONE
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AE008749; AAL20073.1; -.
U43280; AAC43598.1; -.
                                                                                                                                                                                                                                                                                                                                                    49
                                                                                                                                                                                                                                                                                                                                                                                   47
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                 NAKNSDITVGQYGGNNAALVNYDQLVTRVVTHEMAH
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151 AA;
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Pred. No. 0.08
17; Mismatches
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MINOR CURLIN SUBUNIT.
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COMPONENT OF
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J DROWNE J OVO DROME
J DROME
J P51521; Q9XZU4;
T 01-CCT-1996 (Rel. 34, Created)
JT 01-CCT-1996 (Rel. 34, Last sequence update)
JT 01-CCT-2003 (Rel. 42, Last annotation update)
I 0-CCT-2003 (Rel. 42, Last annotation update)

Neoptera; Endopterygota; Diptera; Brachycera; Ephydroidea; Drosophilidae; Drosophila. NCBI_TaxID=7227;

Arthropoda; Hexapoda;

Muscomorpha;

Drosophila melanogaster Eukaryota; Metazoa; Arth

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95021209; PubMed=7935398; Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.; Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.; "Multiple products from the shavenbaby-ovo gene reg melanogaster: relationship to genetic complexity."; mol. Cell. Biol. 14:6809-6818(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PFUUUYS; "..."
SMART; SMO0355; ZnF_C2H2; 4.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
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STRAIN=Oregon-R;
MEDLINE=91993102; PubMed=1712294;
Meyel-Winio M.T.M., Terracol R., 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007087; Znf_C
Pfam; PF00096; zf-C2H2; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U11383; AAB60216.1;
EMBL; X59772; CAB36921.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for female germ line development.";
EMBO J. 10:2259-2266(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TUNCTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF FEMALLINE CELLS: PLAYS A ROLE IN GERM LINE SEX DETERMINATION.
SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
DEVELOPMENTAL STAGE: PIRST APPEARS IN THE GERMARIUM AND ACCUMULATES IN NURSE CELLS DURING COGENESIS. STORED IN THE BUT IS RAPIDLY LOST IN THE EMBRYOS EXCEPT FOR ITS CONTINUED PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS.
SIMILARITY: Contains 4 C2H2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A56038; A56038.
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 regulation
 C2H2.
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POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-ALA.
POLY-GLN.
POLY-GLN.
C2H2-TYPE 1.
C2H2-TYPE 3.
C2H2-TYPE 3.
                                                                                                                                                                                                                                                                                                                              POLY-ALA.
POLY-GLY.
POLY-GLY.
POLY-GLY.
POLY-HIS.
POLY-ASIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat; Nuclear protein;
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            CHAIN
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                                                                                                                                    modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OMPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          006653;
30-MAY-2000
                                        TIGRFAMs; TIGR01414; autotrans_barl; Antigen; S-layer; Cell wall.
                                                                                                           EMBL; AB003681; BAA20138.1; -
                                                                                                                                                                             the European Bioinformatics Institute. These by non-profit institutions as long
                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
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                                                                                                                                                                                                                                                                                                      similarity).
-!- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Alpl
Rickettsiaceae; Rickettsieae;
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                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                  "Sequencing of the gene encoding the protein rOmp
                                                                                                                                                                                                                                                                                                                                                                                                                 Uchiyama T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=YH
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                      japonica."
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SUBCELLULAR LOCATION: Cell wall. This bacterium is layer with hexagonal symmetry.
                                                                                                                                                                                                                                                                                                                                FUNCTION: THE 120 kDa SURFACE-EXPOSED PRO STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE VIRULENCE FACTOR AND/OR IMMUNOGEN DURING
                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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                                                                  Pro; IPR006315; Autotransport.
Pro; IPR005546; Autotransporter.
Pr03797; Autotransporter; 1.
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(Cell surface antigen 5) (Sca5) (rOmpB)
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5; Mismatches
120 kDa SURFACE-EXPOSED
32 kDa BETA PEPTIDE.
POLY-GLY.
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ING INFECTION (By
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-9225987; PubMed-9634230; Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
   EMBL; AE007026; AAK45866.1; PIR; A70762; A70762. TIGR; MT1599; -.
                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                    Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
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Q10778;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 184:5479-5490(2002).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
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MEDLINE=22206494; PubMed=12218036;
                                                                                     EMBL; Z74020; CAA98335.1;
                                                                                                                                                or send an
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15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv1548c/MT1599,
RV1548C OR MT1599 OR MTCY48.17.
Mycobacterium tuberculosis.
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                                                                                                                                          email to license@isb-sib.ch)
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Pred. No. 2.6;
19; Mismatches
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2.6;
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RESULT
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                     at human
Mol. Cell
-!- FUNCT
                                                                                                                           MEDIJINE-20556282; PubMed=10900427,
Chi N.-W., Lodish H.F.;
"Tankyrase is a Golgi-associated mitogen-activated substrate that interacts with IRAP in GLUT4 vesicle substrate that interacts with IRAP in GLUT4 vesicle T Riol. Chem. 275:38437-38444(2000).
                                                               MEDLINE=21602874; PubMed=11739745;
Cook B.D., Dynek J.N., Chang W., Shostak
"Role for the related poly(ADP-Ribose) po
                                                                                                                                                                                                                                                                                   Smith S., de Lange T.;
"Cell cycle dependent localization
to nuclear pre complexes and cent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tankyrase 1 (EC 2.4.2.30) (TANKI) (Tankyrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _HUMAN
                                                                                                                                                                                                                                                                                                                                                                                       Smith S., Giriat I., Schmitt A., de Lange "Tankyrase, a poly(ADP-ribose) polymerase Science 282:1484-1487(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                          FUNCTION,
                                                                                                                                                                                                                                                                                                                                          MEDLINE=99454782;
                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION
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095271; 095272;
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InterPro; IPR002989; Mycobac Pentapep.
Pfam; PF01469; Pentapeptide 2; 11.
Pfam; PF00823; PPE; 1.
Hypothetical protein; Transmembrane; Complete TRANSMEM 14 34 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99040105; PubMed=9822378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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FUNCTION: May regulate vesicle trafficking and modulate subcellular distribution of SLC2A4/GLUT4-vesicles. Has I
                                   uman telomeres.";
Cell. Biol. 22:332-342(2002).
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                                                                                                                                                                                                                                          AND PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AALVNYDQLVTRVVTHEM----AHANNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 678 AA;
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258
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                                                                                                                    MUTAGENESIS OF HIS-1184 AND
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258
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Pred. No. 1.5;
24; Mismatches
                                                                                                                                                                                                                                                                                     action of the telomeric centrosomes.";
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tankyrase
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ALD PRESENTATION OF THE PR

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Nuclear protein; Repeat; ANK repeat; ADP Phosphorylation; Alternative splicing. REPEAT 248 280 ANK 2. REPEAT 248 280 ANK 3. REPEAT 368 400 ANK 5. REPEAT 401 433 ANK 5. REPEAT 521 556 ANK 7. REPEAT 521 556 ANK 7. REPEAT 521 556 ANK 9. REPEAT 683 715 ANK 10. REPEAT 746 748 ANK 11. REPEAT 716 868 ANK 11. REPEAT 836 868 ANK 11. REPEAT 836 868 ANK 11. REPEAT 846 868 ANK 11. REPEAT 859 901 ANK 11. REPEAT 859 901 ANK 12. REPEAT 859 901 ANK 13. REPEAT 859 901 ANK 15.
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SMART; SM00248; ANK; 17.
SMART; SM00454; SAM; 1
PROSITE; PS50088; ANK_REPEAT; 15.
PROSITE; PS50297; ANK_REPEAT; 15.
PROSITE; PS50105; SAM_DOMAIN; 1.
Transferase; GlycosylTransferase; NAD; Golgi stack; Telomere;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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EMBL; AF082557; AAC79842.1; -.
EMBL; AF082558; AAC79843.1; -.
EMBL; AF082559; AAC79844.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00023; ank; 19.
Pfam; PF00536; SAM; 1.
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InterPro; IPR001660; SAM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO:000781; C:chromosome, telomeric region; IDA. GO:0003950; F:NAD ADP-ribosyltransferase activity; GO:0005515; F:protein binding; IPI. GO:0007004; P:telomerase-dependent telomere mainten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regulation of telomere length.

CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl} (N)-acceptor = nicotinamide + {ADP-D-ribosyl} (N+1)-acceptor.

SUBUNIT: Oligomerizes and associates with TNKS2. Interacts with the cytoplasmic domain of LNPEP/Otase in SLC2A4/GLUT4-vesicles. Binds to the N-terminus of telomeric TRF1 via the ANK repeats. SUBCELULAR LOCATION: Cytoplasmic, associated with the Golgi and with juxtanuclear SLC2A4/GLUT4-vesicles. A minor proportion is also found at nuclear pore complexes and around the pericentriolar matrix of mitotic centromeres. During interphase, a small fraction of TNKS is found in the nucleus, associated with TRF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the PARP family.
SIMILARITY: Contains 15 ANK repeats.
SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: Ubiquitous; highest levels in testis. PTM: Upon insulin-stimulation, phosphorylated on serine r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS: Event=Alternative eplicing; Named isoforms=2;
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tote=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                               ADP-ribosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
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RESULT 10
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01-CTT-1996 (Rel. 34, Last sequence upda
28-FEB-2003 (Rel. 41, Last annotation up
Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
Escherichia coli, and
Escherichia coli 0157:H7.
Bacteria, Proteobacteria; Gammaproteobac
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM .... STRAIN-KL2 / MC4100; STRAIN-KL2 / MC4100; MCDLINE-96414468; PubMed-8817489; MEDLINE-96414468; PubMed-8817489; Hammar M., Arnqvist A., Bian Z., Olsen A., Normark S.; Hammar M., Arnqvist A., Bian Z., olsen A., Normark S.; "Expression of two csg operons is required for production "Expression of two csg operons is required for production of two csg operons is required for production "Expression of two csg operons is required for production "Expression of two csg operons is required for production "Expression of two csg operons is required for production "Expression of two csg operons is required for production "Expression of two csg operons is required for production "Expression of two csg operons is required for production "Expression of two csg operons is required for production "Expression of two csg operons is required for production "Expression of two csg operons is required for production "Expression of two csg operons is required for production "Expression of two csg operons is required for production "Expression of two csg operons" is required for production "Expression of two csg operons" is required for production "Expression of two csg operons" is required for production "Expression of two csg operons" is required for production "Expression of two csg operons" is required for production "Expression of two csg operons" is required for production "Expression of two csg operons" is required for production "Expression of two csg operons" is required for two csg operons of two csg operons of two csg operons of two csg operons of two csg operons of two csg operons of two csg operons of two csg operons of two csg operons of two csg operons of two csg operons of two csg operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons operons o
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Mau B., Sha
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Oshima T., Aiba H., Baba T., Pujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto I Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T., Yano M., Horiuchi T., Rajihaka M., Takemoto K., Wada C., Yano M., Horiuchi T.,
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Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., R
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/FTId=VSP 004538.
Missing (In isoform 2).
/FTId=VSP 004539.
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POLY-SER.
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E->A: LOSS OF ACTIVITY;
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Best Local
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                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                SIGNAL
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"Sigma S-dependent growth-phase induction of the c
Escherichia coli can be achieved in vivo by sigma
of the nucleoid-associated protein H-NS.";
Nol. Microbiol. 13:1021-1032(1994).
                                                                                                                                                                                                                                                                                                                                            EMBL; X90754; CAA62281.1;
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[6]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95157246; PubMed=7854117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed-11258796;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=0157:H7 / EDL933 / ATCC 700
MEDLINE=21074935; PubMed=11206551;
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L; D90741; BAA35831.1; -...
L; AE005315; AAC55787.1; -...
L; AE00554; BAB34842.1; -...
; C90806; C90806.
; G85665; G85665.
; S90787; S70787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONE CURLIN MONOMERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a cen the Swiss Institute of Bioinformatics and the EMBL
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SETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIEQNNAKNSDITV
                                        FAVNELSKSSFNQAAII----GQAGTNNSAQLRQGGSKLLAVVAQEGSSNRA-KIDQTGDY
                                                                      FAAIVVSGSAL--AGVVPQWGGGGNHNGGGNSSGPDSTLSIY-QYGSANAALALQSDARK
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Q03646;
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Merozoite surface a
MEDLINE=91156685; PubMed=2000383; Smythe J.A., Coppel R.L., Day K.P., Kemp D.J., Anders R.F.;
                                                                                                          Eukaryota; Alveol
NCBI_TaxID=70150;
                                                                                                                               Plasmodium falciparum Eukaryota; Alveolata;
                                                                  SEQUENCE FROM N.A.
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MEDIINE-87283911; PubMed=3302276;

Riede I., Drexler K., Eschbach M.L., Henning U.;

"DNA sequence of genes 38 encoding a receptor-recognizing pro
bacteriophages T2, K3 and of K3 host range mutants.";

J. Mol. Biol. 194:31-99(1987)

-i- FUNCTION: V938 is at the tip of the long tail fibers and
the phage recognition site for the cellular receptor.

-i- MISCELLANEOUS: THIS PHAGE USE OUTER MEMBRANE PROTEINS OMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR007932; Tail_fibre_GP38. Pfam; PF05268; GP38; 1. Fiber protein; Phage recognition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, T4-like viruses.
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                  Oduola A.M.J.,
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                                                                                                 Hypothetical glycine-rich protein Rv2098c/MT2159/Mb2125c. RV2098C OR MT2159 OR MTCY49.38C OR MB2125C. Mycobacterium tuberculosis, and Mycobacterium howir
SPECIES=M.tuberculosis; STRAIN=H37Rv; MEDLINE=98295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                     SEQUENCE FROM N.A.
                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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SUBCELLULAR LOCATION:
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FUNCTION: May play a role in the merozoite a
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ia; Membrane; Glycoprotein; Antigen;
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MEDLINB=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Kolonay J.F., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.",
                                                                                                                                                                                                                                                                                                                                         EMBL; 273966; CAA98228.1; ALT_FRAME. EMBL; AE007065; AAK46440.1; -. EMBL; EX248341; CAD96978.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
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MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Garnier T., Eiglmeier K., Camus J.-C., Monsempe C., Simon
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature
[2]
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                                                                                                                                                                                                                                                    Pfam; PF00934; PE; 1.
ProDom; PD001223; PE_region; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
-i- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY.
                                                                                                                                                                                                                        Hypothetical protein; CONFLICT 312 31
                                                                                                                                                                                                                                                                        Interpro; IPR000084; P
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SUBFAMILY.

CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 59. Ref.1 sequence has been checked authors in Ref.1 and they report that no errors have been
 265
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                                 75
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                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             an email to license@isb-sib.
YGNGGAAGSGGNGGDAGTGVSSDGF---AGLGGSGGRGGDAGLIGVGGGGGN
                                 YGNGADVGQGAD--NSTIELTQNGFRNNATIDQWNAKNSD---ITVGQYGGN
                                                                   AGLIGHGGAGGNGGDGGHGGSGKAGGSGGSGGFGQFGGAGGLL
                                                                                                 AGVVPQWGGGGN----
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PRINTS; PR00182; ECOLNEIPORIN.
PROSITE; PS00576; GRAM_NEG_PORIN; 1.
Outer membrane; Porin; Transmembrane;
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MEDLINE=93116587; PubMed=1335540;
Zapata G.A., Vann W.F., Rubinstein Y., Frasch C
"Identification of variable region differences
meningitidis class 3 protein sequences among fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ward M.J., Lambden P.R., Heckels J.E.;
"Sequence analysis and relationships between meningococcal class 3 serotype proteins and other porins from pathogenic and non-pathogenic Neisseria species.";
PEMS Microbiol. Lett. 73:283-289(1992).
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P30688;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Major outer membrane protein P.IB precursor (Protein IB) (PIB)
(Porin) (Class 3 protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
Neisseriaceae; Neisseria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein. Outer SIMILARITY: Belongs to the Gram-negative porin family.
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KSDYLGVNKIAEPEARLISVRYDSPEFAGLSGSVQYALNDNAGKY
                                                                                                                                             NAALALQSDARKSETTITQSGYGN
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                                              KNSDITVGQYGGNNAAL--VNYDQLVTRVVTHEMAHANNATANQY
                                                                                            NGLKAIWQVEQKASIAGTDSGWGNRQSFIGLKGGFG--KLRVGRLNSVLKDTGDINPWDS
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Mol. Biol. Evol. 10:127-139(1993).

-i- FUNCTION: Essential for biological clock functions. Determines the period length of circadian and ultradian rhythms; an increase in PER dosage leads to shortened circadian rhythms and a decrease leads to lengthened circadian rhythms. Essential for the circadian rhythmicity of locomotor activity, eclosion behavior, and for the rhythmic component of the male courtship song that originates in the thoracic nervous system. The biological cycle depends on the rhythmic formation and nuclear localization of the TIM. PER complex. Light induces the degradation of TIM, which promotes elimination of PER. Nuclear activity of the heterodimer coordinatively regulates PER and TIM transcription through a negative feedback loop. Behaves as a negative element in circadian transcriptional loop. Does not appear to bind DNA, suggesting indirect transcriptional inhibition (By similarity).

-i- SUBUNIT: Forms heterodimer with timeless (TIM); the complex then translocates into the nucleus (By similarity).

-i- SUBCILLIAR LOCATION: Nuclear at specific periods of the day. First accumulates in the perinuclear region about one hour before translocation into the nucleus. Interaction with Tim is required for nuclear localization (By similarity).

-i- FIMIS THE STABILITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER PER-TIM (BY SIMILARITY).

-i- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.

-i- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
        EMBL; U51055; 
EMBL; U51056; 
EMBL; U51057; 
EMBL; U51058; 
EMBL; U51059; 
EMBL; U51061; 
EMBL; U51061; 
EMBL; U51061; 
EMBL; U51062; 
EMBL; U51062; 
                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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Q03297; O18421; O18422; P91721; P91722;
01-OCT-1993 (Rel. 27, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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MEDLINE=93196482; PubMed=8450754;
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O7x243 citrobacter
O7x240 citrobacter
O7x240 citrobacter
O8cw63 escherichia
O7x237 enterobacte
O54069 salmonella
O983j5 escherichia
O99106 ralatonia s
O8x646 ralatonia s
O7xdr3 oryza sativ
O8eih4 shewanella
O94821 tetrahymena
O9xcj4 salmonella
O9xcj4 salmonella
O8xn57 saalmonella
O8xn57 campylobact
O92uu8 rhizobium m
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			Q9kkb4 rickettsia	Q840u5 rickettsia	Q8ev84 mycoplasma	Q9kka8 rickettsia		Q89ji4 bradyrhizob		Q8u6n9 agrobacteri	Q7x238 enterobacte	Q9kkb1 rickettsia	Q98ln6 rhizobium l	Q9x687 salmonella		Q89ji5 bradyrhizob	Q7uwz8 rhodopirell	Q8mpn4 drosophila			u.	Q7v8s5 prochloroco	Q7x244 citrobacter		Q7x241 citrobacter	Q8efu3 shewanella	Q8nivl neurospora	Q8eih3 shewanella

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Zogaj X., Bol
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                                                                                                                  SEQUENCE
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Enterobacteriaceae; Citrobacter;
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01-OCT-2003
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EMBL: AJ515700; CAD56672.1; -.
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Bacteria; Proteobacteria;
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RX MEDINNE-22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesc RA Rasko D., Burland V., Plunkett G. III, Redford P., Roesc RA Mayhew G.F., Rose D.J., Zhou S.-R., Boutin A., Hackett J., RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.; Perna N.T. RT "Extensive mosaic structure revealed by the complete genome C uropathogenic Escherichia coli.";

PTOC. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

REMBL; AE016759; AAN79779.1; -.
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   STRAIN=Fec39;
Zogaj X., Bok
                               SEQUENCE FROM N.A.
                                                            NCBI_TaxID=28141;
                                                                                            Bacteria; Proteobacteria;
                                                                              Enterobacteriaceae;
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Q9S3J5;
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                   Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cox J.M., Eglezos S., Woolcock J.B.; "Virulence of Salmonella enterities in chickens correlates colony morphology and expression of SEF17 fimbriae."; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Production of Cellulose and Curli Fimbriae Enterobacteriaceae Isolated from the Human G Infect Immun. 72:4151-4158(2003).
EMBL; AJ515702; CAD56678.1; -.
Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEF17 fimbrin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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                                                                                                                                                                                                                                                                                                              IELTQNGFRNNATIDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNGALVDQTASNSTVNVTQIGFGNHATAHQY
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76 AA;
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7704 MW;
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15112 MW; 5D8BB2D872DF15F3 CRC64;
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                   Gammaproteobacteria;
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Last annotation updat
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Q8Y106;
01-MAR-2002
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SEQUENCE
                                                                                                                                                                                                 Pfam; PF05594; Fil haemagg; 20.
Pfam; PF05860; Haemagg_act; 1.
PROSITE; PS01070; NUCLEASE_NON_SPEC; 1.
                                                                                                                                                                                                                                                                                                                     Chandler M., Choisne N., Claudel-Renard C., Cunnac S. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Siguier P., Thebault P., Whalen M., Wincker P., Levy Neissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solar Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21681879; PubMed=11823852;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation updat Probable hemagglutinin-related protein.
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01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
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MEDLINE=99314153; PubMed=10386375;

La Ragione R.M., Collighan R.J., Woodward M.J.;

"Non-curliation of Escherichia coli 078:K80 isolates associated

"Non-tilation of Escherichia coli 078:K80 isolates associated

"Si inserti on in csg8 and reduced persistence in poultry infect

FEMS Microbiol. Lett. 175:247-253(1999).

EMBL; AJ131756; CAB45380.1; -.

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[1]
                                                                                                                                                                                                                                                                    InterPro;
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GO:0004519; F:endonuclease activity;
GO:0003676; F:nucleic acid binding;
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                        KSVQVQARTGDITVSGSGISALSDVDLLAKQGKVDIVAGNDTSSRHED
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                                                                                                                                                                                                                              IPR001604; Endonuclease.
IPR008619; Fil haemagg.
IPR008638; Haemagg_act.
5594; Fil_haemagg; 20.
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121
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89.7%;
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Pred.
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Pred. No. 8.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative glycine-rich protein.
05JNBB0039P10.07G10.
07yza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Plasmid;
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InterPro; IPR008638; Haemagg act.
Pfam; PF05594; Fil haemagg; Zo.
Pfam; PF05860; Haemagg act; 1.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable hemagglutinin-related protein.
RSP0540 OR RS06117.
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Bacteria; Proteobacteria;
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PS01070; NUCLEASE_NON_SPEC;
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Pred. No. 8.4;
19; Mismatches
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Cattolico L.,
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Q8EIH4;
01-MAR-2003
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                                                                                                                                                      Hypothetical
SEQUENCE 5
                                                                                                                                                                                       Shewanella oneidensis.";
Nat. Biotechnol. 20:1118-1123(2002).
EMBL; AE015532; AAN53941.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Alteromonadaceae; Shewane
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01-MAR-2003 (TrEMBLrel.
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STRAIN=cv. Nipponbare;
STRAIN=cv. Nipponbare;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ
EMBL; AE017101; AAD54078.1; -.
101 AA. 17001 MW: 95A246FB11DE3A(
                                                                                                                                                                               TIGR; S00865;
                                                                                                                                                                                                                                                                                                                                                         STRAIN=MR-1;
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                                                                                                                                                                                                                            Genome sequence of the dissimilatory metal ion-reducing
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SEQUENCE FROM N.A.
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                                                                                                                Similarity
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QGDDNDITIKQKGDSNGAEFQVWGDSNDVDLKQRGDANFATFGAYGTDN-DFDLSSKGDN
                       DARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN
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                                                 GDNHTGFVYALAGSENDISMEQEGSNNTAYLSMTTGDDNTVDITQDGDSNTVGDSLIADI
                                                                             GGNHNG---
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Phromosome 10 Sequencing Consultry,
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502 AA; 52441 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Gammaproteobacteria; Alteromonadales;
                                                                                                   15;
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                                                                                                  Score 107; DB
Pred. No. 2.8;
L5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last
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Pred. No. 0.72;
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                                                                                                                                                   proteome.
D08CA23D6C46B62D CRC64;
                                                                       -GGN-----SSGPDSTLSIYQYGSANA---ALALQS
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databases.
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RESULT 13
Q9XCJ4
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ID 7
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Best Local S
Matches 35
Bacteria; Proteobacteria; G
Enterobacteriaceae; Salmone,
NCBI_TaxID=602;
                                                                                                                                               Q9XCJ4;
Q9XCJ4;
01-NOV-1999
01-NOV-1999
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoded by cnjB, a Tetrahymena gene active Nucleic Acids Res. 21:4610-4614(1993). EMBL; X06462; CAB37323.1; -. EMBL; L03710; AAC37171.1; -. PIR; S42136; S42136. HSSP; P05888; 1AAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00939; C2HCZNFINGER.
SMART; SM00343; ZnF C2HC; 7.
PROSITE; PS50158; ZF CCHC; 7.
CONFLICT 251 251 M
CONFLICT 256 256 I
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01-FEB-1997 (TEMBLIFE). 02, Created)
01-FEB-1997 (TEMBLIFE). 02, Last sequence update)
01-OCT-2003 (TrEMBLIFE). 25, Last annotation update
                                                                                                                                 ShdA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=94051569; PubMed=8233798;
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MEDLINE-88189811; PubMed=3357771;
Martindale D.W., Taylor F.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tetrahymena thermophila.
Eukaryota; Alveolata; Cili
Tetrahymenina; Tetrahymena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0003676; F:nucleic acid
InterPro; IPR001878; Znf CCHC.
Pfam; PF00098; zf-CCHC; 7.
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"Retroviral-type zinc fingers and glycine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Multiple introns in a conjugation-specific thermophila.";
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35; Conserv
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                                                                                                                                                                                                                                                                                                                                            QTGGGWGSNDN----
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(TrEMBLrel.
(TrEMBLrel.
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23,
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                                                                  Gammaproteobacteria;
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                                                                                                                                                 Created)
Last sequence Last anno
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H 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      binding;
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                                                                                                                                                   sequence up
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> N (IN REF. 1).
OB03F210104008A3 CRC64;
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ing meiosis
                                                                    Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1748;
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Best Loc
Matches
                            STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21.534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J.,
Courtney L., Porwollik S., Ali J., Dante N
Leonard S., Nguyen C., Scott K., Holmes A.
Ryan E., Sun H., Florea L., Miller W., Sto
                                                                                                                               Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                           Q8ZN57
Q8ZN57;
QRZN57;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar Cothe C-terminal region of AIDA, IcsA, sub
Peyer's patch colonization and shedding factor.
SHDA OR STM2513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-1999) to the EMBL/GenB
EMBL; AF140550; AADZ5110.2; -
InterPro; IPR0063115; Autotransport.
InterPro; IPR005346; Autotransporter.
InterPro; IPR0054899; Pertactin.
InterPro; IPR002173; PfkB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGR01414; autotrans_barl; 3. PROSITE; PS00584; PFKB_KINASES_2; 2. SEQUENCE 2035 AA; 207032 MW; 295DB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kingsley R.A., van Amsterdam K., "The presence of a pathogenicity enterica subspecies I correlates
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF03797; Autotransporter; 1. Pfam; PF03212; Pertactin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genus Salmonella
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STRAIN=ATCC14028;
                       Waterston
                                                                                                                           NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kingeley R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ATCC14028;
  "Complete genome sequence of Salmonella LT2.";
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                                                                                                                                                                                                                                                                                       14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AALYVSGVATVGWQPTTVTGTGLVIETSGGGADDPDGGKYVSNAISLDHYAILELTDAKI
                       R., Wilson R.K.;
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                                 ieth J., Clifton S.W.,
, Dante M., Du F., Hou
Holmes A., Grewal N.,
r W., Stoneking T., Nh
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            serovar Typhimurium
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                                                                    S.W.
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warm blood
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                                               Mulvaney
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S., Laymar
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01-JUN-2003 (
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SEQUENCE FROM N.A. STRAIN=23D;
                                                                                             SEQUENCE FROM
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Pfam; PF03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AEOC
InterPro;
                             Thummuru M.K., Blaser M.J.;
"Characterization of the Campylobacter fetus
that the sapA promoter is deleted in spontane
J. Bacteriol. 174:5916-5922(1992).
                                                                       MEDLINE=92394895; PubMed=1522068;
                                                                                                                   J. Biol.
                                                                                                                              structure
                                                                                                                                                 Blaser M.J.,
                                                                                                                                                           MEDLINE=91035477;
                                                                                                                                                                                  SEQUENCE
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structure.";
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espPro; IPR006315; Autotransporter
espPro; IPR005546; Autotransporter
espPro; IPR004899; Pertactin.
espPro; IPR004899; Pertactin.
espPro; IPR002173; PfkB.
espPo3797; Autotransporter; 1.
espRo3212; Pertactin; 1.
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                                                                                                                                                           PubMed=2229082;
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Campylobacter.
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KB_KINASES_2; 2.
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mutant strains.";
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Matches 44
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                                                                                                                                                                                                                                                                                                                                                             Blaser M.J.;
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99069317; PubMed=9851986; Thompson S.A., Shedd O.L., Ray K.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 "A lipopolysaccharide-binding domain of the Campylobacter layer protein resides within the conserved N terminus of a silent and divergent homologs.", J. Bacteriol. 177:1734-1741(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95204338; PubMed=7896695;
Dworkin J., Tummuru M.K., Blaser M.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Tummuru M.K., Blaser M.J.;
"Rearrangement of sapA homologs with conserved and variable regions
Campylobacter fetus.";
                                                                                                                                                                                                        InterPro;
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Pro; IPR005546; Autotransporter.
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GHSAKDANENSIQI SNGGNINNI VGGHAQDHINLNI IN
                   GNNAALVNYDQL-----VTRVV-THEMAHANNATAN
                                             SANENKVTITE-GTANVADIYGGKSISNNSI
                                                                  DARKSETTITQSGYGNGADV--GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG
                                                                                      QVASENLVIISGGTIN--VPTIGGGSATNATNNQVTISGGKVTSSTIYGGNAN-----K
                                                                                                            KVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNS---SGPDSTLSIYQYGSANAALALQS
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Pred. No. 13;
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Search completed: March 18:40:11

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SUMMARIES

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11.9	11.9	11.9	11.9	11.9	11.9	11.9	12.0	12.0	12.0	12.3	12.6	12.7	13.5	14.1	14.1	14.1	14.6	14.8	
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AAB27212	AAY44402	AAU79539	AAY44404	AAU79538	AAY44403	AAB36331	AAB36328	AAB36336	AAB36323	ABU21488	ABR82645	AAB36342	AAB36344	AAB36319	AAB36324	AAB36340	ABR82644	AAB36320	
Aab27212	Aay44402	Aau79539	Aay44404	Aau79538	Aay44403	Aab36331	Aab36328	Aab36336	Aab36323	Abu21488	Abr82645	Aab36342	Aab36344	Aab36319	Aab36324	Aab36340	Abr82644	Aab36320	
Human tan	Human tan	Truncated	Human tru	Truncated	Human tru	Escherich	Salmonell	Salmonell	Salmonell	Protein e	E. coli c	Salmonell	Escherich	Salmonell	Salmonell	Salmonell	E. coli c	Salmonell	

RESULT 1 AAB36347 ID AAB3 AAB36347 standard; protein; 151 ₿

ALIGNMENTS

26-FEB-2001 AAB36347; AgfA::PT3#2 amino acid sequence SEQ ID NO:14. (first entry)

vaccine; immune response; immunogen. Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;

Salmonella enteritidis. Escherichia coli. 12-OCT-2000 WO200060102-A2 Synthetic.

05-APR-1999; 05-APR-2000; 2000WO-CA000356 99US-0127888P

(UYVI-) UNIV VICTORIA.

Doran JL, Collison SK, Kay WW;

WPI; 2000-672631/65.

N-PSDB; AAC64623.

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 136; 139pp; English.

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CegA and AgfA-homologue fimbria mubunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species,

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RESULT 2
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Best Local
                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                              N-PSDB;
                                                                                                                                                                                          White AP,
                                                                                                                                                    WPI; 2000-672631/65.
                                                                                                                                                                                                                                                                              05-APR-1999;
                                                                                                                                                                                                                                                                                                                  05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                   (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                 12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                            WO200060102-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella; agfA; chromosomal gene replacement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB36352 standard; protein; 151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AgfA::PT3#7 amino acid sequence SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           copy of that gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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                                                                                                                              AAC64628.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKLLKVAAFFAAIVVSGSALAGVVPOWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                          Doran JL,
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nilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                              99US-0127888P
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                                                                                                                                                                                          Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 775; DB 3;
Pred. No. 5.4e-67;
Mismatches 0;
                                                                                                                                                                                        SK,
                                                                                                                                                                                      Kay ww
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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Disclosure; Page 138; 139pp; English

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RESULT 3
AAB36346
ID AAB3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF1/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, combination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene into the chromosome of the back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA grotein containing a replacement segment or segments of foreign amino CC enterobacteriaceae host cell, from the host cell and introducing the polymer into the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation conjunction with a carrier or diluent. (I) is conjuncted the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to immunogenicity and adhesion properties relevant for an efficient live capainst the inserted epitope, and hybrid fimbria are usually strong cimmunogens, which may be important for directing an immune response conjunction of the novement invention. The present sequence is given in the exemplification of the novement invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 144
                                  05-APR-1999;
                                                                       05-APR-2000;
                                                                                                                                                                                                     Salmonella enteritidis.
Escherichia coli.
(UYVI-) UNIV VICTORIA
                                                                                                                                               WO200060102-A2
                                                                                                                                                                                                                                                                 Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36346 standard; protein; 151
                                                                                                              12-OCT-2000
                                                                                                                                                                                                                                                           vaccine;
                                                                                                                                                                                                                                                                                                            AgfA::PT3#1 amino acid sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                  26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                         AAB36346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144;
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                                                                                                                                                                                                                                                           immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVTRVVTHEMAHANOTASDSSVMVRQVGFGNNATANOV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                         2000WO-CA000356.
                                                                                                                                                                                                                                                                                                                                                (first entry)
                                    99US-0127888P
                                                                                                                                                                                                                                                       response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.1%;
91.1%;
                                                                                                                                                                                                                                                       immunogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 714; DB 3;
Pred. No. 4.3e-61;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -SVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                               NO:12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --YDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cc segment of the gene has been replaced by a segment of a foreign DNA cc sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEP17/TAF) nucleation depended cc assembly system of strains of Salmonella, Escherichia coli and colored colo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 141;
                        Salmonella
                                                             Salmonella; AgfA; vaccine
                                                                                                                                             25-MAR-2003
26-JUN-1995
                                                                                                                                                                                                             AAR74625;
                                                                                                                                                                                                                                                AAR74625 standard; protein; 151
                                                                                                    AgfA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a recombinant agfA gene (I) where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              White AP,
                                                                                                                                                                                                                                                                                                                                                                                                    118
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 135; 139pp; English.
                                                                                                                                             (first en
                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 696; DB 3;
Pred. No. 2.4e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
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RESULT 5
AAB36341
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AC AAB3
AC AAB3
AC Salm
XX Salm
XX Salm
XX Salm
XX Salm
XX Salm
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Matches
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  WPI; 2000-672631/65
                                                       White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella; agfA; chromosomal gene replacement; vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                     05-APR-1999;
                                                                                                                                                                                                                          05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                   WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                          Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB36341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36341 standard; protein; 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
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N-PSDB; AAQ87467.
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                                                                                                              (UYVI-) UNIV VICTORIA.
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3; Mismatches 11
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 136; 139pp; English.

WPI; 2000-672631/65. N-PSDB; AAC64623.

White AP,

Doran JL,

Collison SK,

Kay WW;

27 115 14.8 22 3 AAB33320 28 113 14.6 24 7 ABR82644 29 109 14.1 23 3 AAB36324 30 109 14.1 23 3 AAB36324 31 10.9 14.1 23 3 AAB36324 32 104.5 13.5 15.1 3 AAB36324 33 98.5 12.7 15.1 3 AAB36324 34 98 12.6 26 7 ABR82645 35 95 12.3 18.6 6 ABU21488 36 93 12.0 19 3 AAB36323 37 93 12.0 19 3 AAB36323 38 93 12.0 19 3 AAB36323 39 92 11.9 673 3 AAB4403 40 92 11.9 673 3 AAY44404 41 92 11.9 673 5 AAU79539 42 92 11.9 1327 3 AAY44402 45 92 11.9 1327 3 AAY44402 45 92 11.9 1327 3 AAY44402	115 14.8 22 3 11.9 14.1 23 3 1004.5 112.7 151 3 98.5 12.7 151 3 98.5 12.0 19 3 13.2 11.9 13.2 7 3																				
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3 AAB36320 3 AAB36324 3 AAB36324 3 AAB36324 3 AAB36319 3 AAB36319 3 AAB36342 4 AAB36342 7 ABB21488 6 ABB36326 6 AAB36326 6 AAB36326 7 AAB36326 8 AAB36328 8 AAB3		1327	1327	949	949	673	673	23	19	19	19	186	26	151	151	23	23	23	24	22	t
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ALIGNMENTS

RESULT 1 AAB363 AXX AAB33 XXX AAB33 XXX AAB33 XXX AAG6 AYX AAG6 AYX AAG6 AYX Salm OS SSyntn XXX W0200 XX W02 Salmonella; agfA; chromosc vaccine; immune response; Synthetic. Salmonella enteritidis. AAB36347 standard; protein; 05-APR-1999; 05-APR-2000; 2000WO-CA000356 12-OCT-2000. WO200060102-A2 Escherichia AgfA::PT3#2 amino acid sequence SEQ ID NO:14. 26-FEB-2001 (UYVI-) UNIV VICTORIA COL1. (first entry) 99US-0127888P chromosomal gene replacement; fimbrin; epitope; immunogen. 151 AA

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RESULT 8
AAB36353
ID AAB3
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AC AAB3
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DT 26-F
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DE AgfA
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XW Salm
KW vacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 151 AA;
                     Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                          AgfA::PT3#8 amino acid sequence SEQ ID NO:26.
                                                                                                        26-FEB-2001
                                                                                                                                                                                      AAB36353 standard; protein; 151 AA.
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immune response; immunogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 659; DB 3; Pred. No. 9.1e-56;
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                                                                                                                                                                                                                                                                                                                            CC directing recombination of a recombinant gene
CC back into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
CC back into the chromosome of the homologous species, replacing the native
CC copy of that gene; and (4) eliciting an immune response in an animal,
CC comprising separating an amino acid polymer comprising a recombinant AgfA
CC protein containing a replacement segment or segments of foreign amino
CC acid sequence or sequences grown on a Salmonella, E. coli or
CC Enterobacteriaceae host cell, from the host cell and introducing the
CC useful for the expression of recombinant AgfA protein which is useful for
CC eliciting an immune response in an animal. In a fimbrial presentation
CC system the heterologous antigens are presented in high numbers (up to
CC 500,000 copies/cell), the hybrid fimbrin protein possesses both the
CC immunogenicity and adhesion properties relevant for an efficient live
CC vaccine, the carrier fimbrial subunit proteins are usually strong
CC immunogens, which may be important for directing an immune response
CC against the inserted epitope, and hybrid fimbriae are easy and
CC inexpensive to purify in large amount. The present sequence is given in
CC the exemplification of the present invention
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Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence which encodes a foreign epitope or antigen. Also described are:
(1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                            Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-1999;
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121
                                        121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGHHNGGGNSSGPDSTLSIYQYGSANAALALQ
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NNAALVNOTASDSSVMVROVGFGNNATANOY
                                                                                                        SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                              MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Doran JL,
                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                79.0%;
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                                                                                                                                                                                                                                                              Score 612;
Pred. No. 3.
                                                                             VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SK,
                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kay WW;
                                                                                                                                                                                                                                                                DB 3;
                                                                                                                                                                                                                                                                                 Length 151
                                                                                                                                                                                                                                               Indels
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CC back into the chromosome of the homologous species, replacing the native C copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC Enterobacteriaceae host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a carrier or diluent. (1) is CC useful for the expression of recombinant AgfA protein which is useful for CC useful for the expression of recombinant AgfA protein which is useful for CC system the heterologous antigens are presented in high numbers (up to CC 500,000 copies/cell), the hybrid fimbrin protein possesses both the CC immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong CC immunogens, which may be important for directing an immune response CC against the inserted epitope, and hybrid fimbriae are easy and CC inexpensive to purify in large amount. The present sequence is given in the communitation of the averaging fine and the protein contains the contains and the contains and the contains and the contains the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contai
                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SER17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-2000; 2000WO-CA000356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AgfA::PT3#4 amino acid sequence SEQ ID NO:18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine; immune response; immunogen
                                                                                                                                                        exemplification of the present invention
                                  Similarity
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                             78.8%;
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Score 611; DB
Pred. No. 4e-5
6; Mismatches
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                          ; DB 3;
4e-51;
     22; Indels
                                                Length 151;
  ٥,
     Gaps
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MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60

MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ

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RESULT 10
AgfA, (sgA and AgfA-homologue finbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the chomologous species; (3) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant AgfA (2) comprising separating an amino acid polymer comprising a recombinant AgfA (3) crottein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence host cell, from the host cell and introducing the Expolymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for gystem the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid finbrin protein possessee both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid sequence SEQ ID NO:20.
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RESULT 11
AAB36354
ID AAB36
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, (EgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing recombination of a replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or
                                                                                                                                                                                                                                                          Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                  Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                    White AP, Doran JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 AA;
                                                                                                                                                                                                                               Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
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81.5%;
                                                                                                                                                                                                                                                                                                                                                                       Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunogen.
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Pred. No. 6.3e-51
                                                                                                                                                                                                                                                                                                                                                                      SK,
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RESULT 12
AAB36351
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence in given in the present sequence is given in the present sequence is given in the present sequence in given in the present sequence is given in the present sequence is given in the present sequence in given in the present sequence is given in the present sequence in given in the present sequence is given in the present sequence in given in the present sequence is given in the present sequence in the present sequence is given in the present sequence in given in the present sequence is given in the present sequence in the present sequence in the present sequence in the pr
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N-PSDB; AAC64627.
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                                                                                                                                                                                                                                                                                                                                                                     05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid sequence SEQ ID NO:22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                     99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
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                                                                                                                                                                                                                                                                                  Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunogen
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Pred. No. 2.4e-50;
                                                                                                                                                                                                                                                                                  SK,
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described

Disclosure; Page 137; 139pp; English.

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

(1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

N-PSDB; AAC64624

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RESULT 13
AAB36348
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Best Local S
Matches 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            copy of that gene; and (4) eliciting an immune response in an animal, and comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
WPI; 2000-672631/65
                                                                                                                                                                                                                                                                                                      Salmonella; agfA; chromosomal gene replacement;
                                                                                                                              05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                           AAB36348;
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                              White AP,
                                                                                               05-APR-1999;
                                                                                                                                                              12-OCT-2000
                                                                                                                                                                                             WO200060102-A2
                                                                                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                                                                                             Salmonella enteritidis
                                                                                                                                                                                                                                                                                          vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                          AgfA::PT3#3 amino acid sequence SEQ ID
                                                               (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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                            Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA,
                                                                                             99US-0127888P.
                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.7%;
81.5%;
                              Collison
                                                                                                                                                                                                                                                                                          immunogen
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Pred. No. 3e-50;
                              SK,
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                            Kay WW,
                                                                                                                                                                                                                                                                                                                                          NO:16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
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                                                                                                                                                                                                                                                                                                          fimbrin;
                                                                                                                                                                                                                                                                                                          epitope;
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CC directing recombination of a recombinant gene into the chromosome of the Chomologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating a raplacement segment or segments of foreign amino acid polymer comprising a recombinant AgfA C protein containing a replacement segment or segments of foreign amino acid polymer comprising a recombinant AgfA C protein containing a replacement segment or segments of foreign amino acid polymer containing a recombinant AgfA C protein containing a replacement segment or segments of foreign amino acid polymer for a coli or coli or the animal in conjunction with a carrier or diluent. (1) is colymer into the animal in conjunction with a carrier or diluent. (1) is cueful for the expression of recombinant AgfA protein which is useful for cliciting an immune response in an animal. In a fimbrial presentation conjunction which heterologous antigens are presented in high numbers (up to 50,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live capainst the inserted epitope, and hybrid fimbriae are usually strong cidexpensive to purify, in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
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Query Match Best Local S Matches 122 Sequence 151 ĀΆ, 74.6%; Score 578; DB 3; Pred. No. 6.3e-48; Length 151;

122;

Conservative

6

Mismatches

Indels

0

Gaps

Similarity

Ś 밁 Ş 61 \vdash 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ MKLLKVAAFAAI VVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSI YQYGSANAALALQ 60 120 60

121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151

SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG

120

밁

61

121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151

RESULT 14
AAB36343
ID AAB36

AAB36343 standard; protein; 151

26-FEB-2001 (first entry)

Escherichia coli CsgA amino acid sequence SEQ ID NO:7

Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope, vaccine; immune response; immunogen

Escherichia coli.

WO200060102-A2

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RESULT 15
ABR82651
ID ABR82
XX
AC ABR82
XX
DT 04-DE
XX
DE E. CC
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC assembly system of strains of Salmonella, Escherichia coli and C Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene CC back into the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA CC protein containing a replacement segment or segments of foreign amino CC Enterobacteriaceae host cell, from the host cell and introducing the sequence or sequences grown on a Salmonella, E. coli or CC coliciting an immune response in an animal. In a fimbrial presentation CC solonous content for manual in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant AgfA protein which is useful for CC eliciting an immune response in an animal. In a fimbrial presentation CC solonous copies/cell), the hybrid fimbrian protein possesses both the CC immunogenicity and adhesion properties relevant for an efficient live carrier fimbrial subunit protein gan immune response CC against the inserted epitone, and hybrid fimbriae are usually strong CC communogens, which may be important for directing an immune response CC against the inserted epitone, and hybrid fimbriae are assy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches 104
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                    E. coli CsgA subunit 15 kDa protein.
                                                           04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and
                                                                                                                                        ABR82651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                        151
                                                                                                                                   standard; protein;
                                                                                                                                                                                                                                         GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                                                                                                                                                            LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                      SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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                                                           (first entry)
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Pred. No. 4.3e-43;
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Job time :

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Search completed: March 11,

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                                                                                                                                                                                                                                                                   The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABR82642, ABR82648-49. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli 15 kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmor or Shigella infections.
                                                                                                                                                                                                                                        Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 41-42; 42pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bjoerck L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2002; 2002GB-00002275
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DB; ACF36153.
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                                                                                                                                          1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGUHNGGGUSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                            Similarity
GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
                             LVTRVVTHEMAHASVMVRQVGFGNNATANQY
                                                           TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
                                                                                    SDARKSETTITOSGYGNGADVGQGADNSTIELTONGFRNNATIDOWNAKNSDITVGQYDQ
                                                                                                                      MKLLKVEAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
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Pred. No. 1.3e-42;
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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
    GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen
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US-09-186-387-8
US-09-196-387-10
US-09-196-387-2
US-09-196-387-2
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US-09-196-387-2
US-09-196-387-2
US-09-196-387-2
US-09-972-115A-8
US-09-972-115A-8
US-09-252-991A-32096
US-09-252-991A-32096
US-09-072-596-204
US-09-077-596-131
US-09-077-596-204
US-09-077-596-204
US-09-077-596-204
            US-09-252-991A-30227

US-09-540-236-3401

US-09-336-447A-13

US-09-336-447A-5

5187262-1

US-09-043-123-2

US-09-489-039A-11518

US-09-719-402A-2

US-09-841-786-4

US-08-409-995-4

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Sequence 2, Appli
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                                                                                   Sequence 5
Patent No.
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75.5	75.5	75.5	75.5	76.5	76.5	76.5	77	77	77.5	77.5	78.5	78.5	78.5	78.5	78.5	78.5	78.5
9.7	9.7	9.7	9.7	9.9	9.9	9.9	9.9	9.9	10.0	10.0	10.1	10.1	10.1	10.1	10.1	10.1	10.1
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Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 41, Appl	Sequence 21268, A	Sequence 63, Appl	42,	Sequence 39, Appl	Sequence 280, App	Sequence 257, App	Sequence 5818, Ap	Sequence 1, Appli	•	e 47,		Sequence 33, Appl	Sequence 4, Appli	Sequence 33, Appl

ALIGNMENTS

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US-08-233-788A-59
                                                                              US-08-233-788A-59
                                                                                                                                       TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 59, Application US/08233788A Patent No. 5635617
Query Match 89.3%;
Best Local Similarity 90.7%;
Matches 137; Conservative
                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 920043.403C2.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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APPLICANT: Doran,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND CO
                                                                                                 LENGTH: 151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center,
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Score 692; DB 1; Length 15
Pred. No. 3.9e-62;
3; Mismatches 11; Indels
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            Sequence 8, Application US/09196387
Patent No. 6277613
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REFERENCE/DOCKET NUMBER: 9200
TELLECOMMUNICATION INFORMATION:
TELLEPHONE: (206) 622-4900
TELEFAN: (206) 682-6031
TELEFAN: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
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GENERAL INFORMATION:
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APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
King, Joshua
35,
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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STREET: book
CTTY: Seattle
Washing
                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 26-AP
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                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                     61
                                                                                                                                                   82
                                                                                                                                                                                                    22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 81
                                                                                                                                                                                                                                                     97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7, Application US/08233788A 5635617
                                                                                                                                              GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQY 118
                                                                                                              GOGADNSTIELTONGFRNNATIDOWNAKNSDITVGQY
                                                                                                                                                                                VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 60
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                                                                                                                                                                                                                                                                                                                                                                                           120 amino acids
                                                                                                                                                                                                                                                       Conservative
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100.0%; Pr/
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                                                                                                                                                                                                                                                   Score 514; DB 1; pred. No. 2.2e-44; 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                  Length 120;
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                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09841835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                               TITLE OF INVENTION: A
TITLE OF INVENTION: OF
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/0
FILING DATE: June 10, 19
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
FILING DATE:
                                                         STATE: New COUNTRY: US ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
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                                                                                                             CITY: Hackensack
                                                                                                                              STREET:
                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                   158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                   65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
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                                                                                                                                               Klauber & Jackson
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OF USE THEREOF
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                                                                                                                              4th Floor
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                                                                                                                                                                                                                      TRF1 AND METHODS
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Best Local :
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                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
FILING DATE: June 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
LENGTH: 673 amino acids
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APPLICATION NUMBER:
                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
FELECOMMUNICATION INFORMATION:
                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                         COUNTRY: U
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STATE: New Jersey
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                                                                                                                                                                                                                                                                                                                                                                                                                      DDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 KSETTIT----OSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
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Similarity 30.4%;
35; Conservative 1
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Smith, Susan
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                                                                                                                09/095,225
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ER: 600-1-230 CIP1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                            ; MOLECULE TYPE: protein US-09-841-835-10
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GENERAL INFORMATION:
APPLICANT: de Lang
APPLICANT: Smith,
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Matches
                Query Match
Best Local Similarity
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                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                      NAME: Jackson Esq., David A.
REGISTRATION NUMBER: -26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                          LENGTH: 949 amino acids
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                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                             TOPOLOGY:
                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA
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New Jersey
                                                                                                          amino acid
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   Conservative
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Smith, Susan
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                11.9%;
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Pred. No. 0.84
15; Mismatches
                Score 92;
Pred. No.
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.30
                             DB 4;
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   57;
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                               Length 949
   Indels
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6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR

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                                              US-09-841-835-2
                                                             RESULT 8
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US-09-196-387-2
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            Sequence 2, Application US/09841835 Patent No. 6506587
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GENERAL INFORMATION
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MOLECULE TYPE:
HYPOTHETICAL:
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APPLICATION NUMBER: 09/0
FILING DATE: June 10, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 201-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                      Local
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                                                                                                          158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                        65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
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                                                                                                                                                                                                                                                    l Similarity 30.4
35; Conservative
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Smith, Susan
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NO
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APPLICANT: Gregg, Morin B.
APPLICANT: Walter, Funk D.
APPLICANT MICCZYSLAW, Platyszek A.
TITLE OF INVENTION: A Second Mammalian Telomerase FILE REFERENCE: 080/003C
CURRENT APPLICATION UNMBER: US/09/972,115A
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/128,577
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                               US-09-972-115A-8
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INFORMATION FOR SEQ ID NO:
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HYPOTHETICAL:
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STRANDEDNESS: sin
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Smith, Susan
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Pred. No. 1.3;
15; Mismatches
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                                  US-08-864-038A-3
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Query Match
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: May 28, 19;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP
                                                                                                                                                                                                                                  TELEFAX: (212) 953-7733
                                                                                                                                        TOPOLOGY: line MOLECULE TYPE: FOR ORIGINAL SOURCE:
                                     FEATURE: PEPTIDE NAME/KEY: PEPTIDE LOCATION: From 1 to 738 IDENTIFICATION METHOD: /
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 738
                                                                                                                                                                                                                                                                   TELEPHONE: (212) 986-2340
                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskett
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                                                                                                            CELL TYPE:
                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 22
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Word Perfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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ZIP: 514-01
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35; Conserv
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: JAPAN
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VERTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
VERNTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
VENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
VENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
VENTION: TO SAID POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                Bruce Hamburg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                          Pinctada fucata mantle epithelial
                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diskette,
                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                              May 28, 1997
                                                                                                                                                                                                                                                                                                                                                                  15-July-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microsoft Windows
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 11.5%;
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                                               m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.50 inch, 1.44 MB storage
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 Score 89.5;
                                                                                                            cell
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 DB 3;
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Length 738;
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Best Local Similarity
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6214981
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                TOPOLOGY: ur
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: TUCKER, FAPPLICANT: PLOSILA, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212)
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                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212, TELEFAX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 31,232 REFERENCE/DOCKET NUMBER: 79
                                                                                                                                                                                                                                                                                                                              STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: N
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME:
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                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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141 -GFGNNATA 148
                                              156 E---TVQQISELLPIIRGQKALNDIYQLADTNLQKYRRTHAQGHASTAVGAMSYAKGHFS
                                                                          110 NSDITVGQYDQLVTRV-----
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                                                                                                        86
                                                                                                                                                                                                                           48;
                                                                                                                                    57 LALQSDARKSETTITQSGYGNGADVG-QGADNSTI----ELTQNGFRNNA--TIDQWNAK 109
                                                                                                                                                               44 LSFARIAALAVLVIGATLNGSAYAGIGISEADGG--KGGANARG-DKSIAI---GDIAQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 ARKSETTITQSGYGNGADVGQG 84
                                                                                                                                                                                             1 MKLLKVAAFAAIVV----SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAA 56
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                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                      869-8864
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25.4%;
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4; Mismatches
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                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                           62;
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RESULT 13
US-09-056-556-204
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US-09-252-991A-32096
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Best Local Similarity 21.5
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Patent No. 635045
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SEQ ID NO 32096
LENGTH: 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE:
                  ATTORNEY/ĀĞENT INFORMATION:
NAME: MAKI, DAVID J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21(
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A
APPLICANT: Dillon, Davin C
                                                                                                                                                                                                                                                                                                                                                                                                                JUMBER OF SEQUENCES:
                                                                                                                     APPLICATION NUMBER: US/09/056,556 FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                            CITY: Seattle
STATE: Washington
                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TLE OF INVENTION:
                                                                                                                                                                                                                                                                             ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 VNVAAGNFNQQKNDLAAAVSNGQYSTAGSAASQTSTG-NTTVN 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNS----- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 KVSNFGTL--NNASVSGSIKDASGNVGVNVAAGDNNQQANAAALASADASFVFGTATAS- 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WART J. Rubenfield et al.
WENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
WENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09056556
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skeiky, Yasir A.W. Dillon, Davin C.
                                                                                                                                                                                                                                                                                                 USA
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UMBER: US 60/074,788
1998-02-18
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21.5%; Pred. No. 1.
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                    210121.457
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US-09-072-596-199
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Best Local S
Matches 29
Best Local Similarity Matches 29; Conserv
                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                    TELEFAX: (206) 682-60
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (206) 622-4
TELEFAX: (206) 682-603
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                   NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 05-MZ
                                                                                                                                                                                       TELEPHONE:
                                                                               TOPOLOGY:
                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 IGLTGSGLLGF-----GGLNSGTGN-----IGLFNSGTGNVGIGNSGTGNWGIGNSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                               98104-7092
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6458366
                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INVENTION:
                                                                                                                            943 amino acids
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                                                                                                                                                      (206) 682-6031
--- TR NO: 199:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 943 amino acids
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Hendrickson, Ronald C.
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Vedvick, Thomas S.
Twardzik, Daniel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campos-Neto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reed, Steven G.
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682-6031
70: 204:
                                                                                                                                                                                       622-4900
             10.8%; Score 83.5; 25.4%; Pred. No. 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.8%; Score 83.5;
25.4%; Pred. No. 6;
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                                                                                                                                                                                                                                                                                                                                               Version #1.30
                            DB 4;
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                             Length 943;
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Conservative

16;

Mismatches

50;

19;

Gaps

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WS-09-477-135A-131
US-09-477-135A-131
Sequence 131, Application US/09477135A
Patent No. 6572865
GENERAL INFORMATION:
APPLICANT: Mano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
CURRENT FILING DATE: 52888;
CURRENT FILING DATE: 900-01-03
PRIOR APPLICATION NUMBER: US/09/477,135A
CURRENT FILING DATE: 1997-12-15
PRIOR PILING DATE: 1997-12-15
PRIOR PILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
VMMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 131
LENGTH: 943
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-477-135A-131
Search completed: March 11, 2004, 18:44:45
Job time : 34.4 secs
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                                                                                                                       313 NSYNTGFGNSGDANTGFFNSGLANTGVGNAGNYNTGSYNPGNSNTGGFNMGQYN 366
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Result
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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775
           ://gn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
://gn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
://gn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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           GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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   10 US-09-972-115A-8

10 US-01-19-937-4

10 US-09-793-306-1146-9

10 US-09-712-363-156-9

10 US-10-080-170-348-14

14 US-10-156-761-8763-156-15-156-761-8763-156-15-174-363-56-15-174-363-56-15-174-363-56-15-176-1761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9343-14-10-156-761-9348-14-10-156-761-9348-14-10-156-761-9348-14-
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US-09-841-835-8
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Sequence 20638, A
Sequence 8, Appli
Sequence 10, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 146, Appli
Sequence 146, Appli
Sequence 146, Appli
Sequence 156, Appli
Sequence 348, App
Sequence 348, App
Sequence 20619, A
Sequence 20619, A
Sequence 20619, A
Sequence 20619, A
Sequence 20619, A
Sequence 20619, A
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US-10-369-493-20638

Sequence 20638, Application US/10369493 Publication No. US20030233675A1

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78	78.5	78.5	78.5	78.5	78.5	79	79	79.5	79.5	79.5	80	80	80.5	80.5	81	82	82	82	82.5	82.5	83	83	83	83.5	83.5	83.5	u	83.5	84.5
10.1	10.1	10.1	10.1	10.1	•	10.2			•	10.3	10.3		10.4	10.4	10.5	•	10.6	10.6	•	10.6	10.7	10.7	•	•	10.8		10.8		10.9
251	3241	2834	2732	2353	714	594	251	518	253	65	892	255	873	251	812	2893	254	253	2468	407	257	254	254	943	943	943	943	943	271
10	9	14	14	9	9	14	10	9	10	9	10	10	10	10	15	10	10	10	14	14	10	10	10	14	14	10	10	9	14
US-09-880-748-1130	US-09-841-786-1	US-10-085-959-252	US-10-238-075-1119	US-09-797-862-33	US-09-841-786-4	US-10-156-761-13173	US-09-880-748-1122	US-09-976-297-2	US-09-880-748-1850	US-09-996-194-16	US-09-952-267-5	US-09-880-748-1153	US-09-952-267-13	US-09-880-748-1554	US-10-369-493-9134	US-09-882-227-522	US-09-880-748-1226	US-09-880-748-2098	US-10-246-330-4	US-10-156-761-12940	US-09-880-748-1494	US-09-880-748-1165	US-09-880-748-1136	US-10-084-843-204	US-10-193-002-199	US-09-997-181-131	US-09-997-182-131	US-09-996-634-131	US-10-156-761-11721
Sequence 1130, Ap	Sequence 1, Appli	Sequence 252, App	Sequence 1119, Ap	w	Seguence 4, Appli	13173,	Sequence 1122, Ap	Sequence 2, Appli	e 1			115	13,	1554,	9134,	522,	1226,		4, A	12940,	1494,	1165,	Sequence 1136, Ap	204,	199,	131,	e 131,	Sequence 131, App	Sequence 11721, A

ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/03-02-28
PRIOR APPLICATION NUMBER: US/03-039
PRIOR APPLICATION NUMBER: US/03-039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20638
LENGTH: 445
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                                                                                                                                                             Matches
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Best Local (
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                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Rhodopseudomonas palustris
FEATURE:
19 AAFAADSNTVYLNOTGNDQQANITQSGNGNSVGAFNGNSGFLQENGTLSGA-NLLTVKQS
                                                                                                               7 AAFAA-----IVVSGSALAGVVPQWGGGG-----NHNGG-----GNSGFDSTLSIYQY 50
                                                                                                                                                                                  Similarity
                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                        unsure at all Xaa locations
                                                                                                                                                         13.4%; Score 104; DB 15; Length 445; 26.6%; Pred. No. 0.03; tive 25; Mismatches 61; Indels 3
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                                                                                                  US-09-841-835-10
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                                                                                                                     RESULT 3
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US-09-841-835-8
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                                                 Patent No. US20020076 GENERAL INFORMATION:
                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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Patent No. US20020076795A1
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                   APPLICANT: de Lar
APPLICANT: Smith,
     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 201-487-5800
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                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 673 amino acids
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APPLICANT: Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                             158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                10, Application US/09841835
o. US20020076795A1
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                                                                                                                                                                                                                                                          6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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                                                                                                                                                                                                                          VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA
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Hackensack
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Y: linear
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                                 de Lange, Titia
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A PROTEIN THAT BINDS
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30.4%; Pred. No. 0.
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TO TRF1 AND METHODS
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Patent No. US20020076795A1
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APPLICANT: de Lan
APPLICANT: Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                         TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRE1 AND METHODS TITLE OF INVENTION: OF USE THEREOF NUMBER OF SEQUENCES: 12
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELEPHONE: 201-487-5800
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CLASSIFICATION:
PRIOR APPLICATION DATA:
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NUMBER OF SEQUENCES:
                                                                                                  ZIP: 07601
                                                                                                                                                  CITY: Hackensack
                                                                                                                 COUNTRY:
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
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35; Conserv
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Smith, Susan
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30.4%; Pred. No. 1
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   Version #1.30
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CURRENT APPLICATION DATA:

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                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-115A-8
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                                                                                                                                                        Matches
                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
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Best Local S
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CURRENT FILING DATE: 2001-10-05
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PRIOR APPLICATION NUMBER: US 60/128,577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Geron Corporation APPLICANT: Gregg, Morin B.
                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 60/129,123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: A Second Mammalian Telomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 11
MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                ENGTH: 1327
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LENGTH: 1327 amino acids
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STRANDEDNESS: single
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
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158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                     65 KSETTIT----OSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                            99 VAAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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Walter, Funk D.
Mieczyslaw, Piatyszek A.
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                                                                                                                                                    11.9%; Score 92; DB 30.4%; Pred. No. 2; ative 15; Mismatches
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; Pred. No. 2;
15; Mismatches 5
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US-09-793-306-146
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                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 146
LENGTH: 597
Query Match
Best Local Similarity
Matches 33; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/10199937 Publication No. US20030190739A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. US20020098200A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 146,
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                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR FILING DATE: 2000-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 178
SOFTWARE: PatentIn Ver. 2.0
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PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/141,582
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APPLICANT: DeMaggio, Anthony
APPLICANT: Goldman, Phyllis
APPLICANT: McBlligott, David
                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/199,937
                                                                                                                                                                                                                                                                                                                                                                                                             IIILE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
IIILE OF INVENTION: of Tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 014058-008740US
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                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                  TYPE: PRT
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
                                                                                                      OTHER INFORMATION: Description of Artificial Sequence:mTTC#3-His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lodes, Michael
Corixa Corporation
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  Conservative
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                     11.2%; Score 87; I
26.6%; Pred. No. 2
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15;
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  Mismatches
                                          DB 9; Length 597;
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  26;
  Gaps
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RESULT 9
US-09-712-363-156
; Sequence 156, Application US/09712363
; Patent No. US200220164588A1
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APPLICANT: Tucker, Kenneth
APPLICANT: Plosila, Laura
TITLE OF INVENTION: MORAKELLA CATAKRHALIS OUTER MEMBRANE PROTEIN-106 POLYPEPTIDE,
TITLE OF INVENTION: SEQUENCE AND USES THEREOF
FILE REFERENCE: 7969-089-99
CURRENT FILING NUMBER: US/09/813,214A
CURRENT FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: 08/968,685
PRIOR APPLICATION NUMBER: 08/968,685
PRIOR FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 20
SOPTWARE: Patentin version 3.0
SEQ ID NO 9
SEQ ID NO 9
                                                                                                                                                                                      GENERAL INFORMATION:
                                           APPLICANT: Elsenber, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
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Patent No. US20020177200A1
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PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSFARIAALAVLVIGATLNGSAYAGIGISEADGG--KGGANARG-DKSIAI---GDIAQA
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25.4%; Pred. No.
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                                                                                              COMPARATIVE ANALYSIS
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US-10-080-170-348
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US-10-080-170-348
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US-09-712-363-156
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver.
SEQ ID NO 348
LENGTH: 527
                                                                                                                                                                                                                   Best Local Similarity
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SEQ ID NO 156
LENGTH: 527
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PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: COLE, S.T.

TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495.0218

CURRENT APPLICATION NUMBER: US/10/080,170

CURRENT FILING DATE: 2002-06-10

CURRENT FILING DATE: 2002-06-10
                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Mycobacterium tuberculosis
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PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 292
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PRIOR APPLICATION NUMBER: 60/134,092
PRIOR FILING DATE: 1999-05-14
PRIOR PRIOR APPLICATION NUMBER: 60/165,124
PRIOR APPLICATION NUMBER: 60/165,124
PRIOR APPLICATION NUMBER: 60/165,124
PRIOR FILING DATE: 1999-11-12
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FILING DATE: 1999-02-01
APPLICATION NUMBER: 60/126,593
FILING DATE: 1999-03-26
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APPLICATION NUMBER: 60/117,844
FILING DATE: 1999-01-29
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                                                                                                                                             21 GVVPQWGG----GGNHNGGGNSSGPD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  507 WQLADGDVI-------RLGHSEIIVR 525
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                                                                                         GYAPQGGGYAEPAGRDYDYGQSGAPDYGQPAPGGYSGYGQGGYGSAGTSVTLQLDDGSGR 446
                                                    TTITQSG---YGNGADV-----
TYQLREGSNIIGRGQDAQFRLPDTGVSRRHLEIRWDGQVALLADLNSTNGTTVNNAPVQE 506
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22.9%; Pred. No. 2.3;
Live 13; Mismatches
                                                                                                                                                                                          13;
                                                                                                                                                                                                              Score 86.5;
Pred. No. 2
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                                            -GOGADNSTIELTONGFRNNATIDO 105
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                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                 Length
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                                                                                                                                                                                     Gaps
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106 WNAKNSDITVGQYDQLVTRVVTHEMAHASVMVR 138

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Streptomyces avermițilis US-10-156-761-8763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-156-761-8763
                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 8763
                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20619, Application US/10369493 Publication No. US20030233675A1
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                              FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                            TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(486)
OTHER INFORMATION: unsure at all Xaa locations
                                                                           ORGANISM: Rhodopseudomonas
                                                                                                                    LENGTH: 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 AFFATSTFGS---GRVAFWGDSSPIDDGTGQSGNTLYDGWNDTGATNAALALNA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          507 WQLADGDVI------RLGHSEIIVR 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 AFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSE 67
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                                                                                                                                                                                                                                                                                                                 Hinkle, Gregory J.
Slater, Steven C.
Goldman, Barry S.
Chen, Xianfeng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISHIKAWA, JUN
HORIKAWA, HIROSHI
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                                                                             palustrie
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; Pred. No. 2.3;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 14; Length 482;
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                                                           APPLICANT:
                                          PPLICANT
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US-10-374-780A-2086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Microsoft Office 97
SEQ ID NO 56
                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                 Sequence 2086, Application US/10374780A Publication No. US20040019927A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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CURRENT APPLICATION NUMBER: US/10/174,363
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 60/298,973
PRIOR FILING DATE: 2001-06-18
NUMBER OF STO
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Publication No. US20030077623A1
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Best Local Similarity
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                 APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heard, Jacqueline E
APPLICANT: Haake, Volker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Butler, Karlene H.
APPLICANT: Cahoon, Rebecca E
APPLICANT: Harvell, Leslie T.
APPLICANT: Rafalski, Antoni J.
APPLICANT: Sakai, Hajime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                               214 TITPEVTSRGVNRAVMKQLV 233
                                                                                                                                                                                                                                                                                                                          121 LVTRVVTHEMAHASVMVRQV 140
                                                                                                                                                                                                                                                                                                                                                                  154 EQLSVEQGAPSQAIQPIPSSSKAFKFPMRPGKGQSGKRCIVKANHFFAELPDKDLHHYDV 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                               77 NGADVGQGADNSTIE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 GGYGGGRGGGPSSGPPQRQSVPELHQATSPTYQAVSSQPTLSEVSPTQVPEPTVLAQQF- 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 GGGGNHNGGGNSSGPDSTLSI-------YQYGSANAALALQSDARKSETTITQSGYG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 SVVVAGTDYRDIVÄGVLPSLGGVKKAYAIGDGSGPFAPFKDLASDTPFSAPEFGAADGFV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 AIVVSGS----ALAGVVPQWGGGGNHNGGGNSSGP-----DSTLSIYQYGSANAAL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36;
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Similarity 25.7%; Pred. No. 6.8;
36; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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2.3;
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Keddie, James Broun, Pierre E Pilgrim, Marsha L

Reuber, T. Lynne Adam, Luc J Ratcliffe, Oliver Creelman,

Robert A

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RESULT 15
US-10-156-761-9343
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: HISHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER: JP 2001-272697
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CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR PPLICATION NUMBER: 60/310,847
PRIOR PPLICATION NUMBER: 60/336,049
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 10/225,066
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 10/225,066
PRIOR APPLICATION NUMBER: 10/225,066
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PRIOR APPLICATION NUMBER: 10/225,067
PRIOR APPLICATION NUMBER: 10/225,067
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SEQ ID NO 2086
LENGTH: 1048
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APPLICANT: IKEDA, HARUO
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PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
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25.7%; Pred. No. 6.8;
cive 17; Mismatches
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                                                                                                                                                                                                                                                                        ; ORGANISM: Streptomyces avermitilis US-10-156-761-9343
                                                                                                                                                                                                                                                                                                        ; SEQ ID NO 9343
; LENGTH: 438
; TYPE: PRT
                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                      Query Match
Best Local Similarity
   115
                                 97 FRNNATIDOWNAKNSDITVGQYDQLV 122
                                                                                                  59 ---LOSDARKSE------TTITQSGYGNGADVGQGADNSTIELTQNG
                                                                                                                                                                                                        37;
                                                                                                                                  1 MRSIRAAAVGAVTMSLALAASAC----GGGSSTGGGSNDSP-KTLT-YWASNQGASIAVD 54
                                                                                                                                                                  1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALA--
                                                                KKVLQPELDKFEEQTGIKVKLEVVPWSDLLNRILTATTSGQGPDVLNIGNTWSASLQATG 114
                                                                                                                                                                                                        Conservative
-ALLPWDAKNFD-KIGGKDRFV 134
                                                                                                                                                                                                                    11.0%; Score 85;
25.3%; Pred. No. 2
                                                                                                                                                                                                      22;
                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                  DB 14; Length 438;
                                                                                                                                                                                                      51;
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                    36;
                                                                                                                                                                                                    Gaps
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Search completed: March 11, 2004, 19:18:35 Job time: 25.6 secs

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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
                                                                            Database :
                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                 Searched:
PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                              March 11, 2004, 18:24:14; Search time 10.3 Seconds (without alignments) 1410.186 Million cell updates/sec
                                                                                                                                                                                                                                                                               283366 seqs, 96191526 residues
                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                       1 MKLLKVAAFAAIVVSGSALA......HASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                            US-09-543-407-14
775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                               283366
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

4444	39 41 41	36 37 38	3 2 2 1 3 3 4 3 4 3 4 3 4 3 4 4 4 4 4 4 4 4 4
83.5	83 . 5 83 . 5	84.5 84.5 84.8	85.5 86.5 86.5
10.8	10.8 10.8	11.0 10.9 10.8	11.2 11.1 11.1 11.1 11.1
1067 3300	590 602 285	347 967 440 407	645 447 599 575
0000	2277	N N N N	88888
T15352 S35423 D70575	A45621 PL0221 H84219	B39112 S66852 AD1539 T21956	F70825 G84687 B42049 A44951 S35327
hypothetical prote protein kinase sgg probable PPE prote		merozoite 45K surt hypothetical prote probable sugar ABC hypothetical prote	probable PPE prote probable disease r leishmanolysin (EC leishmanolysin (EC protein kinase sgg

ALIGNMENTS

Q	дь	οy	מם	8	Query Match Best Local Matches 13	F;1-20/D F;21-151	A;Descri A;Note:	A; Gene: agfA C; Function:	A;Note: sec	A;Molecu A;Residu	A;Status	A; Contents:	A; Refere	J. Bacte	R;Collin	A;Experi	A;Residu	A; Access	A;Cross-	A;Molecu A:Residu	A; Access	A;Title: A;Refere	J. Bacte	R;Collin	C;Date:	fimbrin C:Specie	RESULT 1
121 LVTRVVTHEMAHASYMVRQVGFGNNATANQY 151 :	61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120	61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120	1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	Query Match 89.4%; Score 693; DB 2; Length 151; Best Local Similarity 90.7%; Pred. No. 5e-52; Matches 137; Conservative 3; Mismatches 11; Indels 0; Gaps 0;	F;1-20/Domain: signal sequence #status predicted <sig> F;21-151/Product: fimbrin protein agfA #status experimental <mat></mat></sig>	A;Description: major component of thin aggregative fimbriae A;Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator C.Voronada: fimbria	agfA lon:	A;Note: sequence extracted from NCBI backbone (NCBIP:45936) C:Genetics:	A;Molecule type: protein A;Residues: 21-33 <co3></co3>	A; Status: preliminary	A;Accessin: A44898	r: A44898; MUID:91310586; PMID:1677357	. Burification and observations of thin aggregative fimbrise from Salmone	R; Collinson, S.K.; Emody, L.; Muller, K.H.; Trust, T.J.; Kay, W.W.))	A;Residues: 21-52 <co2></co2>	A, Accession: PC6015	A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43599.1; PID:g1184714	A;Molecule type: DNA A;Residues: 1-151 <col/>	A;Accession: JC6039	A;11t1e: Salmonella enteritidia agraac operon encoding thin, aggregative iimbilae. A;Reference number: JC6039; MUID:96146512; PMID:8550497		R;COllinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.	Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999	fimbrin protein agfA precursor - Salmonella enteritidis C:Species: Salmonella enteritidis	

121

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N;Alternate names: csgA protein; major curlin protein C:Species: Escherichia coli C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01. C;Accession: S70788; G64846; S31202; S34560; S34559 R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S. Mol. Microbiol. 18, 661-670, 1995 A;Title: Expression of two csg operons is required for production A;Reference number: S70783; MUID:96414468; PMID:8817489
       A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; A;Experimental source: strain K-12, substrain MG1655 R;Olsen, A.; Arngvist, A.; Hammar, M.; Sukupolvi, S.; Norm Mol. Microbiol. 7, 523-536, 1993
                                                                                                                                                                   Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G64846
                                                                                                                                                                                                                              A;Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62282.1; PID:g1147564
A;Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Augu
R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; R
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid;
A;Molecule type: DNA
A;Residues: 1-151 <HAM>
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Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; AiTitle: Complete genome sequence of a multiple drug resistant A; Reference number: ABO502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
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A;Gene: STY1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        major curlin chain precursor [imported] - Salmonella enterica subsp. enteric; Species: Salmonella enterica subsp. enteric sibsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AI0635
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AI0635
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A; Residues: 1-151 < PAR>
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                                                                                                    ;Residues:
                                                                                                                     Molecule type: DNA
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Best Local S
Matches 137
                                                                                                                                          Status: nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references:
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                                                                                                    1-151 <BLAT>
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Pred. No. 5e-52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                              S.; Normark,
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                                                                   PIDN:AAC74126.1;
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Salmonella enterica
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V.; Riley,
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                                                                   PID:g1787279
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A;Atcessampreliminary
A,Status; preliminary
A;Molecule type: DNA
A;Residues: 1-152 cHAY>
A;Residues: 1-152 cHAY>
A;Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:gl3360880;
A;Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:gl3360880;
                                                                                                                                                                                                                                                                                      A;Title: Complete genome sequence of A;Reference number: A99629; MUID:211: A;Accession: D90806
                                                                                                                                                                                                                                                                                                                                          R;Hayashi, T.; Makino, gasawara, N.; Yasunaga, DNA Res. 8, 11-22, 2001
                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: D90806
                                                                                                                                                            A; Gene:
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A;Molecule type: DNA
A;Residues: 1-133,'RQRDSGWLW' <0LS3>
A;Cross-references: EMBL:L04979; NID:g290424;
A;Cross-references: strain K-12, substrain
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R;Olsen, A.N.; Arnqvist, A.M.
submitted to the EMBL Data Library,
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A; Accession: S34559
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                                                                                                                                                                                                                                                                                                                                                              T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii
N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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                                                                                                  Similarity
                        MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL
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MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAL
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                                                                                Conservative
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                                                                                              65.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.1%; Score 528; DB 2; 68.9%; Pred. No. 5.4e-38; cive 20; Mismatches 27
                                                                                                                                                                                                                                                                                                          quence of enterohemorrhagic Escherichia MUID:21156231; PMID:11258796
                                                                              21;
                                                                          Score 506.5; DB 2;
Pred. No. 3.6e-36;
1; Mismatches 28;
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Shinagawa,
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QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYD

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A;Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62281.1; PID:g1147563
A;Experimental source: Strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Augus
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; R.
R, Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                curlin nucleator protein csgB precursor - Escherichia coli (strain K-12) N;Alternate names: csgB protein; curlin nucleation component; minor curl C;Species: Escherichia coli C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01-Mar-2 C;Accession: S70787; P64846
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    A; Molecule type: DNA
A; Residues: 1-151 <BLAT>
A; Cross-references: GB: A
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A;Residues: 1-152 <STO>
A;Cross-references: GB:AE005174; NID:g12514574; PIDN:AAG55788.1;
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                         A;Reference number: A;Accession: F64846
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;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, Perna, N.T.; Dimalanta, E.;
                                                                                                                              Status: nucleic acid sequence not shown; translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, L. Microbiol. 18, 661-670, 1995
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67.1%; Pred. No. 3.6e-36;
cive 21; Mismatches 28
        GB:U00096;
NID:g1787265; PIDN:AAC74125.1;
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Potamousis,
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    PID:g1787278
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K.; Aç
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A; Experimental source: s
C; Genetics:
A; Gene: csgB
A; Map position: 23.15
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      minor curlin subunit precursor CsgB [imported] - Escherichia coli (strain O157:H C;Species: Escherichia coli (C;Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: C90806 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; H gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796
RESULT
G85665
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                                                                                                                                                                                                                                                                                                                                                           A;Experimental source: strain C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-151 <HAY>
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A; Accession: C90806
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                                                                                                                                                                                                                                                                                                                                           A;Gene:
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
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Best Local
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Best Local (
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                                                                               NLAYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQYGTQKTAIVVQRQSQMAIRV
                                                                                                                       SETTITOSGYGNGADVGOGADNSTIELTONGFRNNATIDOWNAKNSDITVGOYDOLVTRV 125
                                                                                                                                                                                                             FAAIVVSGSAL--AGVVPQWGGGGNHNGGGNSSGPDSTLSIY-QYGSANAALALQSDARK 65
                                                                                                                                                                     FAVNELSKSSFNQAAII---GQAGTNNSAQLRQGGSKLLAVVAQEGSSNRA-KIDQTGDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRV 125
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                                                                                                                                                                                                                                                     Score 104.5; DB Pred. No. 0.054; 9; Mismatches !
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K.; A

Apodaca

Mayhe

0157:H

A; Molecule type: DNA A; Residues: 1-151 < S' A; Cross-references: (

1-151 <STO>

GB:AE005174;

NID:g12514573;

PIDN: AAG55787.1;

GSPDB:GN00145;

UWGP: 21

A; Reference number: A; Accession: G85665 A; Status: prelimina:

A85480;

of enterohemorrhagic Escherichia 80; MUID:21074935; PMID:11206551

preliminary

source:

strain O157:H7, substrain EDL933

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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
(;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: D70604
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Experimental;
C;Genetics:
A;Gene: csgB
A; Status: preliminary; nucleic acid sequence not shown; translation not
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C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
C;Accession: JC6040
R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
J. Bacteriol. 178, 662-667, 1996
J. Bacteriol. 178, 662-667, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: minor component of thin aggregative fimbriae \mathbf{A}_i Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator
                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: fimbria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43598.1; A;Experimental source: strain 276755-3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Salmonella enteritidis agfBAC operon encoding A;Reference number: JC6039; MUID:96146512; PMID:8550497 A;Accession: JC6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
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C;Species: Salmonella enteritidis
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Best Local S
Matches 34
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Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;1-21/Domain: signal sequence #status
;1-21/Product: fimbrin protein agfB
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                                                                                                                                                                                                                                                                                                                                                                   OSHMAIRVTO
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Pred. No. 0.054;
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#status predicted <MAT>
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0.17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 151;
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                                                              complete
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                                                                                                                                              Holroyd,
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                                                           genome
                                                                                                                                                လ
                                                         C;Species: Tetrahymená thermophila C;Date: 19-Mar-1997 #sequence revision C;Accession: S42136; S42135; S03650 R;Taylor, F.M.; Martindale, D.W.
A; Reference number: A; Accession: S42136
                                 R; Taylor, F.M.; Martindale, submitted to the EMBL Data
                                                                                                                                         cnjB protein - Tetrahymena thermophila
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RESULT 12
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A; Molecule type: DNA
A; Residues: 1-770 <SCH>
A; Cross-references: EMBL: AL389901; GSPDB: GN00116; NCSP: B7F21.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Schulte, U.; Aign, V.; Hoheisel, submitted to the Protein Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: T51024
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                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: Z25286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: protein B7F21.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   related to C2H2 zinc finger transcription factor D-Sp1 [imported]
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C; Superfamily: Phaseolus
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A;Residues: 1-552 <COL>
A;Cross-references: GB:Z92774; GB:AL123456; NID:g3261729; PIDN:CAB07133.1; PID:g187728.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain H37Rv
                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                               Gene: NCSP:B7F21.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Neurospora crassa
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Best Local !
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                                                                                                                                                                                                       GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADN 87
                                                                                    ---TRVVTHEMAHASV 135
                                                                                                               QSTGLGYHYSSTTRNQHQHHWRNQSNASELSADGSEITHGVASPLVGGSSHARGASGGTS
                                                                                                                                                                         GAGNNNNGSELASPDPNRGYFD----GASPPLPSSSHTTSTTYAGGHNGNGHGMRESVDS 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGSALAGV-----VPQWGGGGNHNGGGNSSGPD---STLSIYQYGSANAALALQSDA 63
                                                                                                                                                                                                                                        Conservative
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Pred. No. 1.8;
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Pred. No. 1
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v 2000
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Library, October 1992

18-Jul-1997

#text_change

07-Dec-1999

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hypothetical glycine-rich protein [imported] - Sinorhizobium meliloti (strain C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: E95965
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-f
A;Reference number: A95842; MUID:21396508; PMID:11481431
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Nucleic Acids Res. 16, 2189-2201, 1988
A;Title: Multiple introns in a conjugation-specific gene
A;Reference number: $03650; MUID:88189811; PMID:3357771
A;Accession: $03650
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A;Residues: 236-250, I', 252-255,'N', 257-773
A;Cross-references: EMBL:X06462
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A;Title: Retroviral-type zinc fingers and glycine-rich repeats
A;Reference number: S42135; MUID:94051569; PMID:8233798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: E95965
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F;1626-1748/Region:
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A; Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-
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A; Molecule type: DN
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;Cross-references: EMBL:L03710; NID:g161751; PID:g161752
;Taylor, F.M.; Martindale, D.W.
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               A;Cross-references:
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R;Garfinkel, M.D.; Wang, J.; Liang, Y.; Mahowald, A.P. Mol. Cell. Biol. 14, 6809-6818, 1994
A;Title: Multiple products from the shavenbaby-ovo gene A;Reference number: A56038; MUID:95021209; PMID:7935398
A;Accession: A56038
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                                                                                                                                                                                                                                                                                                                                            DNA-binding protein ovo - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change
C;Accession: A56038
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                                    A; Molecule type: mRNA
A; Residues: 1-1028 < GAR>
                                                                                                          A;Status: preliminary
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A;Genome: plasmid
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GB:U11383;

Gaps ALALOS	Qy 63 ARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNS 111 Db 105GNGYINCGGVG-GPNNSLDGNNLLNFASVSNYNESNS 141 Search completed: March 11, 2004, 18:42:07 Job time: 11.3 secs	QY 3 LLKVAAFAATVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD 62	Query Matc Best Local Matches	A;Gene: ovo A;Cross-references: FlyBase:FBgn0003028
. # "	AKNS 111 - ESNS 141	YQYGSANAALALQSI NSGGGGGGG	1028; ls 26; Gaps	

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OM protein - protein search, using sw model
                                                            Run on:
March 11, 2004, 18:14:48 ; Search time 6.3 Seconds (without alignments) 1248.031 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Title: Perfect score: Sequence:

US-09-543-407-14 775 1 MKLLKVAAFAAIVVSGSALA......HASVMVRQVGFGNNATANQY 151

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

33339876554 332109876554	11111111111111111111111111111111111111	Result No.
85.5 85.5 85.5 84.8 83.5 83.5 83.5 81.5 81.5 81.5 81.5 81.5 81.5 81.5 81	506.5 506.5 104.5 98.5 99.5 99.5 89.5 88.5	Score
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GP63 LEICH AGO1 ARATH MSA2 PLAF2 GP63 LEIDO GP63 LEIMA PDA6 CABEL SGG DROME P35 MYCPE OMPB RICJA HDC DROMB HME1 HUMAN GRP1 ORYSA RRPO PMMVJ RRP	CSGA_SALTY CSGA_ECOLI CSGA_ECOLI CSGB_ECOLI CSGB_SALTY TNK1_HUMAN OVO_DROME CSGB_SALTI PER_DROWI PER_DROWI VG38_BPT2 PRTC_ERWCH GP63_LEIME YF48_MYCTU	ID .
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P55004	P06997	Q12756	P52302	P34308	P34291	Q04893	Q24180	P30688	P18127	Q8ixf0	P91698	
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SEQUENCE FROM N.A. SPECIES=S.typhi; STRAIN=TY2 / ATCC 700931; MEDLINE=22531367; PubMed=12644504; Deng W., Liou SR., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;	., Barrell B.G.; enome sequence of a multiple drug resistant Salmorovar Typhi CT18."; 848-852(2001).	, Hamlin N , Haque A , Hien T.T., Holroyd S., Ja Jarsen T.S., Leather S., Moule S., O'Gaora P., Pa , Rutherford K., Simmonds M., Skelton J., Stevens	Mungall K.L., Bentley S.D., Holden M.T.G., Sebalnia ham D., Brooks K., Chillingworth T., Connerton P., wis P., Davies R.M., Dowd L., White N., Farrar J.,	Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,	é 41	"Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.":	Leonard S., Nguyen C., SCOCK K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Watasaran B. Wilson B.K.	derson K.E., Spieth J., Clifton S.W., Latreill llik S., Ali J., Dante M., Du F., Hou S., Laym	SEQUENCE FROM N.A. SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609;	regulation.	SEQUENCE FROM N.A. SPECIES=S.typhimurium; STRAIN=SR-11; MEDLINE=98117058; pubMed=9457880; ROMRING U., Bian Z., Hammar M., Sierralta W.D., Normark S.; ROMRING U., Bian A., Hammar M., Sierralta W.D., Normark S.; "Curli fibers are highly conserved between Salmonella typhimurium and	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella. NCBI_TaxID=602, 601, 592; [1]	Salmonella typhimurium, Salmonella typhi, and Salmonella enteritidis.	10-OCT-2003 (Rel. 42, Last annotation update) Major curlin subunit precursor (Fimbrin SEF17). CSGA OR AGFA OR STW1144 OR STY1181 OR T1776.	(Rel. 34, Created)	LT 1 SALTY CSGA_SALTY STANDARD; PRT; 151 AA.

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-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.
COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., 1
"DNA-based diagnostic tests for Salmonella species
the structural gene for thin, aggregative fimbriae.
J. Clin. Microbiol. 31:2263-2273(1993).
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STRAIN=K12 / YMEL;
MEDLINE=93023873; P
Arnqvist A., Olsen.
"The Crl protein ac
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STRAIN-KLZ / MG1655;
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MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMedt G. III, Bloch C.A., Perna N.T., Burlo Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew of the M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew of the M., Collado-Vides J., Glasner J.D., Goeden M.A., Rose D.
Tilev M., Collado-Vides J., Kirkpatrick H.A., Goeden M.A., Rose D.
Salmonella enteritidis.";

J. Bacteriol. 173:4773-4781(1991).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNCOLLED SURFACE STRUCTURES THAT ASSEMBLE TEMPERATURES BELOW 37 DEGREES CELSIUS. C FIBRONECTIN.
                                                                                                                              MEDLINE=91310586; PubMed=1677357;
Collinson S.K., Emoedy L., Trust T.J.,
"Purification and characterization of
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"A 718-kb DNA sequence of the Escherichia corresponding to the 12.7-28.0 min region DNA Res. 3:137-155(1996).
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MEDLINE=96414468; PubMed=8817489;
MEDLINE=96414468; PubMed=8817489;
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Escherichia coli.";
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Best Loca
Matches
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MEDLINE=21218556; PubMed=11319125;
Uhlich G.A., Keen J.E., Elder R.O.;
"Mutations in the csgD promoter associated with variations in expression in certain strains of Escherichia coli 0157:H7.";
Appl. Environ. Microbiol. 67:2367-2370(2001).
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28-FEB-2003
28-FEB-2003
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                 MEDLINE-21074935; PubMed-11205551;
Perna N.T., Plunkett G. II, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."
                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=0157:H7 / E
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Escherichia coli O157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
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28-FEB-2003 (Rel. 41, Last annotation
Major curlin subunit precursor.
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X90754; CAA62282.1; -.
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  :529-533 (2001).
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STRAIN=0157:H7 / RIMD 0509952;

C STRAIN=0157:H7 / RIMD 0509952;

C MEDLINE=21156231; PubMed=11258796;

X MEDLINE=21156231; PubMed=11258796;

X Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama A., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

A Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

A Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.

A Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli T.

"Complete genomic comparison with a laboratory strain K-12.";

DIA Res. 8:11-22 (2001).

DIA Res. 8:11-22 (2001).

L DIA Res. 8:11-22 (2001).

COILED SURPACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWT TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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SEQUENCE FROM N.A.
STRAIN=KL2 / MC4100;
MEDLINE=96414468; PubMed=8817489;
Hammar M., Arngvist A., Bian Z., Olsen A.,
"Expression of two csg operons is required
"Expression and congo red-binding curli po
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CSGB_ECOLI
P39828;
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Escherichia coli O157:H7.
Bacteria; Proteobacteria;
Enterobacteriaceae; Escher
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01-OCT-1996 (Rel. 34, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
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EMBL; AE005315; AAG55788.1;
EMBL; AP002554; BAB34843.1;
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the European Bioinformatics Institute. The
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modified and this statement is not removed.
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Tobe T.,
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                                                                                                                                                                       Armqvist A., Olsen A., Normark S.;

"Sigma S-dependent growth-phase induction of the csgBA promoter in Escherichia coli can be achieved in vivo by sigma 70 in the absence of the nucleoid-associated protein H-NS.";

Mol. Microbiol. 13:1021-1032(1994).

-- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI A TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO CURLIN MONOMERS.

CURLIN MONOMERS.
                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=0157:H7 / RIMD 0509952;

MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H., Khara S., Shiba T., Hattori M., Shinagawa H., Toopelete genome sequence of enterohemorphagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                             MEDLINE=95157246; PubMed=7854117;
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-21 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia corresponding to the 12.7-28.0 min region DNA Res. 3:137-155(1996).
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland I Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97061202; PubMed=8905232;
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Murata T., Tanaka M., Tobe T.,
kawa C., Ogasawara N., Yasunaga T.,
hinagawa H.;
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RESULT 5
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Matches 35
                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SPECIES-S.enteritidis; STRAIN=2,70
MEDLINE=96146512; PubMed=8550497;
Clouthier S.C., D
                                                                                                                                                                             SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 70 MEDLINE-21534948; PubMed=11677609; McClelland M., Sanderson K.E., Spieth J., Clifton S.W. Courtney L., Porwollik S., Ali J., Dante M., Du F., Ho Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Ryan E., Sun H., Florea L., Miller W., Stoneking T., N Waterston R., Wilson R.K.;
                                                                    fimbriae.";
                                                                                                                                            Nature 413:852-856(2001).
[3]
                                                                                                                                                               "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SPECIES-S. typhimurium; STRAIN=SR-11;
MEDLINE=98117058; PubMed=9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark
"Curli fibers are highly conserved between Salmonella ty
Escherichia coli with respect to operon structure and re
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Bacteriol. 180:722-731(1998).
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01-OCT-1996
01-OCT-1996
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Bacteriol. 178:662-667(1996).
- FUNCTION: CURLIN IS THE STRUCTURAL COILED SURFACE STRUCTURES THAT ASSETEMPERATURES BELOW 37 DEGREES CELSIFIERONECTIN. THE MINOR SUBUNIT IS TOURLIN MONOMERS.
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Fimbria;
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3Gene; EG12621; CsgB.
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; D90741; BAA35831.1; -
; AE005315; AAG55787.1; -
; AP002554; BAB34842.1; -
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35; Conservative
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substrate that J. Biol. Chem. [4]
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095271; 095272;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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110-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                    Smith S., de Lange T.;
"Cell cycle dependent localization of the to nuclear pore complexes and centrosomes
                                                                                 MEDLINE=20556282; PubMed=10988299; Chi N.-W., Lodish H.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ002301; CAA05316.1; -. EMBL; AE008749; AAL20073.1; -.
                   "Tankyrase is a Golgi-associated mitogen-activated protein substrate that interacts with IRAP in GLUT4 vesicles."; J. Biol. Chem. 275:38437-38444 (2000).
                                                                                                                                                                                                                                                      MEDLINE=99454782; PubMed=10523501;
                                                                                                                                                                                                                                                                                                                Smith S., Giriat I., Schmitt A., de Lange
"Tankyrase, a poly(ADP-ribose) polymerase
Science 282:1484-1487(1998).
                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99040105; PubMed=9822378; Smith S., Giriat I., Schmitt A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                     Cell Sci. 112:3649-3656(1999).
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Nuclear protein; I
Phosphorylation; I
REPEAT 215
REPEAT 248
REPEAT 281
REPEAT 368
REPEAT 401
REPEAT 401
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EMBL; AF082557; AAC79842.1;
EMBL; AF082558; AAC79843.1;
EMBL; AF082559; AAC79844.1;
HSSP; Q00420; IAWC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                  PROSITE; PS50088; ANK_REPEAT; 15.
PROSITE; PS50297; ANK_REP_REGION;
PROSITE; PS50105; SAM_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                 PRINTS; PRO1415; ANKYRIN. SMART; SM00248; ANK; 17. SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 603303; -.

GO; GO:0000781; C:chromosome, telomeric regio
GO; GO:0003950; F:NAD ADP-ribosyltransferase
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0007004; P:telomerase-dependent telome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restr
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-!- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosy1}(N)-acceptor =
                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00023; ank; 19. Pfam; PF00536; SAM; 1.
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subcellular distribution of SLC2A4/GLUT4-vesicles. Has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at human telomeres.";
Mol. Cell. Biol. 22:332-342(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002110; ANK. InterPro; IPR001660; SAM.
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                                                                                                                                                                                                            fransferase; Glycosyltransferase; NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOId=O95271-2; Sequence=VSP_004538, VSP_004539;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Ubiquitous; highest levels in testis.
PTM: Upon insulin-stimulation, phosphorylated on serine by MAPK kinases.
PTM: ADP-ribosylated (-auto).
SIMILARITY: Belongs to the PARP family.
SIMILARITY: Contains 15 ANK repeats.
SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nicotinamide + {ADP-D-ribosyl}{(N+1)-acceptor.

SUBNNTT: Oligomerizes and associates with TWKS2. Interacts with the Cytoplasmic domain of LNPEP/Otase in SLC2A4/GLUT4-vesicles. Binds to the N-terminus of telomeric TRF1 via the ANK repeats. SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and with juxtanuclear SLC2A4/GLUT4-vesicles. A minor proportion is also found at nuclear pore complexes and around the pericentriolar matrix of mitotic centromeres. During interphase, a small fraction of TNKS is found in the nucleus, associated with TRF1.

ALTERNATIVE PRODUCTS:

Event-Alternative splicing; Named isoforms=2;
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polymerases tankyrase 1 and
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activity;
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                                                                                                                                                                                                                  MEDLINE=95021209; PubMed=7935398; Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.; "Multiple products from the shavenbaby-ovo gene region melanogaster: relationship to genetic complexity."; mol. Cell. Biol. 14:6809-6818(1994).
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01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ovo protein (Shaven baby protein).
OVO OR SVB.
Drosophila melanogaster (Fruit fly).
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P51521; Q9XZ
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01-OCT-1996
10-OCT-2003
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Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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          FUNCTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF I
LINE CELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION.
SUBCELLULAR LOCATION: Nuclear (Potential).
DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND
ACCUMULATES IN NURSE CELLS DURING OFFENERIES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA
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Pred. No. 3.3;
15; Mismatches
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/MISSING (IN 1SOCTOM 2).
/FTIG=VSP_004539.
H->A: LOSS OF ACTIVITY; WHEN ASSOCIATED WITH A-1291.
E->A: LOSS OF ACTIVITY; WHEN ASSOCIATED WITH A-1184.
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        APPEARS IN THE GERMARIUM AND DURING COGENESIS. STORED IN
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PROSITE; PS00028; ZÏNC_FINGER C2H2 1; 3.

PROSITE; PS50157; ZINC_FINGER C2H2 2; 3.

Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;

Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSFAC; T00669; ... F1yBase; FBqn0003028; ovo.
F1yBase; FBqn0003028; znf C2H;
InterPro; IPR007087; Znf C2H2; 3.
SMART; SM00355; Znf C2H2; 4.
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EMBL; X59772; CAB36921.1; ALT_SEQ.
PIR; A56038; A56038.
HSSP, P07248; 2ADR.
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                                                                                                                     Similarity
                        ARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNS
                                                                         LLKVAAFAAIVVSG$ALAGVVPQWGGGGNHNGGGNS$GPDSTL$IYQYGSANAALALQSD
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C2H2-TYPE 1.
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C2H2-TYPE 3.
C2H2-TYPE 4.
A --> R (IN REF. 2).
MW; D7068BB2BC0F6F77 CRC64;
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                                                                                                      Score 91; DB Pred. No. 3; 8; Mismatches
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SEQUENCE FROM N.A.

SETRAIN=TY2 / ATCC 700931;

MEDLINE=22531367; PubMed=12644504;

MEDLINE=22531367; PubMed=12644504;

MEDLINE=22531367; PubMed=12644504;

Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;

"Comparative genomics of Salmonella enterica serovar Typhi strains and CT18.";

J. Bacteriol. 185:2330-2337(2003).

J. Bacteriol. 185:2330-2337(2003).

-i- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI.
-COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWT TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entitles requires a license agreement (See http://www.isb-sib.ch/aror send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Whitehead S., Barrell B.G.; "Complete genome sequence of a enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21534947; PubMed=11677608; Parkhill J., Dougan G., James K.D., Churcher C., Mungall K.L., Bentley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
Enterobacteriaceae; Salmon
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                      Fimbria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 413:848-852(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minor curlin subunit precursor. CSGB OR STY1180 OR T1777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration and the EMBL outstation and the Swiss Institute of Bioinformatics and the EMBL outstation on it.

There are no restrictions on it is in no we
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                                                                                                                                                                                                                                                                              l Similarity
33; Conserv
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                                                                                                         MAHASVMVRQ 139
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                                                                                                                                           ISQSAYGNSA---
                                                                                                                                                                            ITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRVVTHE
                                                                                                                                                                                                             ARVRQEGSKLLSVISQ--EGENNRAKVDQAGNYNFAYIEQTGNAN
                                                                                                                                                                                                                                                                                                                                                     151 AA;
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16254 MW;
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Salmonella.
                                                                                                                                                                                                                                                                                                11.7%;
25.4%;
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Pred. No. 0.36
17; Mismatches
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; 161C54326E573495 CRC64;
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                                                                                                                                                                                                                                                                                                .36;
                                                                                                                                                                                                                                                                                                                    BB
                                                                                                                                                                                                                                                                                                                  1; Length 151;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93196482; PubMed=8450754;
Peixoto A.A., Campesan S., Costa R.H.,
"Molecular evolution of a repetitive r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol.
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Drosophila willistoni (Fruit fly)
Drosophila willistoni (Fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Beoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Penhodroidea: Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PER_DROWI STANDARD: PRT; 1093 AA QO3297; O18421; O18422; P91721; P91722; O1-OCT-1993 (Rel. 27, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Interspecific and intraspecific comparisons of the period locus the Drosophila willistoni sibling species.";
                                                                                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gleason J.M., Powell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Various strains;
MEDLINE=97357421; PubMed=9214747;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PER-TIM (BY SIMILARITY)
MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAIN ATI
SIMILARITY: Contains 2 PAS (PER-ARNY-SIM) dimerization
SIMILARITY: Contains 1 PAS-associated C-terminal (PAC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translocates into the nucleus (By similarity).
SUBCELLULAR LOCATION: Nuclear at specific periods of the
First accumulates in the perinuclear region about one hou
translocation into the nucleus. Interaction with Tim is r
for nuclear localization (By similarity).
FTM: PHOSPHORYLATED WITH A CIRCADIAN RHYTHMICITY, PROBABL
DOUBLE-TIME PROTEIN (DBT). PHOSPHORYLATION COULD BE IMPLI
THE STABILITY OF DER MONOMER AND IN THE FORMATION OF HETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rhythmic component of the male courtship song that originates in the thoracic nervous system. The biological cycle depends on the rhythmic formation and nuclear localization of the TIM-PER complex. Light induces the degradation of TIM, which promotes elimination of PER. Nuclear activity of the heterodimer coordinatively regulates PER and TIM transcription through a negative feedback loop. Behaves are negative element in circadian transcriptional loop. Does not appear to bind DNA, suggesting indirect transcriptional inhibition (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       period length of circadian and ultradian rhythms; an increase in PER dosage leads to shortened circadian rhythms and a decrease leads to lengthened circadian rhythms. Essential for the circadian rhythmicity of locomotor activity, eclosion behavior, and for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Evol. 10:127-139(1993).
FUNCTION: Essential for biological clock functions.
                   US1057;
US1058;
US1059;
US1060;
US1061;
US1062;
US1063;
                                                                                                                                                                                                            U51055;
U51056;
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                                                                      AAB41360.1;
AAB41361.1;
AAB41362.1;
AAB41363.1;
AAB41364.1;
AAB41365.1;
AAB41366.1;
                                                  AAB41367
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EMBL; U51066; AAB41371.1; --
EMBL; U51067; AAB41372.1; --
EMBL; U51068; AAB41373.1; --
EMBL; U51069; AAB41374.1; --
EMBL; U51070; AAB41375.1; --
EMBL; U51071; AAB41375.1; --
EMBL; U51072; AAB41377.1; --
EMBL; U51072; AAB41377.1; --
EMBL; L06342; AAAB4755.1; --
EMBL; L06342; AAAB4755.1; --
EMBL; L06342; AAAB4755.1; --
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InterPro; IPR000014; PAS_domain.
Pfam; PF00999; PAS; 2.
SMART; SM00091; PAS; 2.
PROSITE; PS50112; PAS; 2.
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         recognizing
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                                                                                                                                              GGGGGGGGGGGGLPLFLDVTHTSS-----SSONKGPTGVAAGGAGGGVGGGGG--
                                                                                                                                                                  GGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGAD
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1093
1093
                   (Rel.
                                                                                                                                                                                           Conservative
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733
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718
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617
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724
                                                                                                           --SCSGLGGNGNVGSGNGNNSQPSTNQYTQ
                                                            STANDARD;
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27.7%;
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ALEGRE 1 AND PORTO ALEGRE 2).
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MISSING (IN STRAIN MANAUS 3).
A -> T (IN STRAIN 0811.4).
                   annotati
                           sequence
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PAS 2.

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POLY-LYS.

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POLY-SER.

POLY-ALA.

POLY-ALA.

POLY-ALA.

T -> A (IN STRAIN 0811.4).

S -> F (IN STRAIN 0811.4).

G -> V (IN STRAIN MANAUS 2).

G -> A (IN STRAIN SANTA MARIA).

G -> A (IN STRAIN SANTA MARIA).

MISSING (IN STRAIN PORTO ALEGRE 3).

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MISSING (IN STRAIN SANAUS 1 AND MANAUS 3).

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        (Protein
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Pred. No. 3
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; Mismatches
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MISSING (IN STRAINS GUADELOUPE, MA)
PORTO ALEGRE 2, PORTO ALEGRE 1 AND
                                                           PRT;
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                                                                                                                                                                                                                               AB6DE050267EC187 CRC64;
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                           update)
      update)
1 Gp38).
                                                         262
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3.9;
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                                                                                                           798
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                                                                                                                                                                                                          Length 1093;
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PRTC_ERWCH
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01-AUG-1990
01-NOV-1991
10-OCT-2003
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Delepelaire P., Wandersman C.;
"Protein secretion in Gram-negative bacteria. The ext
metalloprotease B from Erwinia chrysanthemi contains
secretion signal analogous to that of Escherichia col
                      MEDLINE=89255387; PubMed=2722818; Delepelaire P., Wandersman C.;
                                                                  STRAIN=B374;
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Enterobacteriaceae; Pectol
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Viruses; dsDNA v
T4-like viruses.
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Riede I., Drexler K., Eschbach M.L., Henning U.;
Riede I., Drexler K., Eschbach M.L., Henning U.;
"DNA sequence of genes 38 encoding a receptor-recognizing bacteriophages T2, K3 and of K3 host range mutants.";
J. Mol. Biol. 194:31-39(1987).
-i- FUNCTION: V938 is at the tip of the long tail fibers a the phage recognition site for the cellular receptor.
-i- MISCELLANEOUS: THIS PHAGE USE OUTER MEMBRANE PROTEINS
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EMBL; M59229; AAA24860.1; -.
EMBL; J04736; AAA24862.1; -.
EMBL; M60395; AAA63638.1; -.
PIR; A38307; A38307;
PDB; 1GO7; 17-OCT-02.
PDB; 1GO8; 17-OCT-02.
PDB; 1K70; 19-OCT-02.
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Hydrolase; Metalloprotease; Calcium-binding;
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Pfam; PP00353; hemolysinCabind; 3.
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264:9083-9089(1989).
3inds 1 zinc ion and 7 calcium ions per subunit (B
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SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAILNE=93149206; Pub Medina-Acosta E., Kar "Structurally distinc mexicana are developm Mol. Biochem. Parasit -i- FUNCTION: Has an in the mammalian -i- CATALYTIC ACTIVIT -i- Pl' and basic res cleaved at -Ala-T -i- COFACTOR: Binds 1 -i- DEVELOPMENTAL STA	STA 1. 1. 1. 21. gly gly	TVAAYDWIAD TVAAYDWIAD VVTHEMAHAS	Similarity 28 0; Conservativ GGGGNHNGGGNSSG	365 366 368 372 373 373 375 377 381 382 382 383 384 386 386 402 402 412 412 412
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10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv1548c/MT1599,
RV1548C OR MT1599 OR MTCY48.17.
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Pfam; PF01457; Peptidase_M8; 1.
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SIMILARITY: Belongs to peptidase family M8.
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A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Ha
A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
A Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holr
A Hornsby T., Jagels K., Krogl N., McLean J., Moule S., Murphy I
A Hornsby T., Jagels K., Krogl N., McLean J., Moule S., Murphy I
A Hornsby T., Jagels K., Krogl N., Rajandream M.A., Rogers J.,
A Hornsby T., Jagels K., Krogl N., Rajandream M.A., Rogers J.,
A Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
A Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Bulston J.E., Taylor K., Whitehead S., Barrell B.G.,
T "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.",
I Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002989;
Pfam; PF00169; Pentag
Pfam; PF00823; PPE;
Hypothetical protein
TRANSMEM 14
TRANSMEM 180 20
CONFLICT 258 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
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TIGR; MT1599; -.
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EMBL; AE007026; AAK45866.1;
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg & Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000030; Microbac_PPE.
InterPro; IPR002989; Mycobac_pentapep.
Pfam; PF01469; Pentapeptide_2; 11.
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J. Bacteriol. 184:5479-5490(2002).
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STRAIN=CDC 1551 /
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SEQUENCE FROM N.A.
MEDLINE-92112918; Pubmed=1370484;
The property R., Donelson J.E., Pa
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J. Biol. Chem. 267:1888-1895(1992).
-!- FUNCTION: Has an integral role during the infection of macrophages
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"Leishmania gp63 molecule implicated
Arg-Gly-Asp sequence.";
Mol. Blochem. Parasitol. 39:267-274(1
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Eukaryota; Euglenoz
NCBI_TaxID=44271;
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InterPro; IPR001577; PeptIdase_M8.
Pfam; PF01457; Peptidase_M8; 1.
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EMBL; M28527; AAA29235.1;
PIR; A44951; A44951.
HSSP; P08148; 1LML.
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COPACTOR: Binds 1 zinc ion per subunit (By similarity).
SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to peptidase family M8.
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ignal; Cell adhes:
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     adhesion;
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RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Torium M.J., Town C.D.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
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MEDLINE-22954850; PubMed=14593172;

MEDLINE-22954850; PubMed=14593172;

Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

Yamada K., Lim J., Dale J.M., Chen M., Pham P.K., Cheuk R.F.,

Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

Kiranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

Chao Q., Choy N., Enju A., Goldamith A.D., Gurjal M., Hansen N.F.,

Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

Khan S., Koesema E., Ishida J., Jiang P.X., Johnes T., Kawai J.,

Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    development.";
EMBO J. 17:170-180(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Columbia; TISSUB-Leaf;
MEDLINE=98090460; PubMed=9427751;
Bohmert K., Camus I., Bellini C.;
"AGO1 defines a novel locus of Ara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatophyta; Magnoliophyta; eudicotyle eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Argonaute protein.
AGO1 OR AT1G48410 OR F11A17.3 OR T1N15
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15-MAR-2004 (Rel. 43, Last annotation updat
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of Arabidopsis controlling leaf
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edons; core eudicots; rosid
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                                                                                                                                             M.J.,
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Search completed: March 11, 2004, 18:34:54 Job time : 8.3 secs
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Best Local S
Matches 36
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DOMAIN
SEQUENCE
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Science 302:842-846(2003).
Science 302:842-846(2003).
-i-FUNCTION: Essential for proper development of leaves and floral organs, and formation of axillary meristems.
-i-SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-i-ALTERNATIVE PRODUCTS:
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-!- SIMILARITY: Belongs to the argonaute family.
-!- SIMILARITY: Contains 1 PAZ domain.
-!- SIMILARITY: Contains 1 Piwi domain.
-!- CAUTION: Ref. 2 (AAF79718) sequence differs from that shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50821; PAZ; 1.

PROSITE; PS50822; PIWI; 1.

Developmental protein; Alternative splicing.

DOWALN 391 501 PAZ.

DOMAIN 676 997 PIWI.

DOMAIN 13 104 GLY-RICH.
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-!- TISSUE SPECIFICITY: Widely expressed at low levels.
-!- DEVELOPMENTAL STAGE: Expressed throughout all developmental
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                                                                                                             214 TITPEVTSRGVNRAVMKOLV 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                EQLSVEQGAPSQAIQPIPSSSKAFKFPMRPGKGQSGKRCIVKANHFFAELPDKDLHHYDV 213
                                                                                                                                                                                                                                                                                          NGADVGQGADNSTIB-------TQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                             LVTRVVTHEMAHASVMVRQV 140
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1048 AA; 116190 MW; 3E5146343A09C541 CRC64;
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25.7%;
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Listing first 45
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Perfect score:
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2: sp_bacteria:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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sp_organelle:*
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Q8cw63 escherichia
Q7x237 enterobacte
Q54069 salmonella
Q983j5 escherichia
Q3801 salmonella
Q7x238 enterobacte
Q8eih3 shewanella
Q7x241 citrobacter
Q8cw64 escherichia
Q7x244 citrobacter
Q8cw64 escherichia
Q7x244 citrobacter
Q8cx64 shewanella
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Q7ucz1 shigella fl
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Q7x243 citrobacter
Q7x240 citrobacter
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.9	12.0	12.0	12.1	12.1	12.2	12.3	12.3	12.3	12.4	12.4	12.4	12.5	12.5	٠	12.5	٠	•	•	13.0
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Q7XDR3	Q8U6N9	Q8MPN4	Q8SX56	Q8T8L9	Q9W4F0	Q9NGF7	Q9NGF6	Q9XIL0	Q9N6M8	Q92UU8	Q89EV2	Q8EWD6	Q89JI,3	Q8TFA6	Q94821	Q7V8S5	QBNIV1	Q9P3I9	Q88HG0	Q89JI5	Q8XSD6	90TA8Ö	Q8EFU3	Q8VIY0	Q7TW76	P96840	093397	Q8EV84
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Best Local Similarity 89.4%;
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Infect. Immun. 65:5320-5325(1997).
EMBL; AJ000514; CAA04151.1; -.
NON TER 152 152
NON TER 152 152
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MEDLINE=98053981; PubMed=9393832;

Sukupolvi S.S., Lorentz R.G., Gor.

Normark S.J., Rhen M.;

"Expression of thin, aggregative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Expression of thin, aggregative fimbriae promotes interaction of Salmonella typhimurium SR-11 with mouse small intestinal epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
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                                                                                                               SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ
                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSAVAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                     MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 1.2e-47;
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                                                                               Zogaj X., Bokranz W., Nimtz M., Romling U.;
"Production of Cellulose and Curli Fimbriae by Members
Enterobacteriaceae Isolated from the Human Gastrointest
Infect. Immun. 72:4151-4158 (2003).
EMBL; AJ515701; CAD56675.1;
                                                                                                                                                                            Citrobacter freundii
Bacteria; Proteobacteria; Gammap
Enterobacteriaceae; Citrobacter
                                                                                                                                       STRAIN=Fec4
                                                                                                                                                                    Enterobacteriaceae;
NCBI_TaxID=546;
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EMBL; AJ515700; CAD56672.1; -. SEQUENCE 150 AA; 15016 MW; 1D7141B8D6973DC6 CRC64;
                                               Local
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Bacteria; Proteobacteria; Gammap
Enterobacteriaceae; Citrobacter.
                                                                                                                                                 EQUENCE FROM N.A.
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01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                Similarity
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MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                    Conservative
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76.8%;
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                                Score 533; DB
Pred. No. 1.7e
20; Mismatches
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Last
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Pred. No. 3.7
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3; Mismatches
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1.7e-35;
22;
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Best Local 9
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01-OCT-2003
01-OCT-2003
      STRAIN=Fec39;
Zogaj X., Bok
                                           SEQUENCE FROM N.A.
                                                                                                       Enterobacteriaceae;
                                                                                                                         Enterobacter sakazakii.
Bacteria, Proteobacteria,
                                                                                                                                                                                   Curlin-csgA protein.
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MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Ro Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett Moyhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete ge of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
EMBL; AE016759; AAN79779.1; -
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Enterobacteriaceae; Escherichia.
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"Virulence of Salmonella enteritidis in chickens correlates
colony morphology and expression of SEF17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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Infect Immun. 72:4151-4158 (2003).
EMBL; AJ515702; CAD56678 1;
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O1-JAN-1998
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Normark S.J., Rhen M.;
"Expression of thin, a
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La Ragione R.M., Collighan R.J., Woodward M.J.;
"Non-curliation of Escherichia coli O78:K80 isolates associated with
IS1 inserti on in cggB and reduced persistence in poultry infection.";
FEMS Microbiol. Lett. 175:247-253(1999).
EMBL; AJ131756; CAB45380.1; -.
                                                                                                                                                                                                             SEQUENCE
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MEDLINE=98053981; PubMed=9393832;
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Bacteria; Proteobacteria;
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AGFB.
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EMBL; AJ000514; CAA04150.1; -.
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Meldine=2297686; PubMed=12368813;
Meidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
"Genome sequence of the dissimilatory metal ion-reducing bacterium
Nat. Biotechnol. 20:1118-1123(2002).
                                                                                                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 139 AA;
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"Production of Cellulose and Curli Fimbriae by Members of the Enterobacteriaceae Isolated from the Human Gastrointestinal Infect. Immun. 72:4151-4158 (2003).

EMBL; AJ515702; CAD56677.1; -.
SEQUENCE 151 AA; 15985 MW; FOB82BD2A27882B7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 23, 1)
(TrEMBLrel. 23, 1)
(TrEMBLrel. 23, 1)
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subunit
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                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shewanella.
                                                                                                                                                                                                                                                                                                     14811 MW; 41EC1CFA76957920 CRC64;
                                                                                                                                                                                                                                     13.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15985 MW; F0B82BD2A27882B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CsgB, putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.9%; Score 107.5; D; 30.8%; Pred. No. 0.31; tive 14; Mismatches
-IGN-DNLVQ---LNQLGSGNFSIQQIADGAAISITQY
                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gammaproteobacteria; Alteromonadales;
                                                                                                                                                                                                     Score 105; DB 1
Pred. No. 0.45;
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----KIIOKGSGNRANITOYGTOKTAVVVOKOSOMAIRVI
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Best Local !
                                                                                                                                                                                                                                                                                   "Extensive mosaic structure revealed by the complete of uropathogenic Escherichia coli."; Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002). EMBL; AE016759; AAN79778.1; -
                                                                                                                                                                                                                                                                                                                                                                     STRAIN=06:H1 / CFT073 / ATCC 700928;

MEDLINE=22388234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., &
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.,
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Q8CW64;
01-MAR-2003
                                                                                                                                                                                                                                                     SEQUENCE
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01-MAR-2003 (TrEMBLrel. 23, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
Construction subunit precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=217992;
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Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli 06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSGB OR C1305
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"Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158(2003).
EMBL; AJ515701; CAD56674.1; -.
                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriaceae;
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                                                              42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 SNDÁSIKQGSYGNTAVIIQKGSGNKANITQYGTQKTAVVVQRQSQMAIRV
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                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                           proteome.
SETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRV 125
                                            FAVNELSKSSFNQAAII----GQAGTNNSAQLRQGGSKLLTVVAQEGSSNRA-KIDQTGDY
                                                                                      FAAIVVSGSAL--AGVVPQWGGGGNHNGGGNSSGPDSTLSIY-QYGSANAALALQSDARK 65
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                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
component of curlin monomers.
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AA; 16149 MW;
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                                                                                                                                                  19;
                                                                                                                                           Score 104.5; DB
Pred. No. 0.58;
19; Mismatches
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Pred. No. 0.55
L3; Mismatches
                                                                                                                                                                                                                                         49F68448D979B986 CRC64;
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Nat. Biotechnol. 20:1118-1123 (2002).
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NCBI_TaxID=70863;
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STRAIN=2457T / ATCC 700930 / Serotype
MEDLINE=22590274; PubMed=12704152;
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EMBL; AJ515700; CAD56671.1; -.
SEQUENCE 151 AA; 16158 MW; BD0
                                                                                                                                                                                                                                                                                                                                                                                                                                       flexneri serotype 2a strain 2457T.";
Infect. Immun. 71:2775-2786(2003).
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32; Conservative
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28.8%;
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Pred. No. 0.65
20; Mismatches
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Maximum
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Perfect score:
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18
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geneseqp2003as:*
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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FNB curli
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Aab36331	Abu44579	Aae36890	Abr82647	Aab36328	Aab36336	Aab36323	Aae36891	Aaw32312	Abr82645	Abr82649	Aab36319	Aab36324	Aab36340	Aab36337	Aab36327	Aab36322	Aab36342	Aab36320	Aab36339
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ALIGNMENTS

RESULT 1
AAB36348
ID AAB3
XX

AAB36348 standard;

protein;

151

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AAB36348;

26-FEB-2001

(first entry)

AgfA::PT3#3 amino acid sequence

SEQ

ij

NO:16

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WPI; 2000-672631/65.
N-PSDB; AAC64624.
                                                                                                          White AP,
                                                                                                                                                      12-OCT-2000.
                                                                                                                                                                           Synthetic.
                                                                                                                                                                                      Salmonella enteritidis.
                                                                                                                                                                                                      Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                05-APR-1999;
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                                                                                                                                                                WO200060102-A2
                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                vaccine; immune response;
                                                                                                                     (UYVI-) UNIV VICTORIA.
                                                                                                          Doran JL,
                                                                                                                                99US-0127888P
                                                                                                          Collison
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                                                                                                          SX,
                                                                                                          Kay WW;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombination of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 136; 139pp; English.

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RESULT 2
AAR74625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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Best Local
                                                   Eliciting an immune response strains, vector constructs, c
                                                                                              N-PSDB; AAQ87467
                                                                                                                                                                                                              26-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                               AgfA sequence
                                                                                                                                                                   (UYVI-) UNIV VICTORIA INNOVATION & (KING/) KING J.
                                                                                                                                                                                                                                                                                                                                                   Salmonella; AgfA; vaccine.
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26-JUN-1995
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Pred. No. 2.2e-67;
Mismatches 0;
                                                                 Salmonella
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                                                  using attenuated Salmonella
g. fimbrial type proteins.
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The

Salmonella AgfA protein and DNA are used

in vaccine

and genetic

Disclosure; Fig

7B;

95pp; English.

or Or

compsns.

contg.

type

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RESULT 3
AAB36341
ID 36341
ID 36353
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            The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SERI//TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA. CegA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native compositing separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino
   protein containing acid sequence or so
                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-672631/65.
N-PSDB; AAC64617.
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The present sequence represents agfA encoded derived from Salmonella enteritidis 27655-3b.
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                            The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA seguence which encodes a foreign epitope or antigen. Also described a segment of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and system of strains of Salmonella, Escherichia comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprising recombinate comprisi
                                                                                                                                                                                                                                                                                                                                                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                             Disclosure; Page 136; 139pp; English.
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N-PSDB; AAC64625.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
AgfA-homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
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89.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collison
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Pred. No. 5.1e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kay
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                            recombinant
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                                                                                                                                                        are:
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protein useful for eliciting

immune response in animal

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RESULT 6
AAB36346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA comprising a replacement segment or segments of foreign amino acid golymer comprising a recombinant AgfA cold sequence or sequences grown on a Salmonella, E. coli or comprising a recombinant AgfA cold sequence or sequences grown on a Salmonella, E. coli or cold sequence or sequences grown on a Salmonella, E. coli or the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for constant for the expression of recombinant AgfA protein which is useful for gystem the heterologous antigens are presented in high numbers (up to complete/cell), the hybrid fimbrin protein possesses both the communogens, which may be important for directing an immune response constant the inserted epitope, and hybrid fimbriae are usually strong constant the inserted epitope, and hybrid fimbriae are easy and the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 131;
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Best Local
WPI; 2000-672631/65.
N-PSDB; AAC64622.
                                                             White AP,
                                                                                                                                               05-APR-1999;
                                                                                                                                                                                         05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                   12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                     (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                           WO200060102-A2
                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                          Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                vaccine; immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AgfA::PT3#1 amino acid sequence SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB36346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB36346 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGV--------YDQLVTRVVTHEMAHASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATIDOWNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                           Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAH---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                             99US-0127888P
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76.6%;
                                                           Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 618;
Pred. No. 1
                                                           SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                         Кау
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
.6e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
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                                                                                                                                                                                                                                                                             Query Match
Best Local Simi
Matches 121;
                                                                                                                                                                                                                                                                                                                                                                                immunogens, which may be important. The present sequence is given inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                         Sequence 151
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    121
                                                121
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                                                                                                                                       61
                                                                                                                                                                                                           1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                     Similarity
                                      NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
NNAALVNYDOLVTRVVTHEMAHANNATANOY 151
                                                                                    SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                            MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                         A.
                                                                                                                                                                                                                                                                                                76.6%;
                                                                                                                                                                                                                                                                     Score 580; DB 3; L
Pred. No. 9.8e-50;
                                                                                                                                                                                                                                                                                                                 Length 151;
                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                        Gaps
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RESULT 7
AAB36347
AgfA::PT3#2
                                                                        26-FEB-2001
                                                                                 AAB36347;
                                                                                          AAB36347 standard; protein; 151
                                                              amino acid sequence SEQ ID NO:14.
                                                                       (first entry)
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05-APR-2000; 2000WO-CA000356 Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; Escherichia coli. Synthetic. Salmonella enteritidis. 12-OCT-2000 WO200060102-A2 vaccine; immune response; immunogen

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA

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ARBJ6353
ID AABJ
XX
AC AABJ
XX
DT 26-F
XX
XX
DE AGEA
XX
XX
VACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene cc back into the chromosome of the homologous species, replacing the native compyrising separating an amino acid polymer comprising a recombinant AgfA cromprising separating an amino acid polymer comprising a recombinant AgfA cromprising sequences grown on a Salmonella, E. coli or enterobacteriaceae host cell, from the host cell and introducing the colymer into the animal in conjunction with a carrier or diluent. (1) is cusful for the expression of recombinant AgfA protein which is useful for the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the carrier fimbrial subunit proteins are usually strong companient the inserted epitope, and hybrid fimbriae are usually strong consensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 151 AA
               Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                      AgfA::PT3#8 amino acid sequence SEQ ID NO:26
                                                                                                                                                                   AAB36353 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SER17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein useful for eliciting immune response in animal.
                                                                                             26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                      121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                              LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                            SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                    SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                         (first entry)
response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.4%;
80.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 578; DB 3; Pred. No. 1.5e-49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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                                                                                                                                                                                                                                                           Matches 122;
                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                             Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAC64629
                                                                                                                                                                                                                                                                                                                                                                                        the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                           nexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
121
                                        121
                                                                                   61
                                                                                                                                                                                                                μ
                                                                                                                                                                                                                                                                                Similarity
                                        NNAALVNOTASDSSVMVROVGFGNNATANOY 151
                                                                                                                          SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                MKILKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                     MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Doran JL,
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0127888P
                                                                                                                                                                                                                                                                         76.2%;
80.8%;
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                                                                                                                                                                                                                                                                                                                                                                                        present invention
                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                         Score 577; DB 3; Length 151.
Pred. No. 1.9e-49;
5; Mismatches 24; Indels
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                                                                                                                                                                                            CC assembly system of strains of Salmonella, Escherichia coli and CR Enterobacteriaceae for the production of fimbriae comprising recombinant CR Agfa, CsgA and Agfa-homologue fimbria subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immure response in an animal, CC comprising as replacement segment or segments of foreign amino acid polymer comprising a recombinant Agfa coli sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the useful for the expression of recombinant Agfa protein which is useful for copiumer into the animal in conjunction with a carrier or diluent. (I) is celliciting an immure response in an animal. In a fimbrial presentation composes/celly, the hybrid fimbrin protein possesses both the immunogens, which may be important for directing an immune response conspines the inserted epitope, and hybrid fimbriae are usually strong immunogens, which may be important for directing an immune response conspines the inserted epitope, and hybrid fimbriae are easy and conspined the presention of the present sequence is given in the presention of the presention of the presention. The present sequence is given in the presention of the presention of the presention of the presention.
                                                                                     Matches
                                                                                                                        Query Match
                                                                                                                                                         Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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N-PSDB; AAC64628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AgfA::PT3#7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB36352 standard; protein;
                                                                                                       Local
                                                                                     123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΑP,
                                                                                                     Similarity
                                   MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agfA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosomal gene replacement; fimbrin; epitope;
                                                                                                 76.0%;
81.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collison SK,
                                                                                                                                                                                          present invention
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                                                                                 5
                                                                             Score 575; DB 3;
Pred. No. 3.1e-49;
5; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO:24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kay WW;
                                                                                                                Length 151;
                                                                               Indels
                                                                           0;
                                                                           Gaps
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directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA (2) comprising separating an amino acid polymer comprising a recombinant AgfA (3) containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or miterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong against the inserted epitope, and hybrid fimbrine are easy and inexpensive to purify in large amount. The present sequence is given in
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AAB36350
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                                                                                                                                                                                                                                                                                                                                     The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF1/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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N-PSDB; AAC64626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella enteritidis.
Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDARKSETTÍTÓSGYGNGADVGÓGADNSTÍBLTÓNGFRNNATÍDÓWNAKNYDÓLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ımmunogen.
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Best Local Simi
Matches 122;
The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella Escherichia coli and Enterobacteriaces for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 138; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AgfA::PT3#9 amino acid sequence SEQ ID NO:28
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)B; AAC64630.
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80.8%;
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Pred. No. 3.9e-49;
6; Mismatches 23
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XW WO200
XW SO-AF
XW WO210
XW UVVI
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XW WPI;
DR WPSI
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DR WPSI
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DR WPSI
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Best Local S
Matches 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                      05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the exemplification of the present invention
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                                                                                                                                                    2000-672631/65.
DB; AAC64627.
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The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign DI sequence which encodes a foreign epitope or antigen. Also describe

foreign DNA so described

Disclosure; Page 137; 139pp; English

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

N-PSDB; AAC64631.

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RESULT 13
AAB36355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC assembly system of strains of Salmonella, Escherichia coli and CE Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the CE homologous species; (3) directing recombinant gene into the chromosome of the back into the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E coli or CC eliciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to System the heterologous antigens are presented in high numbers (up to immunogenicity and adhesion properties relevant for an efficient live CC vaccine, the carrier fimbrial subunit protein passesses both the carrier fimbrial subunit proteins are usually strong CC immunogens, which may be important for directing an immune response consists the inserted epitope, and hybrid fimbriae are usually strong the inserted epitope, and hybrid fimbriae are easy and conspensive to purify in large amount. The present sequence is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
WPI; 2000-672631/65
                                                      White AP,
                                                                                                                                                                      05-APR-1999;
                                                                                                                                                                                                                       05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                                                                                      12-OCT-2000
                                                                                                                                                                                                                                                                                                                                             WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                       synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                             (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AgfA::PT3#10 amino acid sequence SEQ ID NO:30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB36355 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ımmune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDARKSETTITOSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                   Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                      99US-0127888P
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80.8%;
                                                      Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 567; DB Pred. No. 1.9e-5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>5</u>
                                                   SK,
                                                   Kay WW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
.9e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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AgfA sequence

10-NOV-1994 WO9425598-A2. Salmonella enteritidis Salmonella; AgfA; vaccine 27-AUG-2003 25-MAR-2003 26-JUN-1995

(revised) (first entry) (revised) AAR62761;

AAR62761 standard; protein; 120 AA

RESULT 14

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                                                                                                                                                                                                                                                                                                                                                        CC Agfa, CspA and Agfa homologue fimbrin subunits, respectively; (2)
CC directing recombination of a recombinant gene into the chromosome of the CC directing recombination of a recombinant gene into the chromosome of the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant Agfa CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, B. coli or CC Enterobacteriaceae host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant Agfa protein which is useful for CC system the heterologous antigens are presented in high numbers (up to CC 500,000 copies/cell), the hybrid fimbrin protein possesses both the carrier fimbrial subunit proteins are usually strong which are immune response in an immune response in an immune response or sequence.
                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 122
                                                                                                                                                                                                                                                                                                                                                        Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 139; 139pp; English.
  121
                                         121
                                                                                                                                                                                                                                                                122;
                                                                                      13
                                                                                                                                61
                                                                                                                                                                                                                                                                                          Similarity
                           NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                      SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
NNAALVNOTASDSSVMVRQVGFGNNATANQY
                                                                                   SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                   74.8%;
                                                                                                                                                                                                                                                                5.
                                                                                                                                                                                                                                                           Score 566; DB 3;
Pred. No. 2.4e-48;
5; Mismatches 24
                                                                                                                                                                                                                                                                24;
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RESULT 15
AAW23569
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Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents the Salmonella enteritis 27655-3b TnphoA mutant strain AgfA protein. The encoding DNA and isolated AgfA protein are used in genetic immunization vaccine ossitions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enteritidis 27655-3b InphoA mutant agfA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 7A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kay WW
                          Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
                                                                                                           WPI; 1997-309886/28
N-PSDB; AAT74141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
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29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW23569;
                                                                                                                                                                                                                                                                                                       26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                              26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW23569 standard; protein; 120 AA.
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                                                                                                                                                                                                                                                (UYVI-) UNIV VICTORIA INNOVATION &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 NSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 HASGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYGQGADNSTIELTQNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95;
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                                                                                                                                                                                            SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
                                                                                                                                                                                                                                                                                                       93US-00054452.
                                                                                                                                                                                                                                                                                                                                                              94US-00233788
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Pred. No. 1.3e-40;
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                                                                                                                                                                                                                              Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents an agfA fragment encoded by an agfA gene fragment derived from Salmonella enteritidis 27655-3b TnphoA mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Fig 7;
                                                                                                                                                                       Local Similarity
                                     97
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                                                                                                 HASGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNG
                                     FRNNATIDOWNAKNSDITYGOYGGNNAALVNOTASDS 133
                                                                             NSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNG
FRNNATIDOWNAKNSDITYGOYGGNNAALVNOTASDS 112
                                                                                                                                                     Conservative
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Search completed: March 11, 2004, 18:33:37 Job time : 46.9 secs

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and is derived by analysis of the total score distribution.
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US-09-233-681A-26438
US-09-252-991A-26438
US-09-252-991A-26438
US-09-262-991A-2648B-7
US-08-614-377A-7
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US-09-336-115C-6
US-09-336-115C-6
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  Sequence 59, Appl
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Query Match Query Match Best Local Similarity Best Local Similari	In Release # DATA: DATA: US/08/23 APR-1994 435 BER: 35,570 NUMBER: 920 NUMBER: 920 NEORMATION: 622-4900 182-6031 SEEDANBERRY INC: 59: STICS: TO acids classing acids classi	-08-233-788A-59 sequence 59, Application US/08233788A Patent No. 5635617 GENERAL INFORMATION: APPLICANT: Doran, James L. APPLICANT: Kay, William W. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Clouthier, Sharon C. APPLICANT: Collinson, Geren S. APPLICANT: Collinson, OF SALMONELLA NUMBER OF INVENTION: OF SALMONELLA NUMBER OF SEQUENCES: 61 CORRESPONDENCE ADDRESS: ADDRESSE: Seed and Berry STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle STATE: Washington COUNTRY: U.S.A. ZIP: 98104-7092 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk MEDIUM TYPE: Floppy disk OPERATING SYSTEM: PC-DOS/MS-DOS	28 78 10.3 1864 2 US-08-804-227C-3 29 77.5 10.2 518 3 US-09-043-123-2 30 77.5 10.2 2314 4 US-09-268-347-49 30 77.5 10.2 2314 4 US-09-268-347-49 31 77 10.2 1612 1 US-08-169-297-2 32 77 10.2 1612 1 US-08-169-297-2 33 76.5 10.1 892 4 US-09-134-001C-3159 34 76.5 10.0 273 4 US-09-328-352-6167 36 76 10.0 741 4 US-09-328-352-6167 37 76 10.0 906 1 US-08-687-379-2 38 76 10.0 906 1 US-08-687-379-2 40 76 10.0 906 1 US-08-687-379-4 41 76 10.0 906 4 US-08-687-379-4 42 76 10.0 906 4 US-08-172-332-1 43 76 10.0 906 4 US-08-163-26-204 44 76 10.0 943 4 US-09-072-596-199 45 75 9.9 359 4 US-09-328-352-6562 45 75 9.9 359 4 US-09-328-352-6562
Indels 0; Gaps		DETECTION	sequence 3, Appli sequence 2, Appli sequence 32096, A sequence 32096, A sequence 3159, Ap sequence 5, Appli sequence 6167, Ap sequence 7854, Ap sequence 2, Appli sequence 2, Appli sequence 4, Appli sequence 2, Appli sequence 2, Appli sequence 2, Appli sequence 204, App sequence 204, App

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Sequence 5434, Application US/09543681A Patent No. 6605709 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920
TELECOMMUNICATION INFORMATION: (206) 622,4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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FILING DATE: 26-APR-1994
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                                                                                                              FRNNATIDQWNAKUSDITVGQYGGNNAALVNQTASDS 133
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                                                                                                                                                                                                                                                                                                                           120 amino acids
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                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Joshua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n, James L.
William W.
                                                                                                                                                                                                                         64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/233,788A
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                                                                                                                                                                                                            Score 487; DB 1;
Pred. No. 2.5e-43;
2; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version
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                                                                                                                                                                                                                                       Length 120;
                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                 ; LENGTH: 943
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-477-135A-131
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                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6572865
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 131, Application US/09477135A
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1995-0
NUMBER OF SEQ ID NOS: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 5434
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1996-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 52888
CURRENT APPLICATION NUMBER: US/09/477,135A
CURRENT FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08990823
PRIOR FILING DATE: 1997-12-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycob
TITLE OF INVENTION: immur
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABII
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION UNUMBER: US 60/128,706
PRIOR PILLNG DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
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TYPE: PRT
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                                                                                                                                                                                                                                            Local
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                                                                           156
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                                                                                                     57 L----ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD 112
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                                                                                                                                                                                                                           39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 DQLYTRVVTHEMAHASGPD-STLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVG
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                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2315
                                                                                                                                         ALFVSLVVSNILGQNAPAIAATEAAYEQMWAQDVAAMFGYHAGASAAVSALTPFGQALPT 155
                                                                                                                                                                            AAFAAIVVSG-----SALAGVYDQLVTRVVTHEMAHASGPDSTLS-IYQYGSANAA 56
                                                                     VAGGGALVSAAAAQVTTRVFRNLGL-ANVGEGN-----VGNGNVGNFNLGSANIGNGN
IGSGNIGSSNIGFGN-VGPGLTAALNNIGFGNTGSNN 243
                                  ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
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Similarity 28.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium Tuberculosis DNA Sequences Encoding immunostimulatory Peptides
                                                                                                                                                                                                                     11.4%; Score 86.5; D
24.8%; Pred. No. 2.4;
tive 22; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 5500353
GENERAL INFORMATION:
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Garvey, George A
REGISTRATION NUMBER: 17737
REFERENCE/DOCKET NUMBER: 5:
                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Smit, John
APPLICANT: Bingle, Wade H
TITLE OF INVENTION: Bacterial surface protein expression
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                   CURRENT APPLICATION DATA:
                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
TELEPHONE:
                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                FILING DATE:
                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                            CITY: Arlington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08194290
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AVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

AVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                            Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                  3000 South Eads Street
  703-684-5600
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                                                                                                                                                                US/08/194,290
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US-08-614-377A-7
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                                                             TELEFAX: 617-542-8906 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: No. 59768
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/194,290
FILING DATE: 09-FEB-1994
ATE: 09-FEB-1994
                                              SEQUENCE CHARACTERISTICS:
                                                                                                           REFERENCE/DOCKET NUMBER: 08
TELECOMMUNICATION INFORMATION:
                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TBAO, Y. ROCKY
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                                                                                                                                                                                                 CLASSIFICATION: 435
APPLICATION NUMBER: US 07/895,367
FILING DATE: 09-JUNE-1992
TYPE: amino STRANDEDNESS:
                                                                                            TELEPHONE:
                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 463 AAATAGATVAGRVNGAVT--ITDSAAASATTAGKIATVTLGSFGAA----TIDSSAL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 NAA--LVNQTASDSSVM 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 TTITQSGYGNGADVGQGA-----DNSTIELTQNGFRNNATI-DQWNAKNSDITVGQYGGN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 AIVVSGSALAGVYDQLVTRVVTHEMAHA---SGPDSTLSIYQYGSANAALALQSDARKSE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boston
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                  amino acid
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                                 1026 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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No. 5976864ellini, John F.
VENTION: EXPRESSION AND SECRETION OF
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                                                                                              617-542-5070
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24.8%; Pred. No. 7
                                                                                                                                           34053
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                                                                                                                             08106/002001
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RESULT 9
US-09-134-001C-3214
   Sequence 3214, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn DOUCETte-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-142-648B-7
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Best Local
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SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Patent No. 6210948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT.
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 1996-03-12
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 08106/002002
CURRENT APPLICATION NUMBER: US/09/142,648B
CURRENT FILING DATE: 1999-03-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT: NO. 6210948ellini, John F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
                                                                                                                                                                                                                                                                                       TTVNLSGTGTSLGIGRGALTATPTANTLTLNVNGLTTTGAITDSEAAADDGFTTINIAGS
                                                                                                                                                                                                                                                                                                                                                 AAATAGATVAGRVNGAVT---ITDSAAASATTAGKIATVTLGSFGAA----TIDSSAL---
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                                                                                                                                                                                                                                                                                                                  TTITQSGYGNGADYGOGA-----DNSTIELTQNGFRNNATI-DQWNAKNSDITYGQYGGN 121
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No. 6210948ellini,
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IMBER: US 07/614,377
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                                             US-09-336-115C-12
                                                               RESULT 11
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Sequence 12, Application US/09336115C Patent No. 6576244 GENERAL INFORMATION:
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NAME/KEY: SIGNAL
LOCATION: (1)...(18)
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; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3214
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APPLICANT: Guy, Bruno
TITLE OF INVENTION: LT and CT in Parenteral
TITLE OF INVENTION: Methods Against Helicob
FILE REFERENCE: 06132/055002
CURRENT APPLICATION NUMBER: US/09/336,115C
CURRENT FILING DATE: 1999-06-18
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PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3214
LENGTH: 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/100,258
PRIOR FILING DATE: 1998-06-19
NUMBER OF SEQ ID NOS: 24
213 NNIIEHYYTENGKEIPVSYSGGSSFSPTIQLTYHNNAENLLQQAATIMQVLITQ 266
                                                                               159 GILSIDEYOKLNOAYQI-----IQTALNONQGGGMPALNDTTKTGVVNIQQTNYRTTTQ 212
                                        99 NNATIDQWNAKNSDITVGQYGG------NNAA-LVNQTASDSSVMVRQ 139
                                                                                                                          43 STISIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFR---- 98
                                                                                                                                                                     99 AYQAVALALNAAVGMWQVIALFIGCGPGPTNNQSYQSFGNTPALNGTTTTCNQAYGTGPN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        612 GFSPEYTMSVWMGFNK---VKOYGTNS 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   566 KAYGSAYGH------GVSGVNMGAKTGTGTYGQEIYEKYNLPDNAAKDVWIN 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       511 SĀFĀĀĪ-----ĀNGGTYNNAHSIQKVVTHEGDTIBYEHTSHKAMKDYTSYMLAEILKGTF 565
                                                                                                                                                                                                                       8 AFAAIVVSGSALAGVYDQLVTRV------
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                                                                                                                                                                                                                                                             10.7%; Score 81;
19.0%; Pred. No...
7ative 27; Mismato
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Pred. No. 5.7;
12; Mismatches
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Best Local S
Matches 33
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SEQ ID NO 6
LENGTH: 745
                                                                             Matches
                                                                                                                   Query Match
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Patent No. 6576244
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LENGTH: 691
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TITLE OF INVENTION: LT and CT in Parenteral Immunization
TITLE OF INVENTION: Methods Against Helicobacter Infection
FILE REFERENCE: 06.132/055002
CURRENT APPLICATION NUMBER: US/09/336,115C
CURRENT FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 09/100,258 PRIOR FILING DATE: 1998-06-19
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TITLE OF INVENTION: LT and CT in Parenteral Immunization
TITLE OF INVENTION: Methods Against Helicobacter Infection
FILE REFERENCE: 06.132/055002
CURRENT APPLICATION NUMBER: US/09/336,115C
CURRENT FILING DATE: 1999-06-18
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PRIOR APPLICATION NUMBER: US 09/100,258
PRIOR FILING DATE: 1998-06-19
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                                                                                                                                                                                                                                                       NAME/KEY: SIGNAL LOCATION: (1)...(20)
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ORGANISM: Helicobacter pylori
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                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                   NAME/KEY: VARIANT
LOCATION: 721
                                                                                                                                                                                                                                                                                                                      ORGANISM: Helicobacter pylori
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                                                                                                  Local Similarity
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    152
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                                     31 VTHEMAHASGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYGQGADNSTI 90
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ITCNRFESTGPGKSMSIDEFKKLNEAYQIIQQALKNQSGFPELG-GNGTKV---SVNYNY 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09336115C
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                                                                               Conservative
                                                                                                10.7%;
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19.0%; Pred. No. 5.7,
ative 27; Mismatches
                                                                           18; Mismatches
                                                                                                Score 81;
Pred. No.
                                                                                                                   DB 4; Length 745;
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                                                                             4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 69
LENGTH: 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Applic Patent No. 5549897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/038,682
FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High TITLE OF INVENTION: Molecular Weight Proteins EILE REFERENCE: 1038-861 MIS:jb CURRENT APPLICATION UNMBER: US/09/206,942 CURRENT FILING DATE: 1998-12-08 EARLIER APPLICATION NUMBER: 09/167,568 EARLIER FILING DATE: 1998-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 69,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Loosmore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BARENKAMD, STEPHEN J
APPLICANT: ST. GEME III, JOSEPH W
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
TITLE OF INVENTION: OF NON-TYPEABLE HARMODUTTIFS
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                     STREET: 2001 Jefferson Davis Hwy.,
STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                ZIP: 22202-0286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08038682
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01 Jefferson Davis Hwy., 1203 Crystal Plaza
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26.4%; Pred. No. 12;
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                                                                    Version
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ATTORNEY/AGENT INFORMATION:

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RESULT 15
US-08-302-832-2
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TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1536 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,832
FILING DATE: 16-SEP-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: GB 9205704.1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 9205704.1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US DET/US93/02166
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US DET/US93/02166
PRIOR APPLICATION NUMBER: US DET/US93/02166
APPLICATION NUMBER: US DET/US93/02166
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APPLICATION NUMBER: US DET/US93/02166
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INFORMATION FOR SEQ ID NO:
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Patent No. 5603938
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                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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CITY: Arlington
STATE: Viroin:
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                                                                                          NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 22202-0286
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REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1281 NTVNVTANAGDLTV-----GNGAEIN 1301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
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Similarity 26.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virginia
: U.S.A.
                           (703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WENTION: High Molecular Weight Surface Proteins
WENTION: of No. 5603938-Typeable Haemophilus
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Pred. No. 20;
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                                                                                                                                                                                                                                           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1536 amino acids
                                                                                                                                                                                                                                                                                                                                    LENGTH: 1536 amino ac
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
1281 NTVNVTANAGDLTV-----GNGAEIN 1301
                                                                  1226 TSSÓSG-----DIGGTISGGTVEVKATESLTTÓSNSKIKATTGEANVTSATGTIGGTISG 1280
                                                                                                                                          1168 TGSILGGIESSSGSVTLTATEGALAVSNISG--NTVTVTANSGALTTLAGSTIKGTESVT
                                   122 NAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                             15 SGSALAGVYDQ--LVTRVVTH---EMAHASGPDSTLSIYQYGSANAALALQS-DARKSET 68
                                                                                                   69 TITQSGYGNGADVGQGADNSTIBL-----TQNGFRNNATIDQWNAKNSDITVGQYGGN 121
                                                                                                                                                                                                                       Ch 10.6%; Score 80.5; 1 Similarity 26.4%; Pred. No. 20; 39; Conservative 22; Mismatches
                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                     60;
                                                                                                                                                                                                                                                      Length 1536;
                                                                                                                                                                                                                   Indels 27;
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1225

Search completed: March 11, 2004, 18:44:50 Job time: 17.4 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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1: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10B.PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10B.PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

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Copyright (c) 1993 - 2004 Compugen Ltd
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US-09-997-181-131
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US-10-238-075-1549
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Sequence 20638, A Sequence 1549, App Sequence 131, App Sequence 131, App Sequence 131, App Sequence 131, App Sequence 1, Appli Sequence 1, Appli Sequence 9411, App Sequence 10, Appli Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 1373, A
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Sequence 2, Appli Sequence 199, App		e 5, A	5044. 7	Sequence 1717. Ap	7187	ddw 'r	e 1		e 560,		Sequence 28, Appl	13909,	374	Sequence 21, Appl	395	230	352,	63	Sequence 2, Appli	e 65,	Sequence 6, Appli	22	12,	10	e 7	7,	Sequence 5343, Ap

ALIGNMENTS

US-10-369-493-20638

Sequence 20638, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:

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APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US/10/360,039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20638
LENGTH: 445
TYPB: PRT
ORGANISM: Rhodopseudomonas palustris
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(445)
OTHER INFORMATION: unsure at all xaa locations
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                                                                                                                                        Matches
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Best Local (
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                      59
                                                                                                                                    46;
                                                                                                                                                          Similarity
                                                         LFFVTASVLVLSSSAAFAADSNTVY------LNQTGNDQQANITQSGNGNSVGA
                -----LOSDARKSETTI-----
                                                                                            LLKVAAFAAIVVSGSALAG----VYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALA 58
                                                                                                                                        Conservative
                                                                                                                                                          15.0%; Score 113.5; DB 15; 25.0%; Pred. No. 0.00077;
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RESULT 3
US-09-793-306-146
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US-10-238-075-1549
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US-10-238-075-1549
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                       SEQ ID NO 146
LENGTH: 597
                                               APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
TITLE OF INVENTION: of Tuberculosis
FILE REFERENCE: 014058-008740US
CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT EILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR FILING DATE: 2000-02-25
PRIOR FILING DATE: 2000-08-08
RIOR FILING DATE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 0003145
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1549
LENGTH: 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL
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Publication No. US20030148324A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Campos-Neto, Antonio
APPLICANT: Skeiky, Yasir
APPLICANT: Ovendale, Pamela
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CURRENT FILING DATE: 2002-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides a FILE REFERENCE: BLANDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: I.N.S.E.R.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IKVIALATEVSAVFAGSAMA--YDGTITETGKVVAQTCTVNTSDKDLAVTL----PTVAT 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jen, Shyian
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                                                                                                                                                                                                                                                                                                                                                                                                                 Lodes, Michael
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24.5%;
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0.11;
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US-09-997-182-131
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                       Sequence 131, Application US/09997182
Publication No. US20030049263A1
GENERAL INFORMATION:
APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences
TITLE OF INVENTION: immunostimulatory Peptides
FILE REFERENCE: 61258
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Best Local :
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GENERAL INFORMATION:
APPLICANT: Nano, FI
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CURRENT APPLICATION NUMBER: US/09/997,182
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NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 2.0
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es 39; Conserv
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CURRENT APPLICATION NUMBER: US/09/996,634
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR FILING DATE: 1097-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
PRIOR FILING DATE: 1996-06-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding TITLE OF INVENTION: immunostimulatory Peptides FILE REFERENCE: 61260
                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mycobacterium tuberculosis
                                      113 ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                    156 VAGGGALVSAAAAQVTTRVFRNLGL-ANVGEGN-----VGNGNVGNFNLGSANIGNGN
                                                                                                                           57 L----ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD 112
                                                                                                                                                                            96 ALFVSLVVSNILGQNAPAIAATEAAYEQMWAQDVAAMFGYHAGASAAVSALTPFGQALPT 155
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IGSGNIGSSNIGFGN-VGPGLTAALNNIGFGNTGSNN
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35.9%;
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Pred. No. 0.62;
7; Mismatches
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243
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CURRENT FILING DATE:

2001-11-28

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CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR APPLICATION NUMBER: 06/000,254
PRIOR APPLICATION NUMBER: 60/000,254
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Best Local S
Matches 39
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NUMBER OF SEQ ID NOS: 169
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 131
LENGTH: 943
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                                                                                                                                                                                                                                                    ORGANISM: Mycobacterium tuberculosis -09-997-181-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding TITLE OF INVENTION: immunostimulatory Peptides
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PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
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FILING DATE: 2000-01-03
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156 VAGGGÁLVSAÁAAQVTTRVFRNLGL-ÁNVGEGN-----VGNGNVGNFNLGSANIGNGN
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                                       57 L----ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD 112
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                                                                                                                        7 AAFAAIVVSG-----SALAGVYDQLVTRVVTHEMAHASGPDSTLS-IYQYGSANAA 56
                                                                                                                                                                Similarity 24.8
39; Conservative
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                                                                               ALFVSLVVSNLLGQNAPAIAATEAAYEQMWAQDVAAMFGYHAGASAAVSALTPFGQALPT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGSGNIGSSNIGFGN-VGPGLTAALNNIGFGNTGSNN 243
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b. US20030049269A1
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24.8%; Pred. No. 1.9;
ative 22; Mismatches
                                                                                                                                                                11.4%; Score 86.5; D; 24.8%; Pred. No. 1.9; tive 22; Mismatches
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                                                                                                                                                                                                          DB 10;
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                                                                                                                                                                                                        Length 943;
                                                                                                                                                                  Indels
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US-09-984-334-1
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SEQ ID NO 1
LENGTH: 385
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                                                                                                                                                                    SOFTWARE: PatentIn Ver. SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
Query Match
Best Local Similarity
Matches 30; Conserv
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Best Local
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CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHOD FOR PRODUCING 4-CYANO-3-OXOBUTANOATE AND TITLE OF INVENTION: 4-CTANO-3-HYDROXYBUTANOATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WAKITA, RYUHEI APPLICANT: ITO, NOBUYA
                                                                                                                                                                                                         PRIOR FILING DATE: 2001-06-11
NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PROCESS FOR PRODUCING OPTICALLY ACTIVE TITLE OF INVENTION: 4-HALO-3-HYDROXYBUTANOATE FILE REFERENCE: 7372-72249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: JP 2001-175175
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PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: JP 2001-026594
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: JP 2000-372704 PRIOR FILING DATE: 2000-12-07
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                                                                                                     ORGANISM: Corynebacterium sp
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                                                                                                                           TYPE: PRT
                                                                                                                                              LENGTH: 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QSDARKSETTITQSGYGNGADV-----GQGADNSTIELTQNGFRNNATIDQWNAKN 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MATSUMURA, KENJI
SHIMIZU, MASATOSHI
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    Conservative
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                       25.9%;
                       11.1%; Score 84; I
25.9%; Pred. No. 1;
    21;
    Mismatches
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                                         DB 14; Length 385;
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    Gaps
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US-10-156-761-9411
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SEQ ID NO 9411
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                   PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                        CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                           CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                        APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: JP 2001-395884
PRIOR FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: JP 2001-395885
PRIOR FILING DATE: 2001-12-27
PRIOR PRIOR APPLICATION NUMBER: JP 2002-107648
PRIOR PILING DATE: 2002-04-10
NUMBER OF SEQ ID NOS: 15
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CURRENT APPLICATION NUMBER: US/10/327,108
CURRENT FILING DATE: 2002-12-24
CURRENT FILING DATE: 2002-12-24
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TYPE: PRT
ORGANISM: Corynebacterium pseudodiphtheriticum
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                                                                                                                                                                                                                                                        ISHIKAWA, JUN
HORIKAWA, HIROSHI
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RESULT 12
US-10-185-990-11
Sequence 11, Application US/10185990
Publication No. US20030073109A1
GENERAL INFORMATION:
APPLICANT: PAN, Jae-Gu
FILE REFERENCE: 02589.00100
CURRENT APPLICATION NUMBER: US/10/185,990
CURRENT FILING DATE: 2002-06-28
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                                                                 NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH
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US-10-185-990-10
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LENGTH: 1626
TYPE: PRT
ORGANISM: Bacillus subtilis
10-185-990-11
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 02589.000100
CURRENT APPLICATION NUMBER: US/10/185,990
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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TITLE OF INVENTION: JAE GU PAN ET
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Best Local :
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ORGANISM: BACILLUS SUBTILIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 1621
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                                                                                                                                                                                                                                                                                                                 516 ---SGSESSLTAG-YGS-----TQTAQQGSVLTS--GYGSTQTA 548
                                                                                                                                                                                                                                                                                                                                              104 DQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 PVTTGGQESQWTALPSDTRDGE--ARNGAADPSGAAD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 VAAFAAIVVSG--SALAGVYDQLVTR-----VVTHEMAHASGPDSTLSIYQYGSANAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IEAGPOSSEETEAQLRLGGNDDAGAAADGETARMPSDGDFDGGATGAAGPPAQWEVDGQC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 -----RKSETTITQSGYGNGADVGQGADNSTIELTQNG-FRNNAT-----ID---- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 AIVVSGSALAGVYDQLVTRVVTHEMAHASGPDS-----TLSIYQYGSANAALALQSDA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44;
                                                                                                                                                                                                                                                                                                                                                                                  IAGYGSTQTSGSDŠÁLTAGYGSTQTAQEGSNLTAGYGSTGTAGADSSL-IAGYGSTQTS- 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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26.7%; Pred. No. 8.6;
tive 21; Mismatches
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28.0%; Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-996-194-16
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                                APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 202-05-29
CURRENT FILING DATE: 202-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 22
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 65
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                    Sequence 13173, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                        APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/253,878
PRIOR FILING DATE: 2000-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/250,348
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/250,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 35800/240590
CURRENT APPLICATION NUMBER: US/09/996,194
CURRENT FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bandaru, Rajasehkar
TITLE OF INVENTION: 84242, 8035, 55304, 52999, and 21999,
TITLE OF INVENTION: No. US20020151696A1el Human Proteins and Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/250,338
APPLICATION NUMBER: JP 2001-204089 FILING DATE: 2001-05-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               469 -----GSESSLT-AGYGSTQTAREGSTLTAGYGSTGTAGADSSLIA----GYGSTQT- 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  411 IAGYGSTQTSGSDSALTAGYGSTQTAQEGSNLTAGYGSTGTAGADSSL-IAGYGSTQTS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
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Similarity 88.9%;
16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---SGSESSLTAG-YGS-----TQTAQQGSVLTS--GYGSTQTA 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09996194
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Pred. No.
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; NAME/KEY: unsure
; LOCATION: (1)..(273)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-20096
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US-10-369-493-20096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20096
LENGTH: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20096, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 13173
LENGTH: 594
                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: No. US20030233675Altoc punctiforme
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                                                                                                                                                               Local Similarity es 32; Conserv
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209
                                      141
                                                                           151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
                                                                                                                  84
                                                                                                                                                                                      43 STLSIYQYGSANA-ALALQS------DARKSETTITQSG-----YGNGADVGQ 83
                                                                                                                                                         92 TTLDL-QFGSTNSDDVTLKPNQTLFAGDGADFVEGTKGNTIVTGNGEDTVLVGSGSSVST 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 TQSGYGNGADVGQG----ADNSTIELTQNGFRNNATIDQWNAKNSDIT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 AIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARKSETTI 70
SFGGS 213
                                      GFGNN 145
                                                                           GDGNDQVFIGVNSPASNTSADGGNG-NDEVTVVEANGSN-NLFGGAGADTLTVVEGSRQL
                                                                                                              GADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMV----RQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETS---RGAEAVGGPSAADLSQQNIAQEGRQNNACANH-NGLNADVTGARQDTACVTVDR
                                                                                                                                                                                                                                   Conservative
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Pred. No. 0.
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                                                                                                                                                                                                                                   44; Indels
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                                                                                                                                                                                                                                                                        Length 273;
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                                                                             208
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Search completed: March 11, Job time: 25.6 secs

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GB:U43280; NID:g1184712; PIDN:AAC43599.1; PID:g1184714

aggregative fimbriae.

ReBult No.

Minimum Maximum

88

Searched

Database

Sequence:

OM protein -

The second secon						
hypothetical r		N	760	10.8	81.5	5
hypothetical prote	C90739	N	760	10.8	81.5	4
cell wall surface	E95206	N	4776	_	82	ພ
hemolysin [import	AI0452	N	1635	10.	82	42
S-layer protein	C87374	N	1073	10.	82	ä
paracrystalline	A48995	N	1026	10.8	82	ö
hypothetical prote	T32020	N	534	10	82	39
hypothetical prote	869589	N	528	10.8	82	38
ice nucleation pro	SNPSO	Д	1200		83.5	37
probable PPE prote	E70969	N	3716	11.1	84	36
nucleoskeletal-lik	S14055	N	823	11.1	84	5
ice nucleation	A25547	N	1210	11.3	85.5	4
probable PPE prote	D70575	N	3300	11.4	86.5	ຜ
F3F19.21 protein	C86266	N	573	11.5	87	32
hypothetical prote	C29349	N	455	11.5	87	ĭ
outer membrane	S21408	N	331	11.5	87	ö

ALIGNMENTS

A;Description: major component of thin aggregative fimbriae A;Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen C;Keywords: fimbria F;1-20/Domain: signal sequence #status predicted <SIG> F;21-151/Product: fimbrin protein agfA #status experimental <MAT> A;Molecule type: protein
A;Residues: 21-52 <CO2>
A;Experimental source: strain 27655-3b
A;Rote: the authors translated the codon ACG for residue 44 as Ile
R;Collinson, S.K.; Emody, L.; Muller, K.H.; Trust, T.J.; Kay, W.W.
J. Bacteriol. 173, 4773-4781, 1991
A;Title: Purification and characterization of thin, aggregative fimbriae from Salmonell.
A;Reference number: A44898; MUID:91310586; PMID:1677357
A;Contents: 27655 A;Status: preliminary A;Molecule type: protein A;Residues: 21-33 <CO3> A;Note: sequence extracted A; Accession: A44898 Local Similarity NNAALVNQTASDSSVMVRQVGFGNNATANQY SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ Conservative 86.9**%;** 90.1**%**; from NCBI backbone (NCBIP: 45936) ω -Score 658; DB 2; Pred. No. 7.5e-52; Mismatches Length 151; Indels 0 Gaps activator 60 60 120 120

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121

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N;Alternate names:
C;Species: Escheric
C;Date: 12-Feb-1998
C;Accession: S70788
                                                                                                                                                                                                                    A;Cross references: EMBL:X90754; NID:g1147558; PIDN A;Experimental source: strain Kl2, substrain W3110 A;Note: the nucleotide sequence was submitted to the R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Pe A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
    A;Cross-references: GB:AB000205; GB:U00096; NID:g1787265; A;Experimental source: strain K-12, substrain MG1655 R;Olsen, A.; Arnqvist, A.; Hammar, M.; Sukupolvi, S.; Norn Mol. Microbiol. 7, 523-536, 1993
                                                                                                                                                         A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G64846
                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 12-Fab-1998 #sequence revision 20-Fab-1998 #text_change 01 C;Accession: S70788; G64846; S31202; S34560; S34559 R;Hammarr, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S. Mol. Microbiol. 18, 661-670, 1995 A;Title: Expression of two csg operons is required for production A;Reference number: S70783; MUID:96414468; PMID:8817489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
S70788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ourlin protein csgA precursor - Escherichia
N;Alternate names: csgA protein; major curli
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S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Title: Complete genome Sequence of a multiple drug resistant
A;Title: Complete genome Sequence of a multiple drug resistant
                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-151 < HAM>
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R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pi th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-151 < PAR>
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                                                                                                 Molecule type: DNA
Residues: 1-151 <BLAT>
                                                                                                                                    Status: nucleic acid sequence not shown; translation
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Pred.
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                         S.; Normark,
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L.; White, N.;
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V., Riley,
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Matches

100;

Conservative

19;

Mismatches

32;

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Gaps

59

119 60

QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG MKLLKVAATAATVFSGSALAGVVPQYGGGGGNHGGGGGNNSGPNSELNTYQYGGGNSALAL MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTH-EMAHASGPDSTLSIYQYGSANAALAL

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R;Hayashi, T.; Makino, K.; Umitshi, F.; Shiba, T.; Hattori, M.; Shi gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shi DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D90806
                                                                                     A;Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                               C;Species: Escherich
C;Date: 18-Jul-2001
C;Accession: D90806
                                                                      A;Gene:
                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-152 < HAY>
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D90806
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A;Molecule type: DNA
A;Residues: 1-133,'RQRDSGWLW' <0LS3>
A;Cross references: EMBL:L04979; NID:9290424;
A;Cross references: strain K-12, substrain
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A;Residues: 21-42;44-50 <OLS2>
R;Olsen, A.N.; Armqvist, A.M.
submitted to the EMBL Data Library,
A;Reference number: S34559
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A:Residues: 1-6,'V',8-151 <OLS1>
A:Cross-references: EMBL:L04979
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;Function:
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    62.7%;
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Score 474.5; DB 2;
Pred. No. 2e-35;
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Pred. No. 2.7e-36;
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M.; Shinagawa,
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A;Experimental source: Etrain K[2], substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Aug R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F64846
                                                                                                                                                                                                                                                                                                                                                   R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S. Mol. Microbiol. 18, 661-670, 1995
A;Title: Expression of two csg operons is required for production A;Reference number: S70783; MUID:96414468; PMID:8817489
A;Accession: S70787
                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: csgB protein; curlin nucleation component; mi
C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change
C;Accession: S70787; F64846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              curlin nucleator protein csgB precursor - Escherichia coli (strain K-12)
N;Alternate names: csgB protein; curlin nucleation component; minor curl
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C; Accession: H85665
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                                             Molecule type: DNA
                                                                  Status: nucleic acid sequence
                                                                                                                                                                                                                                                               Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62281.1; PID:g1147563
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      GB
    AE000205;
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                                                                  not shown;
                                                                                                                                                                                                                                                                                                                                 not shown; translation not shown
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    GB:U00096;
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Pred. No. 2e-3
L9; Mismatches
                                                                  translation not
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NID: g1787265;
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    PIDN: AAC74125.1;
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Potamousis, K.; Ap
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  PID:g1787278;
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                                                                                                                           iller, L.; Grotbeck, E.J.; Davis, Nature 409, 529-533, 2001
A;Title: Genome sequence of enter
                      A; Molecule type: DNA
A; Residues: 1-151 < STO>
                                                                                    A; Reference number: A85480; A; Accession: G85665
                                                                                                                                                                          R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.;
                                                                                                                                                                                                                      C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: G85665
                                                                                                                                                                                                                                                                 C;Species: Escherichia coli
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                                                                  A;Status: preliminary
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GB:AE005174;

NID:g12514573;

PIDN: AAG55787.1;

GSPDB:GN00145;

UWGP: Z16

enterohemorrhagic Escherichia MUID:21074935; PMID:11206551

coli

0157:H7

J.D.; Rose, Potamousis,

D.J.; Mayhew K.; Apodaca,

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C; Genetics:
A; Gene: csgB
A; Map position:
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A;Molecule type: DNA
A;Residues: 1-151 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:g13360879; GSPDB:GN00154
A;Cross-referencal source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A:Reference number: A99629; MUID:21156231; PMID:11258796
curlin minor chain precursor, CsgA homolog
                     G85665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A99629; A; Accession: C90806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gasawara, N.; Yasunaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Hayashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  minor curlin subunit precursor CsgB [imported] - C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Description: minor component of wild-type curli; interaction between CsgA and CsgB tri A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-21/Domain: signal sequence #status predicted <SIG>F;22-151/Product: minor curlin chain #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
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Best Local
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37; Conserv
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                                                                                                EGSSNRAKIDQTGDYNL-AYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY 129
                                                                                                                                        NGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                IAAAAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Makino,
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T.; Kuhara,
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                                                                                                                                                                                                                                                              Score 118.5; DB
Pred. No. 0.0014;
3; Mismatches 6
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Pred. No. 0.0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M.; Kurokawa, I
S.; Shiba, T.;
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[imported] - Escherichia coli (strain
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A;Accession: AH0635
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-151 <PZ
A;Cross-references: (
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                                                                                                                                        nucleation component of curlin monomers [imported] - Salmonella enterica sub C; Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AH0635
C;Parskhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, Cth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, S.; Moule, S.; O'Gaora, P.
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A; Gene: csgB
                                                     S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AH0635
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A; Residues: 1-151 < COL>
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C;Species: Salmonella enteritidis
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Residues: 1-151 <P.
                                                  Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description: minor component of thin aggregative fimbriae, Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
37; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                          NGFRNNATIDOWNAKNSDIT-VGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                         GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ
                                                                                                                                                                                                                                                                                                                                                                                                                                         GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST-----IELTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAHASGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGSSNRAKIDOTGDYNL-AYIDOAGSANDASISOGAYGNTAMIIOKGSGNKANITOY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                    <PAR>
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     GB:AL513382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB:U43280; NID:g1184712; PIDN:AAC43598.1; PID:g1184713
ce: strain 276755-3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strain O157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.7%;
31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.7%;
                                                                                                                                                                                                                                                                                                                                          -AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13,
   PIDN:CAD08267.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 111.5; DB Pred. No. 0.0057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 118.5; DB 
Pred. No. 0.0014; 
3; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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 PID:g16502314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46;
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                                                                                                                                                              D.; Wain, J
, L.; White,
   GSPDB:GN00176
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                                                                                                                                                                Churcher,
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N;Alternaté names: glycoprotein gp63, s
C;Species: Leishmania chagasi
C;Date: 10-Mar-1994 #sequence_revision
C;Accession: B42049
                                                                             B42049
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                                                           leishmanolysin (EC 3.4.24.36) precursor, stationary phase -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A45621;
A; Accession: A45621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-590 < WEB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A45621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Leishmania donovani
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                                           stationary
               07-Apr-1994
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F;566-590/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;48,251,255,321/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F;112-129,118-217,301_373,380-443,393-412,402-477,454-498,503-553,523-546/Disulfide bon
F;251,255,321/Binding site: zinc, catalytic (His) (active) #status predicted
F;252/Active site: Glu #status predicted
F;252/Active site: Glu #status predicted
F;265/Modified site: carbohydrate (Asn) (covalent) #status predicted
F;565/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Description: catalyzes the hydrolysis of peptide bonds between two hydrophobic A;Note: the activated form can activate the proenzyme form C;Superfamily: leishmanolysin C;Keywords: blocked carboxyl end; cell adhesion; glycoprotein; hydrolase; lipopro F;1-39/Domain: signal sequence #status predicted <SIG>F;40-87/Domain: activation peptide #status predicted <ATP>F;88-565/Product: leishmanolysin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Biochem. Parasitol. 48, 173-184, 1991
A;Title: Heterogeneity of the genes encoding the major surface glycoprotein
A;Reference number: A45621; MUID:92107220; PMID:1762629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jan-2000 C;Accession: A45621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         leishmanolysin (EC 3.4.24.36) precursor - Leishmania on N_fAlternate names: surfase endopeptidase glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST----IELTQ
                                                                                                                                    DVPVINSSTAVAKAREQYGCGTLEYLEMEDQGGAGSAGSHIKM----
                                                                                                                                                                                                                                                                        AVGVINIPAANIASRYDQLVTRVVTHEMAHALG----FSVVFFRDARILESISNVRHKDF 281
                                                                NSDITVGQYGGNNAALVNQTA---SDSSVMVRQVGFGNNA 146
                                                                                                                                                                                                        -----SETTITQS--GYGNGA------DVGQGADNSTIELTQNGFRNNATIDQWNAK 109
                                                                                                                                                                                                                                                                                                                                     AFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAPGIATATNYDLARSEYNFAVNELSKSSFNOAAIIGOVGTDNSARVROEGSKLLSVISO 73
AGYYSALTMÁIFQDLGFYQADFS-KAEEMPWGRNÁ 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.7%; Score 111.5; DB 30.5%; Pred. No. 0.0057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from NCBI backbone (NCBIN:74958, NCBIP:74959)
                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.24;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 101.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                             59;
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                                                                                                                                    RNAQ-DELMAP 334
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Leishmania chagasi

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22-Jun-1999

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C;Superfamily: leishmanolysin
C;Superfamily: leishmanolysin
C;Keywords: cell adhesion; glycoprotein; hydrolase; membrane bound; metalloproteinase;
F;1-39/Domain: signal sequence #status predicted <SIG>
F;40-97/Domain: signal sequence #status predicted <ATP>
F;40-97/Domain: activation peptide #status predicted <MATP
F;98-599/Product: leishmanolysin #status predicted <MATP
F;48,261,265,331/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F;122-139,188-227,311-383,390-451,403-422,412-486,463-507,512-562,532-555/Disulfide bor
F;261,265,331/Binding site: zinc, catalytic (His) (active) #status predicted
F;262/Active site: Glu #status predicted
F;262/Active site: Glu #status predicted
F;267,394/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;1-39/Domain: signal sequence #status predicted <SIG>
F;1-39/Domain: activation peptide #status predicted <ANT
F;98-574/Product: leishmanolysin #status predicted <ANT
F;575-599/Domain: carboxyl-terminal propeptide #status pr
F;48,261,265,331/Binding site: zinc, catalytic (Cys, His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Ramamoorthy, R.; Donelson, J.E.; Paetz, K.E.; Maybodi, M. Biol. Chem. 267, 1888-1895, 1992
A;Title: Three distinct RNAs for the surface protease gp63 A;Reference number: A42049; MUID:92112918; PMID:1370484
A;Accession: A42049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Miller, R.A.; Reed, S.G.; Parsons, M.
Mol. Blochem. Parasitol. 39, 267-274, 1990
A;Title: Leishmania gp63 molecule implicated in cellular A;Reference number: A44951; MUID:90205976; PMID:2320059
A;Accession: A44951
                                                                                                                                                                                               A; Note: the C; Superfamil
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A; Residues: 1-599 <MIL>
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                                                                                                                                                                                                                            A;Description: catalyzes the hydrolysis of peptide bonds between A;Note: the activated form can activate the proenzyme form
                                                                                                                                                                                                                                                                                                                         A_iNote: sequence extracted from NCBI backbone ( A_iNote: the source is designated as Leishmania
                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M80672; NID:g159328; PIDN:AAA29238.1; PID:g159329
A;Note: sequence extracted from NCBI backbone (NCBIN:76040, NCBIP:76041)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M28527; NID:g159322; PIDN:AAA29235.1; PID:g159323
R;Ramamoorthy, R.; Donelson, J.E.; Paetz, K.E.; Maybodi, M.; Roberts, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leishmanolysin (EC 3.4.24.36) precursor, log phase - Leishmania chagasi
N;Alternate names: glycoprotein gp63; surface metalloproteinase, log ph
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                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
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Best Local S
Matches 32
                                                                                                                                                              ;Note: the activated form can activate the proen;Superfamily: leishmanolysin;Keywords: blocked carboxyl end; cell adhesion;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ramamoorthy, R., Donelson, J.E.
Biol. Chem. 267, 1888-1895, 19
Title: Three distinct RNAs for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary
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95, 1992
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Pred. No. 0.27;
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             #status
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                             leishmanolysin (EC 3.4.24.36) precursor - Leishmania mexic NyAlternate names: surface metalloproteinase glycoprotein C;Species: Leishmania mexicana C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_cC;Accession: S19916; A48564 R;Medina-Acosta, E.; Karess, R.E.; Russell, D. submitted to the EMBL Data Library, February 1992 A;Description: Structurally distinct genes for the surface A;Description: Structurally distinct genes for the surface
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S19916
      A; Reference
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
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;Experimental source: strain H37Rv
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296
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                                        SSVMVRQVGFGNNATAN 149
                                                                                    GNFGSGNGRAGLPGSGNVGNGNLGNSNLGSGNTGNSNVGFGNTGNNNVGTGNAGSGNIGA
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23.4%;
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Leishmania mexicana

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10-Sep-1999

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protease

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Leishmania

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Search completed: March 11, 2004, 18:42:08 Job time: 11.3 secs
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R;Medina-Acosta, E.; Karess, R.E.; Russell, D.G.
MOI. Biochem. Parasitol. 57, 31-45, 1993
MOI. Biochem. Parasitol. 57, 31-45, 1993
A;Title: Structurally distinct genes for the surface protease of Leishmania mexicana are A;Reference number: A48564; MUID:93149206; PMID:8426614
A;Accession: A48564
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A;Molecule type: mRNA
A;Residues: 1-646 <MED>
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A, Map position: 700kb chromosomal band
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1 drosophila
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0 escherichia
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9 azotobacter
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6 homo sapien
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5 pseudomonas
5 pseudomonas
7 saccharomyc
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RESULT 1 CSGA SALTY		45	44	43	42	41	40	39	38	37	36	35	34	
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	ALIGNMENTS	PANE_HALN1	ARGJ CORGL	OMB_NEIMB	OMPB_RICPR	Y281_MYCPN	GLR1_RAT	GLR1_MOUSE	OMPB_RICRI	120K_RICRI	7B4C_PSESP	GP63_LEIGU	NRF1 MOUSE	
		Q9hrf0 halobacteri	Q59280 corynebacte	P30690 neisseria m		P75383 mycoplasma		P23818 mus musculu		P14914 rickettsia	P07662 pseudomonas	Q00689 leishmania	Q9wu00 mus musculu	

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Query Match
Best Local Similarity
Matches 136; Conser
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EMBL; AE008749; AAL20074.1; --
EMBL; AL627269; CAD08268.1; --
EMBL; AE016840; AA069399.1; --
EMBL; U43280; AAC43599.1; --
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Fimbria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COllinson S.K., Emoedy L., Mueller K.-M., Trust T.J., Kay W.W. Purification and characterization of thin, aggregative fimbr Salmonella enteritidis.",

J. Bacteriol. 173:4773-4781 (1991).

-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Doran J.L., Collinson S.K., Burian J., Sarlos G., Todd E.C.D., Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.; "DNA-based diagnostic tests for Salmonella species targeting agfa, the structural gene for thin, aggregative fimbriae."; J. Clin. Microbiol. 31:2263-2273(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=S.enteritidis; STRAIN=27655-3B; MEDLINE=91310586; PubMed=1677357; Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson & Front Collinson 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=S.enteritidis; STRAIN=27655-3B; MEDLINE=96146512; PubMed=8550497; Collinson S.K., Clouthier S.C., Doran J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [5]
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SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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280; AAv.,
039; UC6039.
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1 20
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                                                       NNAAL VNOTASDSSVMVROVGFGNNATANQY
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                                                                                 NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                        SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATI
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Pred. No. 4.9e-50;
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SVMVRQVGFGNNATANQY ->
REF. 6).
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encoding thin, aggregative
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RESULT 2
CSGA_ECOLI
                                                                                                                                                                              SEQUENCE OF 21-40.
STRAIN=K12 / YMEL;
MEDLINE=93023873; PubMed=1357528;
Arnqvist A., Olsen A., Pfeifer J., Rumrhe Crl protein activates cryptic gribronectin binding in Escherichia compol. Microbiol. 6:2443-2452(1992).
   J. Bacteriol. 173:4773-4781(1991).
J. Bacteriol. 173:4773-4781(1991).
-i- FUNCTION: CURLIN IS THE STRUCTURAL
COILED SURPACE STRUCTURES THAT ASSE
TEMPERATURES BELOW 37 DEGREES CELS!
                                                                                           MEDLINE=91310586; PubMed=1677357; Collinson S.K., Emoedy L., Trust T. "Purification and characterization"
                                                                                                                                                                                                                                                                                                                                                                 Yano M., H.
"A 718-kb
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Yano M., Horiuchi T.;
"A 716 Lb. """
                                                                                                                                                        SEQUENCE OF
                                                                                                                                                                                                                                                                                                                            "A 718-kb DNA sequence of the I corresponding to the 12.7-28.0 DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkeet G. III, Bloch C.A., Perna N.T.
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., M
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A.,
Mau B., Shao Y.;
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Escherichia coli.";
Mol. Microbiol. 7:5:
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STRAIN=K12
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MEDLINE=93211294; PubMed=8459772;
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Enterobacteriaceae; Eschei
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01-DEC-1992
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B-2003 (Rel. 41, Last annotation
curlin subunit precursor.
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RESULT 3
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Best Local S
Matches 101
            MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohamman."
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Q93UZ4;
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SIGNAL
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EMBL;
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                                                                                                                                                                                                                                                                                 STRAIN=0157:H7 / ATCC 43895;
MEDLINE=21218556; PubMed=11319125;
Uhlich G.A., Keen J.E., Elder R.O.;
Uhlich g.A., Keen J.E. Belder R.O.;
"Mutations in the cegD promoter associated with variations expression in certain strains of Escherichia coli 0157:H7.'
Appl. Environ. Microbiol. 67:2367-2370(2001).
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Escherichia coli O157:H7.
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28-FEB-2003
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X90754; CAA62282.1; -.
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C STRAIN=0157:H7 / RIMD 0509952;

K MEDLINE=21156231; PubMed=11258796;

X MEDLINE=21156231; PubMed=11258796;

X HAYASHI T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama A. Han, C.,—G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

A Hida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.
A Kuhara S., Shiba T., Hattori M., Shinagawa H.;
T. "Complete genome sequence of enterohemorrhagic Escherichia coli
T. O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).

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COILED SURFACE STRUCTURAL SUBUNIT OF THE CURLI. CURLI
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SEQUENCE
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P39828;
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28-FEB-2003 (Rel. 41, Last annotation
Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
Hammar M., Arnqvist A., Bian Z., Olsen A., "Expression of two csg operons is required fibronectin- and congo red-binding curli po
                                                                                                SEQUENCE FROM N.A.
STRAIN=K12 / MC410
                                                                                                                                                                                                             Escherichia coli, and
Escherichia coli O157:H7.
Bacteria, Proteobacteria,
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EMBL; AE005315; AAG55788.1;
EMBL; AP002554; BAB34843.1;
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ka M., Tobe
<sup>V</sup>., Yasunaga <sup>h</sup>
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino E., Ohnishi M., Kurokawa T., Tanaka M., Tobe Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
NA Res. 8:11-22(2001).
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MEDLINE-21074935; PubMed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Melch R.A., Blattner F.R.;

"Genome sequence of enteronaemorrhagic Escherichia coli 0157:H7."
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"A 718-kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita
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                         email to license@isb-sib.ch)
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                                                                                        J. Bacteriol. 185:2330-2337(2003).
-!- FUNCTION: CURLIN IS THE STRUCTURAL
-COILED SURFACE STRUCTURES THAT ASSE
TEMPERATURES BELOW 37 DEGREES CELSI
FIBRONECTIN. THE MINOR SUBUNIT IS T
                                                                                                                                                                          STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains and CT18.";
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28-FEB-2003 (Rel. 41, Last
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EMBL; AE005315; AAG55787.1;
EMBL; AP002554; BAB34842.1;
PIR; C90806; C90806.
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PIR; S70787; S70787.
                                                       CURLIN MONOMERS.
SIMILARITY: BELONGS
SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEF17
CSGB OR AGFB OR STM1143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609; McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Lat Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulv Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.
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SPECIES-S. typhimurium; STRAIN-SR-11;

SPECIES-S. typhimurium; STRAIN-SR-11;

SPECIES-S. typhimurium; STRAIN-SR-11;

MEDLINE-99117058; PubMed-9457880;

Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;

"Curli fibers are highly conserved between Salmonella typhing the structure and regulation of the second second regulation of the second second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation of the second regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation regulation re
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                                                                                                                                                                                                                                     MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A.,
"Salmonella enteritidis agfBAC operon encoding thin, agg
                                                                                                                                                                                                                                                                                                                                             SPECIES=S.enteritidis; STRAIN=27655-3B;
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an email to license@isb-sib.ch).
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e agreement (See tageisb-eit
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Pred. No. 0.00
17; Mismatches
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P23223;
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Fimbria;
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SEQUENCE
EMBL; M60048;
HSSP; P08148;
                                                                                                                      This
                                                                                                                                                                                                                                     Webb J.R., Button L.L., McMaster R.W.;
"Heterogeneity of the genes encoding the rof Leishmania donovani.";
Mol. Biochem. Parasitol. 48:173-184(1991)
-i- FUNCTION: Has an integral role during
                                                                                                                                                                                                                                                                                                                                                          Leishmania donovani.
Eukaryota; Euglenozoa;
NCBI_TaxID=5661;
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EMBL; AE008749; AAL20073.1; -.
EMBL; U43280; AAC43598.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. Uentities requires a license agreement (See htterities requires a license agreement)
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                                                                 modified and this statement is not
                                                                                                                                                                                                                                                                                                          WEDLINE=92107220;
                                                                                                                                                                                                                                                                                                                          STRAIN=LV9
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              Leishmanolysin precursor (EC (Major surface glycoprotein)
                                                                                                                                           COFACTOR: Binds 1 zinc ion per subunit (By sims SUBCELLULAR LOCATION: Attached to the membrane SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                      in the mammalian host.

CATALYTIC ACTIVITY: Preference for hydrophobic P1' and basic residues at P2 and P3'. A model r cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.

COPACTOR: Binds 1 zinc ion per subunit (By simi
                                                                                                        SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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Signal; Complete proteome
1 21 POTEN
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                                       equires a license agreement email to license@isb-sib.cl
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(Rel. 20, Last sequence update)
(Rel. 42, Last annotation update)
(Rel. 43, Last annotation (BC 34,24,36) (Cell
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             AAA29244.1;
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30.5%;
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rane by a GPI-anchor.
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SEQUENCE FROM ...
MEDLINE=92112918; Pubmeu-_
Ramamoorthy R., Donelson J
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01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell
(Major surface glycoprotein) (GP63 protein) (Rendopeptidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GP63 LEICH
P15706;
01-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEICH
                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=90205976; PubMed=2320059;

Miller R.A., Reed S.G., Parsons M.;

"Leishmania gp63 molecule implicated in cellular

Arg-Gly-Asp sequence.";

Mol. Biochem. Parasitol. 39:267-274(1990).
                                                                                                                                                                                                                                                                                                                            Leishmania chagasi.
Eukaryota; Eugleno:
NCBI_TaxID=44271;
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PROSITE; PS00142; ZINC_PROTEASE; 1.
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InterPro; IPR001577;
Pfam; PF01457; Peptio
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PRINTS; PR00782; LSHMANOLYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
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J. Biol. Chem. 267:1888-1895(1992)
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                                                                                                                                                                                                                                                                   Gaps
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AC AC

GP63_LEIME P43150;

STANDARD;

PRT;

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u1-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin C1 precursor (EC 3.4.24.36) (Cell surface p
(Major surface glycoprotein) (GP63 protein) (Promastigote
endopeptidase).
GP63-C1.
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PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a checken the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93149206; PubMed=8426614; Medina-Acosta E., Karess R.E., Russell D.G.; "Structurally distinct genes for the surface mexicana are developmentally regulated."; Mol. Blochem. Parasitol. 57:31-46(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlycoSuiteDB; P43150; -... Zn BS. InterPro; IPR005025; Pept M Zn BS. InterPro; IPR001577; PeptIdase_M8. Pfam; PF01457; Peptidase_M8; 1. PRINTS; PR00782; LSHMANOLYSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X64394; CAA45733.1; -. PIR; S19916; S19916.
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STRAIN=MNYC/BZ/62/M379;
                                                                                                                                                                                                                                                                                                                                   METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leishmania mexicana.
Bukaryota; Euglenozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; M08.001; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: Preference for hydrophobic p1' and basic residues at p2 and p3'. A model n cleaved at -Ala-Tyr-|-Lou-Lys-Lys-COFACTOR: Binds 1 zinc ion per subunit (By simi DEVELOPMENTAL STAGE: Expressed in both the prom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amastigote forms.
SIMILARITY: Belongs to peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Has an integral role during the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P08148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metalloprottease; Glycoprotein; Metal-binding; ignal; Cell adhesion; Multigene family.
                                                                    518
538
86
297
299
409
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103
266
270
270
270
336
1127
1127
1193
316
408
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                   69054
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                                           ACTIVATION PEPTIDE (POTENTIAL).

LEISHMANOLYSIN C1.

ZINC (CATALYTIC) (BY SIMILARITY).

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                 (GLCNAC. .
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promastigote
                                                                                                                                                                                                                                                                                                                               SIMILARITY)
SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zinc;
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MRL outstation -
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RESULT 10
OMPB_RICJA
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Best Local S
Matches 40
Query Match
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Matches 42
                                                                CHAIN
DOMAIN
                                                                                         CHAIN
                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases - 1- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A N - STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKET VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rompB)
(romp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OMPB_RI
                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Prote
Rickettsiaceae;
                                                   SEQUENCE
                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=35790;
                                                                                                                                                                                                                                                                                                                                                                                                                                     japonica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rickettsia japonica.
                                                                                                                                          interPro;
                                                                                                                                                                                                                                                                                                   (By similarity).
SUBCELLULAR LOCATION: Cell wall. This bacterium is cover subcertith hexagonal symmetry.
SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                        FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RICJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
                                                                                                                                                                      AB003681; BAA20138.1;
                                                                                                                                PF03797;
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             Similarity
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                                                                                                                                                                                                                        non-profit institutions as long and this statement is not removed.
                                                                                                    S-layer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proteobacteria; Alphaproteobacteria; aceae; Rickettsieae; Rickettsia.
                                                                                                                                         IPR006315; Autotransport. IPR005546; Autotransporter.
                                                                                                                 TIGR01414; autot
                                                   1656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                      Cell wall.
                                                                                                                                                                                                                                                                                                                                                                                                                                               gene encoding the protein rOmp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132
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            13.1%;
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                                                                                                                 rans_barl;
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                                                   MW;
                                                              32 kDa BE
POLY-GLY.
            Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                               120 kDa SURFACE-EXPOSED
32 kDa BETA PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                     3132A69C9DD5999F
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No. 0
                        99;
                                                                            BETA
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                                                                                                                                                                                                           oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                              There are no
                         DB 1;
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.33;
                                                                             PEPTIDE
                                                                                                                                                                                                                                    as
                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN IS A MAJOR
DLE AS A RICKETTSIAL
ING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66;
                                                                                                                                                                                                                                   its content
                         Length 1656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rickettsiales;
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                                                               Query Match
Best Local (
                                                      Matches
                                                                                                                     PRINTS; PRO0327; ICENUCLEAIN.

PROSITE; PS00314; ICE NUCLEATION, 34.

ICE NUCLEATION, 34.

ICE nucleation; Repeat; Outer membrane.

DOMAIN 162 993 OCTAPEPTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: Ice nucleation proteins enable crystallization in supercooled water.
-!- SUBCELIGUAR LOCATION: Outer membrane.
-!- DOMAIN: CONTAINS IMPERFECT REPEATS OF A CA-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE
                                                                                                          SEQUENCE
                                                                                                                                                                                                                   EMBL; D14992; BAA03636.1; PIR; JC2143; JC2143.
                                                                                                                                                                                                                                                            or send
                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biosci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uredovora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94264407: PubMed=7764866; Michigami Y., Watabe S., Abe K., Obata H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ICEN PANAN
Q47879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
Enterobacteriaceae; Panto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pantoea ananas (Erwinia uredovora)
                                                                                                                                                                                                      HSSP; P06620; 1INA.
                                                                                                                                                                       nterPro; IPR000258; Ice_nucleatn.
fam; PF00818; Ice_nucleation; 51.
                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                            PERIODICITY IS SUPERIMPOSED.

MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
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GP63_LEIMA
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Button L.L., Morney
"Molecular cloning of the "Molecular cloning of the Med. 167:724-729(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                           "The crystal structure of the Leishmania leishmanolysin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schneider P., Ferguson M.A.J., PULLURYLLE....,
Homans S.W., Bordler C.;
"Structure of the glycosyl-phosphatidylinositol
"Structure of the symmetriante surface protes
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01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell
(Major surface glycoprotein) (GP63 protein) (FR63 protein)
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Schlagenhauf E., Etges
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in the mammalian host.

CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 are P1 and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.

COPACTOR: Binds I zinc ion per subunit.

SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. PTM: THE PHOSPHATIDYLINOSITOL MOIETY OF THE GPI-ANCHOR CONTAINS PTM: THE PHOSPHATIDYLINOSITOL MOIETY OF THE GPI-ANCHOR CONTAINS FULLY SATURATED, UNBRANCHED 1-O-ALKYL CHAIN (MAINLY C24:0) AND FULLY SATURATED UNBRANCHED 2-O-ACYL CHAINS (C12:0, C14:0, C16:0, AND C18:0).
s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no wa
                                                                                                                  SIMILARITY: Belongs to peptidase family M8.
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171:589-589(1990)
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R PROSITE; P800142; ZINC_PROTEASE; 1.
PYTOCHASE; Metalloprotease; Glycoprotein; Metal-binding; Zinc;
W Zymogen; Signal; Cell adhesion; GPI-anchor; 3D-structure; Lipoprotein.
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Erwinia herbicola.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
NCBI_TaxID=549;
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                                                                                                                                                                                                                                                                                                                                                                                             12.7%;
llarity 59.5%;
Conservative
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; Pred. No. 0.56
3; Mismatches
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01-FEB-1991
16-OCT-2001
              SEQUENCE FROM N.A.
MEDLINE=90092494; PubMed=2599095;
Abe K., Watabe S., Emori Y., Watar
                                                                 NCBI_TaxID=553;
                                                                               Enterobacteriaceae;
                                                                                          Pantoea ananas (Erwinia uredovora)
Bacteria; Proteobacteria; Gammaprot
                                                                                                                                                                                   P20469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 65.
PRINTS; PR00327; ICENUCLEAIN.
PROSITE; PS00314; ICE_NUCLEATION; 45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M26382; AAA24823.1;
PIR; JQ0188; JQ0188.
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SEQUENCE FROM N.A.
STRAIN=M1;
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                                                                                                                               nucleation protein inaA.
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SUBCELLULAR LOCATION: Outer membrane.
DOMALN: CONTAINS 126 IMPERFECT REPEARS OF A CONSENSUS OCTA
A-G-Y-G-S-T-X-T, FURTHER ON A 16-RESIDUE AND A REGIONAL 48
PERIODICITY IS SUPERIMPOSED.
MISCELLANBOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH TH
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF
SIMILARITY: Belongs to the bacterial ice nucleation protein
family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleation; Repeat; Outer membrane.
AIN 162 1217 OCTAPEPTIDE PERIODICITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                consensus sequence of ice nucleation proteins from Erwinia
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     nucleation
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Pred. No. 1.6;
24; Mismatches
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  of Erwinia
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P18127;
Xanthomonas campestris pv. translucens.";

Mol. Gen. Genet. 223:163-166(1990).

-i-FUNCTION: Ice nucleation proteins enable bacteria to nucleate crystallization in supercooled water.

-i- SUBCELLULAR LOCATION: Outer membrane (By similarity).

-i- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
                                                                                                                                                                                                                  MEDLINE=91080859;
                                                                                                                                                                                                                                             STRAIN=X56S;
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01-NOV-1990 (Rel.
16-OCT-2001 (Rel.
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                                                                                                                                                                                         Zhao J.,
                                                                                                                                                          Zhao J., Orser C.S.;
'Conserved repetition in the ice nucleation
                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=343;
                                                                                                                                                                                                                                                                                                                                                                                                Kanthomonas campestris (pv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ice nucleation; Repeat; Outer membrane.
162 1281 OCTAPEPTID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X17316; CAA35194.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S07053; S07053.
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FEBS Lett. 258:297-300(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleation protein.
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FUNCTION: Ice nucleation proteins enable bacteria to nucleat FUNCTION: Ice nucleation in supercooled water.

SUBCELLULAR LOCATION: Outer membrane (By similarity).

DOWALN: CONTAINS MANY IMPERFECT REPEATS OF THE CONSENSUS OCTAMEBRIDE A-G-Y-G-S-T-X-T; FUNTTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.

SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209
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Pro; IPR000258; Ice_nucleatn.
PF00818; Ice_nucleation; 69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71
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16, Last sequence update)
40, Last annotation update)
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29.3%;
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131094 MW; 89B0EE24AA837039 CRO
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Pred. No. 2.1;
20; Mismatches
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Search completed: March 11, 2004, 18:34:55 Job time: 7.3 secs
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Best Local Similarity
Matches 43; Conserv
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HSSP; P06620; IINA.
InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 81.
PRINTS; PR00327; ICENUCLBATN.
PROSITE; PS00314; ICE_NUCLEATION; 57.
ICE_nucleation; Repeat; Outer membrane.
SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                           1169
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29.9%; Pred. No. 3;
ative 26; Mismatches
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	t Query Match Length	DB	ID	Description
1	649	85.7	152	ง i	033802	O33802 salmonella
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σ	340	44.9	76	N	Q54069	Q54069 salmonella
7	133	17.6	502	16	Q8EIH4	Q8eih4 shewanella
89	120	15.9	160	16	Q8CW64	Q8cw64 escherichia
9	120	15.9	160	16	Q83RU7	
10	118.5	15.7	151	16	Q7UCZ1	Q7uczl shigella fl
11	118.5	15.7	153	16	Q89JI6	Q89ji6 bradyrhizob
12	116	15.3	171	16	Q89JI3	Q89ji3 bradyrhizob
13	115	15.2	139	16	Q8EIH3	
14	110	14.5	130	16	Q89JI4	Q89ji4 bradyrhizob
15	108.5	14.3	151	N	Q7X244	Q7x244 citrobacter
16	107.5	14.2	154	16	Q89JI5	Q89ji5 bradyrhizob

4 4 5 4	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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12.6 12.6	12.6	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.8	12.8	12.9	12.9	13.0	13.1	13.1	13.1	13.1	13.1	13.1	13.3	13.4	13.5	13.9
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121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151	61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120	61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120	1 MKLLKVAAFAAIVVSGSAVAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ 60	Query Match 85.7%; Score 649; DB 2; Length 152; Best Local Similarity 88.7%; Pred. No. 1.1e-44; Matches 134; Conservative 4; Mismatches 13; Indels 0; Gaps 0;	E 152 AA;	EMBL; AJ000514; CAA04151.1; NON TER 152 152	. Immun. 6	cells.";	n mouse small inter	"Expression of thin, aggregative fimbriae promotes interaction of		Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z., Pfeifer J.D.,		SEQUENCE FROM N.A.	[E] =	NCBI TaxID=602;		Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	Salmonella typhimurium.			(TrEMBLrel. 19, Last annotation	(TrEMBLrel. 05,	01-JAN-1998 (TrEMBLrel. 05, Created)	033802;	O33802 PRELIMINARY; PRT; 152 AA.	02	IT 1

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                                                                                                                                                                                                                                                                                     STRAIN=Fec4;
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Enterobacteriaceae; Citrol
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Bacteria, Proteobacteria,
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                         SEQUENCE FROM N.A. STRAIN=Fec39;
                                                                                    Enterobacteriaceae;
NCBI_TaxID=28141;
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SEQUENCE
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                                                                                                                                       Bacteria; Proteobacteria;
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CSGA OR C1306.
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MEDLINE=22388234; PubMed=12471157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKILKVAAIAAIVFSGSALAGVVPQYGGGGUHGGGGUNNSGPNSELNIYQYGGGNSALAQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTH-EMAHASGPDSTLSIYQYGSANAALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteome.
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  Bokranz
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A protein.
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Escherichia.
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25,
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  Romling
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R., Boutin A., Hackett
Schwartz D.C., Perna 1
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                                                                                                                                     Enterobacteriales;
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RESULT 7
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Matches 67
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Best Local S
Matches 95
                                                                       Q8EIH4;
Q8EIH4;
01-MAR-2003
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                               Conserved
S00865.
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Q54069;
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                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella enteritidis.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
         Bacteria;
                      Shewanella oneidensis.
                                                  01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                            SEQÜENCE
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EMBL; AJ515702; CAD56678.1; -.
                                                                                                                                                                                                                                                                                                                                                               STRAIN-SE30;
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=592;
                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                          NSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNG
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                                                                                                                                                                      FRNNATIDO 105
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 Proteobacteria; Gammaproteobacteria; Alteromonadales;
adaceae; Shewanella.
                                        hypothetical
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76 AA;
                                                  (TrEMBLrel.
                                                                         (TrEMBLrel.
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                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                             7704 MW;
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97.18;
                                       protein.
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                                                  Last sequence update)
                                                                                                                                                                                                                                 Score 340; DB Pred. No. 3.1e-2; Mismatches
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Pred. No. 4.
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SEQUENCE
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Q8CW64;
01-MAR-2003
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                                                                                                                            STRAIN=O6:H1 / CFT073 / ATCC 700928;

MEDLINE=22388234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Rc

Welch R.A., Burkles E.L., Liou S.-R., Boutin A., Hackett

Rasko D., Buckles E.L., Zhou S., Schwartz D.C., Perna N

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete ge

of uropathogenic Escherichia coll.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

EMBL; AE016759; AAN79778.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22297686; PubMed=12368813;
Heidelberg J.F., Pauleen I.T., Nelson K.E., Gaidos E.J., Nelson W.C. Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Baanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium characteristics."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
SEQUENCE 5
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       Enterobacteriaceae;
NCBI_TaxID=217992;
                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                Escherichia
                                                                                                                                                                                                                                                                                                                                                CSGB OR C1305.
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37; Conser
                                                              Similarity
                          VYDQ----
                                                                                                                 proteome.
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MYDQVQGDNMKNKLLFMMLTILGAPGIAAAAGYDLANSEYNF---
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502 AA; 52441 MW;
                                                                                                     160 AA;
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                                                  Conservative
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                                                                                                     16963 MW;
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                                                             15.9%;
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                                                                                                                                                                                                                                                                                                                                                            precursor.
                         ----LVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARKSET
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                                                17;
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Last
                                                  Score 120; DB
Pred. No. 0.03
L7; Mismatches
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STRAIN=2457T / ATCC 700930 / Serotype 2a;
MEDLINE=22590274; PubMed=12704152;
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01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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CSGB OR S1108.
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Enterobacteriaceae; Shige
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STRAIN=301 / Serotype 2a;

MEDLINE=22272406; PubMed=12384590;

Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang Yang J., Yang G., Wu H., Yang J., Yang G., Wu H., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen
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01-JUN-2003
01-JUN-2003
01-JUN-2003
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Enterobacteriaceae; Shigella.
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Hou Y.,
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Bacteria; Proteobacteria; Alphaproteobacteria;
Bradyrhizobiaceae; Bradyrhizobium.
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"Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T.";
Infect. Immun. 71:2775-2786(2003).
EMBL; AE016981; AAP16542.1; -.
SEQUENCE 151 AA; 15868 MW; 5D5D266B964014A0 CRC64;
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153 AA;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
Minor curlin subunit CsgB, putative.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., U
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M.
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H.,
                                                                                                                                                                                                                                    "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis.";
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NCBI_TaxID=70863;
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139 AA;
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               Conservative
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SEQUENCE
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MEDLINE=22484998; PubMed=12597275;
Maneko T., Nakamura Y., Sato S., Minamisawa K., Ucl
Kaneko T., Nakamura Y., Idesawa K., Iriguchi M.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wi
Tabata S.;
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Bacteria; Proteobacteria;
Bradyrhizobiaceae; Bradyrh
                                   Enterobacteriaceae;
NCBI_TaxID=213763;
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ALIGNMENTS

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AC A WPI; 2000-672631/65. N-PSDB; AAC64625. 05-APR-2000; 2000WO-CA000356 Synthetic. Salmonella enteritidis Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; White AP, 05-APR-1999; WO200060102-A2 vaccine; immune response; 26-FEB-2001 AAB36349; AAB36349 standard; (UYVI-) UNIV VICTORIA. 12-OCT-2000 Escherichia coli. AgfA::PT3#4 amino acid sequence SEQ ID NO:18 Doran JL, (first 99US-0127888P protein; entry) Collison immunogen. 151 SK, ₿ Kay WW;

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CegA and AgfA-homologue fimbria mubunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene

the

chromosome

o H

the

homologous

species,

recombinant gene

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 136; 139pp; English.

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RESULT 2
AAR74625
ID AAR7
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AC AAR7
XX AAR7
XX AAR7
AC AAR7
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                         Disclosure; Fig 7B; 95pp; English.
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                                                                                                                        Eliciting an
                                                                                                                                                                    WPI; 1994-358275/44.
N-PSDB; AAQ87467.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella; AgfA; vaccine.
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26-JUN-1995
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                                                                3 an immune response to Salmonella - using vector constructs, or compsns. contg. fimt
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The Salmonella AgfA protein and DNA are used in vaccine

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The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbriae (SERIT/TAF) nucleation depended compared to the production of fimbriae conjurising recombinant directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species, (a) directing recombinant gene combinant gene compositing species, (a) directing recombinant of a recombinant gene of the CC back into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant gene combinant gene in an animal, are constining a replacement segment or segments of foreign amino cc acid sequence or sequences grown on a Salmonella, E. coli or
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AAB36341
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                                                                                                                                                                                                                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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N-PSDB; AAC64617.
                                                                                                                                                                                                                                                                                                                                                                         White AP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella; agfa; chromosomal gene replacement; fimbrin; epitope;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunization compositions, respectively, to elicit an immune response Salmonella in animals (e.g. food producing animals) and humans. (Updat on 25-MAR-2003 to correct PN field.)
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Pred. No. 6.
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Best Local S
Matches 137
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The present sequence represents agfA encoded derived from Salmonella enteritidis 27655-3b.
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29-SEP-1997
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                                                                                                                                                                                                                                                                                           Collinson
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                                                                            Example 2; Fig 7; 85pp; English
                                                                                                                              enteropathogenic
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thogenic bacteria
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "Encoded by GCC"
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90.7%;
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Pred. No. 6.8e-59;
3; Mismatches 11
                                                                                                                                 used for diagnosis of Salmonella e Enterobacteria family.
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he full agfA gene
nucleic acid can
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Best Local S
Matches 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriacese for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                             Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                   Disclosure; Page 138; 139pp;
                                                                                                                                                                                                                                                                                                                                          05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AgfA::PT3#8 amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine;
                                                                                                                                                                                                          2000-672631/65.
DB; AAC64629.
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                                                                                                                                                                                                                                                  Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agfA; chromosomal gene replacement;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         response;
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90.1%;
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Pred.
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No. 2.1e-58;
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Best Local Similarity
Matches 136; Conserv
Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA
                                                                                                                                                                                             White AP, Doran JL,
                                                                                                                   N-PSDB; AAC64626.
                                                                                                                                             WPI; 2000-672631/65
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Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AgfA::PT3#5 amino acid sequence SEQ ID NO:20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB36350 standard; protein; 151 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVTRVVTHEMAHA------GYGNGADVGQGADNSTIELTQNGFENNATIDQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WNAKNŚDITYGQYGGNNAALVNOTASDSSVMVROVGFGNNATANOV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                    99US-0127888P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 response;
                                                                                                                                                                                                Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.5%;
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Pred. No. 2.4e-57;
0; Mismatches 0; Indels
                                                                                                                                                                                                SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 151;
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RESULT 7
AAB36348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC Agfa, CsgA and Agfa-homologue fimbrin subunits, respectively, (2)
CC homologous species; (3) directing recombinant gene into the chromosome of the CC back into the chromosome of the homologous species, and (4) eliciting an immune response in an animal;
CC copy of that gene; and (4) eliciting an immune response in an animal;
CC protein containing a replacement segment or segments of foreign amino acid polymer comprising a recombinant Agfa (2) grotein containing a replacement segment or segments of foreign amino CC Enterobacteriaceae host cell, from the host cell and introducing the useful for the expression of recombinant Agfa protein which is useful for celliciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to immunogenicity and adhesion properties relevant for an efficient live immunogens, which may be importent for directing an immune response considered the inserted epitope, and hybrid fimbriae are usually strong considered to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
     05-APR-2000; 2000WO-CA000356.
                                              12-OCT-2000
                                                                               WO200060102-A2
                                                                                                                                 Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                         Salmonella; agfA; chromosomal gene replacement; fimbrin;
                                                                                                                                                                                vaccine; immune response;
                                                                                                                                                                                                                            AgfA::PT3#3 amino acid sequence SEQ ID NO:16.
                                                                                                                                                                                                                                                                         26-FEB-2001
                                                                                                                                                                                                                                                                                                                                    AAB36348 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 151 AA;
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(1) use of thin aggregative fimbriae (SEF1/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SDARKYDQLVTRVVTHEMAHA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVÁAFAÁTVVSGSÁLAGVVÞQWGGGGNHNGGGNSSGÞDSTLSTYQYGSANAALALQ
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28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        RNNATIDOWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                  RNNATIDOWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----YDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADVSTIELTQNGF 97
                                                                                                                                                                                                                                                                   (first entry)
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73.6%;
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Pred. No. 3.3e-52;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GQGADNSTIELTQNGF
                                                                                                                                                                                           epitope;
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05-APR-1999;

99US-0127888P

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RESULT 8
AAB36346
ID AAB3
XX
AC AAB3
XX
DT 26-F
XX
DE Agf#
XX
KW Salm
KW vacc
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and the accomplished to purify in large amount. The present sequence is given in the accomplished to the present incompliance are cased and the present in the present sequence is given in the accomplished to the present incompliance are cased and the present sequence is given in the accomplished the present incomplished the present sequence is given in the accomplished the present incomplished the pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 151 AA;
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                             Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                   AgfA::PT3#1 amino acid sequence SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segmence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended
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vaccine; immune response; immunogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                            (first entry)
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76.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNN
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Pred. No. 8e-52;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               back into the Chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier imbrial subunit proteins are usually strong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CegA and AgfA-homologue fimbria subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombination of a secombination of a recombination of the homologous species; (3) directing recombination of a recombination of a recombination of a recombination of the homologous species; (3) directing recombination of a recombination of the combination                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 135; 139pp; English.
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Escherichia coli.
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121
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                                                                                                                                                                                                                                                                                                                                                                               122;
                                                                                                                       61
                                                                                                                                                                                                                                                                                                                <u>س</u>
                                                                                                                                                                                                                                                                                  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                        NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                        SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
NNAALVNYDQLVTRVVTHEMAHANNATANQY
                                                                                                                                                                                                                                                 MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         78.6%;
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                                                                                                                   YGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD
                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 613; DB 3; Length 151
Pred. No. 2.4e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SK,
                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT

120

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CC assembly system of strains of Salmonella, Escherichia coli and CC Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CsgA and AgfA homologue fimbrin subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the CC homologous species; (3) directing recombinant gene into the chromosome of the back into the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant AgfA protein which is useful for celiciting an immune response in an animal. In a fimbrial presentation consistent the heterologous antigens are presented in high numbers (up to complete cell), the hybrid fimbria protein possesses both the communogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong against the inserted epitope, and hybrid fimbriae are easy and consistent to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB36347
                                                         Matches
                                                                         Query Match
Best Local Similarity
                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        White AP, Doran JL,
                                                                                                                                                                 inexpensive to purify in large amount. The present sequence the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 136; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein useful for eliciting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AgfA::PT3#2 amino acid sequence SEQ ID NO:14
1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                    151 AA;
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                       78.3%;
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                                                  Score 611; DB 3;
Pred. No. 3.8e-51;
6; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune response in animal.
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                                                                                     Length 151;
                                                     Indels
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                                                                                                                                                                                     is given in
                                                Gaps
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MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ

60

to purify

The present sequence is given

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RESULT 10
AAB36352
        directing recombination of a recombinant gene into the chromosome of the Chomologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein seems both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response
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                                                                                                                                                                                                                                                                                                                                                          The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            White AP, Doran JL,
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ARBSULT 11
AAB36354
ID AAB36554
XX AAB36
XX AAB36
XX SAlmo
XX Salmo
XX Salmo
XX Salmo
XX Salmo
XX Salmo
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XX WO200
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XX WO200
XX WO200
XX WO5-AE
XX WHI;
DR N-PSI
XX WHI;
DR N-PSI
XX WHI;
DR N-PSI
XX WHI;
CC Segun
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CC Agfa
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Best Local Similarity 82.9
Matches 124; Conservative
              The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CegA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene homologous species; (3) directing recombination of a recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene back into the chromosome of the homologous species in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino
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                                                                                                                                                                                                                                                                                                            Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA
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 grown on a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 608; DB Pred. No. 7.4e-5; Mismatches
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                                                                                                                                                                                                                                                                                              response
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                                                                                                                                                                                                                                                                                                 animal.
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RESULT 12
AAB36351
ID AAB36
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful, for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                       Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 151 AA;
                                                                                                                                                                                                                   05-APR-1999;
                                                                                                                                                                                                                                           05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                              WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                          vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                AgfA::PT3#6 amino acid sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the exemplification of the present invention
                                                                                                                                                                                           (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                    Sscherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKILKVAAFAAIVVSGSALAGVVPQWGGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                Doran JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                    99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.1%;
80.8%;
                                                                                                                                                                 Collison
                                                                                                                                                                                                                                                                                                                                                                          ımmunogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151
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Pred. No. 3.
                                                                                                                                                                 SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                 Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                  NO:22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 151;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described

Disclosure; Page 137; 139pp; English.

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

WPI; 2000-672631/65. N-PSDB; AAC64627.

N-PSDB; AAC64631.

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RESULT 13
AAB36355
ID AAB36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC copy of that gene; and (4) eliciting an immune response in an animal, and (a) eliciting an immune response in an animal, and (but of the gene; and (c) eliciting an immune response in an animal, and comprising a recombinant AgfA comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the complymer into the animal in conjunction with a carrier or diluent. (I) is consequence segments of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for celliciting an immune response in an animal. In a fimbrial presentation consequence (up to a system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein sets both the communogenicity and adhesion properties relevant for an efficient live immunogens, which may be important for directing an immune response consequence in the inserted epitope, and hybrid fimbriae are easy and consequence in a system in the present sequence is given in the present in the inserted epitope.
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Best Local (
WPI; 2000-672631/65
                            White AP, Doran JL,
                                                                                                      05-APR-1999;
                                                                                                                                       05-APR-2000; 2000WO-CA000356
                                                                  (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                               Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                    AgfA::PT3#10 amino acid sequence SEQ ID NO:30
                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2001 (first entry)
                                                                                                                                                                               12-OCT-2000
                                                                                                                                                                                                                   WO200060102-A2
                                                                                                                                                                                                                                                                    Escherichia coli.
                                                                                                                                                                                                                                                                                                                          vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB36355 standard; protein; 151
                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                      Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                          immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKLLKVAAFAAI VVSGSALAGVVPOWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                      99US-0127888P
                                                                                                                                                                                                                                                                                                                      response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.9%;
81.5%;
                                Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 600; DB Pred. No. 4.4e 5; Mismatches
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                              SK,
                            Kay
                              WW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
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The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEFI7/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC AgfA, CsgA and AgfA-homologue fimbriae in the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species, (2) CC chomologous species; (3) directing recombinant gene into the chromosome of the comprising a recombinant gene CC copy of that gene; and (4) eliciting an immune response in an animal. CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the cuseful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to immunogenicity and adhesion properties relevant for an efficient live conditions the carrier fibbrial subunit protein are usually strong companish the inserted epitope, and hybrid fimbriae are usually strong conditions which may be important for directing an immune response in an immune response conditions are usually strong conditions. The present sequence is given in the expressive to purify in large amount. The present sequence is given in the examination of the present invention.
Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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В Query Match Best Local S Matches 123 121 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151 123; 61 61 н Similarity SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG MKLLKVAAFAAIVVSGSALAGVVFQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ NNAALVNOTASDSSVMVROVGFGNNATANOY 151 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG Conservative 76.8%; 81.5%; <u>υ</u> Score 599; DB 3; Pred. No. 5.5e-50; 5; Mismatches 23 Length 151 Indels 0 Gaps 120 120 60 60 0

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RESULT 14
AAB36343
ID AAB36
Escherichia coli CsgA amino acid sequence SEQ ID NO:7
                                                    vaccine;
                                                            Salmonella;
                                                                                          26~FEB-2001
                                                                                                          AAB36343;
                                                                                                                      AAB36343 standard; protein; 151 AA
                                                   immune
                                                           agfA;
                                                                                        (first entry)
                                                   response;
                                                       chromosomal gene replacement; fimbrin; epitope;
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12-OCT-2000

Escherichia coli

WO200060102-A2.

05-APR-2000;

2000WO-CA000356

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RESULT 15
ABR82651
ID ABR82
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AC ABR82
XX
DT 04-DE
XX
DE E CO
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Best Local S
Matches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                back into the chromosome of the homologous species, replacing the native copy of that gene, and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong
                E, coli CsgA subunit 15 kDa protein.
                                                          04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                segment of the gene has been replaced by a beginning. Also described a sequence which encodes a foreign epitope or antigen. Also described a sequence which encodes a foreign epitope or antigen. Also described a sequence which encodes a foreign expension of salmonella. Escherichia coli and
                                                                                                  ABR82651
                                                                                                                                       ABR82651 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                            GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                                                                                                                                                         NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                         TDARNSDLTITOHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
                                                                                                                                                                                                                                                                                                                                                SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 AA
                                                                                                                                                                                                                                                                                                                                                                                                    MKLLKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGGNNSGPNSELNIYQYGGGNSALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention describes a recombinant agfA gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 135;
                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0127888P
                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.1%; Score 523; DB 3; 68.9%; Pred. No. 1.2e-42; tive 20; Mismatches 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 151;
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Search completed: March 11, Job time: 46.9 secs

2004, 18:33:38

121

GNGAAVDOTASNSSVNVTOVGFGNNATAHOY

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                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                           The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABR82642, ABR82648-49. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infections.
                                                                                                                                                                                                                                Sequence
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N-PSDB; ACF36153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bjoerck L,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 41-42; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JAN-2002; 2002GB-00002275
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                                                         SDARKSETTITQSGYGNGADVGQGADNSTIBLTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                     MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
                                                                                                  MKLLKVEAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
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                                                                                                                                                                                66.4%; Score 518; DB 7; 68.2%; Pred. No. 3.8e-42;
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
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  Issued_Patents_AA:*
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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RESULT 1
US-08-233-788A-59
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Query Match
Best Local S
Matches 136
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Patent No. 5635617
GENERAL INFORMATION:
APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: OF SALMONELLA
                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.

ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
                                                                                                                                                                                         TELEX: 3723836 SEEDANBERRY INFORMATION FOR SEQ ID NO: 59:
                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-631
                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                TYPE: amino acid
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CITY: Seattle
STATE: Washington
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6300 Columbia Center,
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ilarity 90.1%;
Conservative
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Score 686; DB 1; I
Pred. No. 2.2e-62;
3; Mismatches 12;
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US-08-233-788A-57
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Sequence 4764, Application US/09328352 Patent No. 6562958 GENERAL INFORMATION:
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APPLICANT: Doran,
APPLICANT: Kay, Wil
APPLICANT: Collins
APPLICANT: Clouthic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 57, Application US/08233788A Patent No. 5635617
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206) 682-603
TELEX: 3723836 SEEDANE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: King, Joshua
REGISTAGN NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,78;
FILING DATE: 26-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                               y Match 64.9%;
Local Similarity 87.5%;
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                                                                                                                                                                                                                  VVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADV
                                                                                                                    GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 112
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Kay, William W.

Collinson, Karen S.

Clouthier, Sharon C.

AVENTION: METHODS AND COMPOSITIONS FOR DETECTION

VENTION: OF SALMONELLA
                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4764
                                                                                                                                                                                           APPLICATION NUMBER: US/08/254,573
FILING DATE: 06-UUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,611
FILING DATE: 10-UUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                      REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION DATA:
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TYPE: PRT
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION
           TYPE: ami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER OF SEQUENCES:
                                                                                                          TELEPHONE: (703)683-4109
                                                                                                      TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 SGSALAGVVPQWGGGGNHNGG-GNSSGPDYDQLVTRVVTHEM-----AHALQSDA 63
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                            amino acids
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KAMBOJ, kaj
ELIOTT, Candace
'""T, Stephen
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Pred. No. 0.75;
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                                                                                                                                                                                                                                                                                                                                                                                   Version #1
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Sequence, Patent No. 57500.

Patent No. 57500.

GENERAL INFORMATION:

APPLICANT: Hoeger, Thomas

APPLICANT: Ultsch, Andreas

APPLICANT: Bach, Alfred

APPLICANT: Sterrer, Sylvia

APPLICANT: Lemaire, Hans-Georg

APPLICANT: Lemaire, Hans-Georg

TTTLE OF INVENTION: Subunits of Glutamate Receptors, Their

TOTAL OF INVENTION: Preparation and Their Use
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Best Local S
Matches 45
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Best Local (
                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 906 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.5 inch, 720 Kb storage
COMPUTER: IBM AT-compatible, 80286 processor
OPERATING SYSTEM: MS-DOS version 6.0
SOFTWARE: WordPerfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,379
FILING DATE: 05-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 110-
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                    Local Similarity
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                                       301 AEAFQSLRRQ---RIDISRRGNAGDCLANPAVPWGQGIDIQRALQQVRFEGLTGNVQFNE
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                                                                             56 AHALQSDARKSETTITQSGYGNGADV------GQGAD------NSTIELTQ
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                                                                                                                                                                                                                  11.5%; Score 90; DB 1; Length 906; 22.6%; Pred. No. 1.1;
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-----IDQWNAKNSDI---TVGQYGGNNAALVNQT-----ASD
                                                                                                                                                                                                 26; Mismatches
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US-08-687-379-4
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                                                                                                          RESULT 7
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Sequence 1, Application US/08172332
Patent No. 6313279
GENERAL INFORMATION:
APPLICANT: Burnett, J. Paul
APPLICANT: Mayne, Nancy G
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INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette-3.5 inch, 720 Kb storak COMPUTER: IBM AT-compatible, 80286 processor OPERATING SYSTEM: MS-DOS VERSION 6.0 SOFTWARE: WordPerfect version 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/687,379
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APPLICANT:
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APPLICANT: Sterrer, Sylvia
APPLICANT: Lemaire, Hans-Georg
TITLE OF INVENTION: Subunits of Glutamate Receptors, Their
TITLE OF INVENTION: Preparation and Their Use
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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1101 Connecticut Avenue
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Andreas
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Pred. No.
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US-08-216-326-2
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                   APPLICANT: KAMBOJ, Rajender
APPLICANT: ELIOTT, Candace
APPLICANT: NUTT, Stephen
TITLE OF INVENTION: AMPA-BINDING
                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
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LENGTH: 906 amino acid
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TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
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APPLICANT: Sharp, Robert I
TITLE OF INVENTION: HUMAN
TITLE OF INVENTION: COMPOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
ADDRESSEE: Foley & Lardner STREET: 3000 K Street N.W., CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Leeds, James P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/879,688 FILING DATE: May 1, 1992
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                                                                                                                                                                                                                                                                                                                                                   358 KGRRINYTLHVIEMKHDGIRKIGYWNEDDKFVPAATDAQAGGDNSSVQNRTYIVTTILED 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 VTGFQLVNYTDTIPAKIMQQW------KNSDARDHTRVDWKRPKYTSALTYDGVKVM 300
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                                                                                                                                                                                                                                                                                                                                                                                              NGFRNNAT----
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Lilly Corporate Center
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SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN GLUTAMATE RECEPTOR AND RELATED DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/172,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                    -----IDQWNAKNSDI----TVGQYGGNNAALVNQT-----ASD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 90; DB 4; Length 906; Pred. No. 1.1; 6; Mismatches 56; Indels
                Suite 500
                                                                                   HUMAN Glur1 RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version
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RESULT 9
US-08-864-038A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08864038A Patent No. 6001592
GENERAL INFORMATION:
APPLICANT: Kunio NAKASHTMA at all arters are all all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters are all arters ar
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                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KUMÍO NAKASHIMA et al.
TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
TITLE OF INVENTION: TO SAID POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FLOS PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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APPLICATION NUMBER: US/08/216,326
APPLICATION NUMBER: US/08/216,326
FILING DATE: 23-MAR-1994
PRIOR APPLICATION TUBERTA:
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                                                                                                                                                                                                                                                              STREET: Isshind
       COMPUTER: IBM CO-
OPERATING SYSTEM:
                                                                                                                                                        COUNTRY: JAPAN
ZIP: 514-01
                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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ZIP: 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358
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IBM Compatible
SYSTEM: Microsoft Windows 95
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                                                                          3.50 inch, 1.44 MB
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Pred. No.
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SOPTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:

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RESULT 10
US-09-336-447A-5
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// TYPE: PRT
// ORGANISM: Moraxella catarrhalis
US-09-336-447A-5

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Best Local Similarity 25.6
 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09336447A Patent No. 6310190 GENERAL INFORMATION:
                                                                                                                                           SOFTWARE: Patentin Ver. SEQ ID NO 5
               Query Match
Best Local Similarity
                                                                                                                                                                                                                                               APPLICANT: HANSEN, ERIC J.
APPLICANT: ABBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: PISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
APPLICANT: FREDENBURG, ROSS A.
APPLICANT: TREDENBURG, ROSS A.
                                                                                                                                                                             FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
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TELEFAX: (212)953-7733
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                          LENGTH: 892
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LENGTH: 738
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APPLICATION NUMBER: JP 8-
PILING DATE: 15-July-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: peptide
LOCATION: from 1 to 738
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REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELL TYPE: mantle epithelial cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/864,038A FILING DATE: May 28, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGGNNAALVNQTASDSS-----VMVRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARKSETTITQSGYGNGADVGQGADNSTIELTQ-----NGFRNNATIDQWNAKNSDITVGQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pinctada fucata
10.8%; Score 84; DB 26.8%; Pred. No. 4.3; tive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.2%; Score 87.5; D
25.6%; Pred. No. 1.5;
Live 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP 8-184459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22,389
3ER: F-5610
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                                   DB 4;
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                                                                                                                                                                                                                                                         OF MORAXELLA CATARRHALIS
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   55
                                 Length 892
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   Indels
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US-07-718-575-2
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Patent No. 52
                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 9103330318
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 907 amino acid
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: 9318
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jensen Ph.D., Jan
TITLE OF INVENTION: GLUTAMA:
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 444 So. F. CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/718,575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                      310 Q---RIDISRRGNAGDCLANPAVPWGQGIDIQRALQQVRFEGLTGNVQFNEKGRRTNYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 NNSTVAGGSHNQATGEGSF---AAGVENKANAN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 IGGGYYSRAIGDSSTIGGGYYNQATGEKSTVAGGRNN----QATGNNSTVAGGSYNQATG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <sup>7</sup>5
                                                                                                          65 KSETTITQSGYGNGADV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
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                                                                                                                                                                                                                  43;
                                                                                                                                                                           6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGG-NSSGPDYDQLVTRVVTHEMAHALQSDAR
HVIEMKHDGIRKIGYWNEDDKFVPAATDAQAGGDNSSVQNRTYIVTTILEDPYVMLKK--
                                   -----IDQWNAKNSDI---TVGQYGGNNAALVNQT-----ASDSSVMVRQVG 141
                                                                                                                                           VTGFQLVNYTDTIPARIMQQWRTSDSRDHTRVDWKRPKYTSALTYDGVKVMAEAFQSLRR
                                                                                                                                                                                                                                                                                                                                       AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGQG-----ADNSTI------ELTQNGFRNNATIDQWNAKNSDITVGQYG---G
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                                                                                                                                                                                                                                                                                                                                                        907 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                  (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States
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VENTION: GLUTAMATE RECEPTOR
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Hollmann Ph.D., Michael NMN
Bettler Ph.D., Bernhard NMN
                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19910813
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                                                                                                                                                                                                                                 10.8%;
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                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P31 8962
                                                                                                                                                                                                                               Score 84; DB 1; Length 907; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stephen F.
                                                                                                                                                                                                                  Mismatches
                                                                                                          GQGAD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version
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                                                                                                                                                                                                                69;
                                                                                                                                                                                                                  Indels
                                                                                                        ---NSTIELTQNGFRNNAT- 102
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                                                                                                                                                                                                              Gaps
                                                                                                                                             309
     424
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RESULT 12 US-08-481-206-2

GENERAL INFORMATION:

STREET: 444 SO. FI CITY: Los Angeles STATE: California

COUNTRY:

90071-2921

United States

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425 142

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APPLICANT: Hollmann Ph.D., Mid
APPLICANT: Bettler Ph.D., Berr
APPLICANT: Jensen Ph.D., Jan
TITLE OF INVENTION: GLUTAMATE
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Reiter Ph.D., Stephen E. REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,206
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Pretty, Schroeder
STREET: 444 So. Flower St.,
                                                                              367 HVIEMKHDGIRKÍGYMNEDDKFVÞAATDAQAGGDNSSVQNRTYIVTTILEDÞYVNLKK--
                                                                                                                                                   310 Q---RIDIŚRRĆNAGÓCLANPAVPWGQGIDIQRALQQVRFEGLTGNVQFNEKĠRRTNYTL 366
                                                                                                                                                                                        65 KSETTITQSGYGNGADV------GQGAD------NSTIELTQNGFRNNAT- 102
                                                                                                                                                                                                                                                               6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGG-NSSGPDYDQLVTRVVTHEWAHALQSDAR 64
                                                                                                    ------IDQWNAKNSDI---TVGQYGGNNAALVNOT-----ASDSSVMVRQVG 141
                                                                                                                                                                                                                            VTGFQLVNYTDTIPÄRIMQQWRTSDSRDHTRVDWKRPKYTSALTYDGVKVWAEAFQSLRR 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08481206
                                                                                                                                                                                                                                                                                                                  10.8%; Score 84; DB 1; Length 907, ilarity 22.6%; Pred. No. 4.4; Conservative 24; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bettler Ph.D., Bernharu AFT.,
Jensen Ph.D., Jan E.
VENTION: GLUTAMATE RECEPTOR COMPOSITIONS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heinemann Ph.D., Stephen F.
Boulter Ph.D., James R.
Hollmann Ph.D., Michael NMN
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                                                                                                                                                                                                                                                                                                            Mismatches
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Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.25
                                                                                                                                                                                                                                                                                                          69;
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                        54;
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                                                                                                                                                                                                                        Query Match 10.8%; Score 84; DB 2; Length 907 Best Local Similarity 22.6%; Pred. No. 4.4; Matches 43; Conservative 24; Mismatches 69; Indels
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US-08-486-269A-2
                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 907 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/013,767
FILING DATE: 04-FEB-1993
APPLICATION NUMBER: 07/718,575
FILING DATE: 21-JUN-1991
FILING DATE: 25-OCT-1990
APPLICATION NUMBER: 07/428,116
FILING DATE: 27-OCT-1989
APPLICATION NUMBER: 07/428,116
ATTORNEY/AGENT INFORMATION:
NAME: Reiter. Stanhon R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows DEMON
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,269A
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Reiter, Stephen REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                           250 VTGFQLVNYTDT1PÅRIMQQWRTSDSRDHTRVDWKRPKYTSALTYDGVKVMÅBÅFQSLRR 309
                                                                                                                                                                              6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGG-NSSGPDYDQLVTRVVTHEMAHALQSDAR 64
HVIEMKHDGIRKIGYMNEDDKFVPAATDAQAGGDNSSVQNRTYIVTTILEDPYVMLKK--
                                                                      Q---RIDISRRGNAGDCLANPAVPWGQGIDIQRALQQVRFEGLTGNVQFNEKGRRTNYTL 366
                                                                                                                   KSETTITQSGYGNGADV-------GQGAD----
                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          San Diego
CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           619-677-1465
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4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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Bettler, Bernhard
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Boulter, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                  amino acids
                                 IDQWNAKNSDI---TVGQYGGNNAALVNQT----ASDSSVMVRQVG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Jan E.

GLUTAMATE RECEPTOR COMPOSITIONS
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for Windows DEMONSTRATION Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT/US90/06153
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                                                                                                        -----NSTIELTQNGFRNNAT- 102
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142 FGNNATANOY 151

425

----NANQF 429

; MOLECULE TYPE: protein US-08-481-206-2

TYPE: amino acid

LENGTH:

907 amino acids

MOLECULE

TELEX: 9103330318
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

TELEFAX:

(619)535-8949

(619)

535-9001

TELEPHONE:

CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: 1

ATTORNEY/AGENT INFORMATION:

Matches Query Match

250

Local Similarity es 43; Conserv

24;

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                                                                                                                          US-09-072-596-199
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                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVID J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPAN: (206) 622-4900
TELEPAN: (206) 682-6031
INFORMATION FOR SEQ ID NO: 204:
                                                                           Sequence 199, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 204, App.
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                                             APPLICANT:
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APPLICANT: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS
                               APPLICANT:
APPLICANT:
               PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 943 amino acids
TYPE: amino acid
STRANDEDNESS:
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FILING DATE: 07-APR-1998
CLASSIFICATION:
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31; Conservative
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             Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
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Search completed: March 11, 2004, 18:44:51
Job time :
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELECHONE: (206) 622-4900
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
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STREET: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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TOPOLOGY: 13
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                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                              212 FGNSGDANTGFFNSGTANTGVGNAGNYNTGSYNPGNSNTGGFNMGQYNTGYLNSGNYNTG
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Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
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Pred. No. 4.7;
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Perfect score:
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seq length: 2000000000
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: /cgn2 6/ptcdata/1/pubpaa/US06_PUBCOMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-793-306-1146

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US-09-810-264-28

US-09-952-267-5

US-09-996-634-131

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   US-09-952-267-13
US-10-238-075-1549
US-09-820-843A-21
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Sequence 20638, A
Sequence 146, App
Sequence 2, Appli
Sequence 28, Appli
Sequence 12833, A
Sequence 131, App
Sequence 131, App
Sequence 111, App
Sequence 199, App
Sequence 204, App
Sequence 16, Appl
Sequence 16, Appl
Sequence 179, App
Sequence 179, App
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Sequence 180, Appl
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-10-156-7	US-10-085-959-252	US-10-238-075-1119	US-10-093-037-63	- 1	-10-156-761-	-10-156-761-	-10-156	9-493-	-10	US-10-076-604-101	US-10-076-604-103	US-10-156-761-11286	52	ശ	US-09-809-517A-26	US-09-809-517A-23	US-09-809-517A-25	US-10-045-674-591	US-09-884-767A-213	US-09-884-767A-215	US-10-033-399B-12	US-09-809-517A-27	US-09-809-517A-24	0	US-10-016-986-34	٩	US-09-797-862-33	8	US-09-9/6-29/-2
Sequence 9107, Ap	e 252	1119	e 63,	Sequence 63, Appl	119	12605,	13173,	20096	Sequence 105, App	101,		11286	527,	e 27	26,	23,	25,	e 59		15	e 12	27,	24, 1	16,	34,	ce 594	e 33, 1	176,	*

ALIGNMENTS

Q	Qy da	Query Match Best Local Matches 4	; NAME, ; LOCA; ; OTHEI US-10-36;	; TYPE: PYPE: ; PRIOR ; NUMBEI ; SEQ ID	; FILE OF ; FILE REFE ; CURRENT F ; CURRENT E ; PRIOR APE	APPLICANT: APPLICANT: APPLICANT: ITTLE OF I	; Sequence 20 ; Publication ; GENERAL INF ; APPLICANT: ; APPLICANT:	RESULT 1 US-10-369	
51 VTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKN 110 :	7 AAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRV 50	Query Match 13.9%; Score 108.5; DB 15; Length 445; Best Local Similarity 27.5%; Pred. No. 0.0089; Matches 46; Conservative 19; Mismatches 61; Indels 41; Gaps 6;	; NAME/KEY: unsure; NAME/KEY: unsure; LOCATION: (1)(445); LOCATION: (1)(445); OTHER INFORMATION: unsure at all Xaa locations US-10-369-493-20638	TYPE: PRT ORGANISM: Rhodopseudomonas palustris FEATURE:	PRIOR FILING DATE: 2002-02-21 NUMBER OF SEQ ID NOS: 47374 SEQ ID NO 20638 1FMCTH. 445	FILE REFERENCE: 38-10 (52052)B CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28 PRIOR APPLICATION NUMBER: US 60/360,039	Goldman, Chen, Xia Chen, Xia INVENTION: I	Sequence 20638, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION: APPLICANT: Cao, Yongwei APPLICANT: Hinkle, Gregory J.	RESULT 1 US-10-369-493-20638

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CURRENT APPLICATION NUMBER: US/10/251,661
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/193,614
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: PCT/US01/10661
PRIOR FILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                RESULT 3
US-10-251-661-2
Sequence 2, Application US/10251661
Publication No. US2003016555A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 146
LENGTH: 597
TYPE: PRT
ORGANISM: Artificial Sequence
PRATURE: PRT
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                                                                                                                                                                       TITLE OF INVENTION: Methods and Compositions for TITLE OF INVENTION: Memory Consolidation FILE REFERENCE: 3499.1001-003
                                                                                                                                                                                                                                   APPLICANT: Alberini, Cristina M. APPLICANT: Bear, Mark F.
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TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
TITLE OF INVENTION: of Tuberculosis
FILE REFERENCE: 014058-008740US
CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT FILING DATE: 2001-02-26
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APPLICANT:
APPLICANT:
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APPLICANT: Skeiky, Yasir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNSTIELTQNGFRNNATIDQ--WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFG 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----VKQSGNSNSVGRDIQGKQSGAGNSAAIFQEGTGSDVELQQTGTSNGAVPSGWNWTN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lodes, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jen, Shyian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.7%; Score 91; DB 9; Length 597; 27.8%; Pred. No. 0.8;
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GENERAL INFORMATION
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US-10-369-493-12833
; Sequence 12833, Application US/10369493
; Publication No. US20030233675A1
                                                             RESULT
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-661-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 278
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                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhang, Lingyu
TITLE OF INVENTION: WRKY Transcription Factors and Methods
TITLE OF INVENTION: of Use
FILE REFERENCE: 1183
CURRENT APPLICATION NUMBER: US/09/810,264
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/190,467
PRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence 28,
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APPLICANT:
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APPLICANT: Crane, Virginia C.

Pamodu. Omolayo O.
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                                                                                                                                                                                                                                                                                                                                    Local Similarity es 35; Conserv
                                                                                                      182 VGCPVRKHVERASHDNRÁVITTYEGRHSHDVPVGRGAGASRALPTSSSSDSSVVV 236
                                                                                                                                                                           122 DNEGSSGTGACVKPVREPRLVVQTLSDIDILDDGFRWRKYGQKVVKGNPNPRSYYKCTT
                                                                                                                                                                                                                                                                                    15 SG$ALAGYVPQWGGGGNHNGGGNS$GPDYDQLVTRVVTHEMAHALQSDARKSETTITQSG 74
                                                                                                                                                                                                                                                 71 NSSGCAAVIAE-----DHTNGSEHSGPTPENSSVTFGDDEADNGAEPETKRRK----EHG
                                                                                                                                                                                                                      75 YGNGADVGQGA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 AEAFQSLRRQ---RIDISRRGNAGDCLANPAVPWGQGIDIQRALQQVAFEGLTGNVQFNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 VTGFQLVNYTDTIPÄKIMQOW------KNSDARDHTRVDWKRPKYTSALTYDGVKVM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 AHALQSDARKSETTITQSGYGNGADV------GQGAD------NSTIELTQ
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                                                                                                                                     NNATIDQWNAKNS-DITVGQYGGNNAALVNQTASDSSVMV 137
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Pred. No. 1
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SEQ ID NO 5
LENGTH: 852
TYPE PRT
ORGANISM: Moraxella catarrhalis
US-09-952-267-5
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; LOCATION: (1)..(408)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-12833
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                                                                                                                                                                 Query Match
Best Local Similarity
Matches 41; Conserv
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Best Local :
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SEQ ID NO 12833
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                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/952,267
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 09/336,447
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HANSEN, APPLICANT: AEBI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
PILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Aspergillus nidulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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133 IGGGYYSRAIGDSSTIGGGYYNQATGEKSTVAGGRNN----QATGNNSTVAGGSYNQATG 188
                                      81 VGQG-----ADNSTI-----G 120
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                                                                                                                        28 GGGNHNGGGNSS----GPDYDQLVTRVVTHEMAHALQSDARKSETTI----TQSGYGNGAD
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                                                                                GGKDNEAKGNYSTVGGGDYNEAKGNYST--VGGGSSNTAKGEKSTIGGGDTNDANGTYST 132
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No. US20030032772A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGFTNSSSFDPINIGGKDITITTTEGSVIDGNGQAYWDGLGSNGGV 117
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COPE, LESLIE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Slater, Steven C. Goldman, Barry S.
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Slater, Steven C.
                                                                                                                                                                   Conservative
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28.3%; Pred. No. 2.3;
                                                                                                                                                                 10.8%; Score 84; DB 26.8%; Pred. No. 7; tive 17; Mismatches
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                                                                                                                                                                                                           DB 10; Length 892;
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US-09-996-634-131
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US-09-996-634-131
                                                                                        PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/900,823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
SOFTWARE: PatentIn
SEQ ID NO 131
LENGTH: 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 131
LENGTH: 943
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Patent No. US20020172684A1
GENERAL INFORMATION:
APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Namo, Fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 131, A Publication No.
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CURRENT FILING DATE: 2001-11-28
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PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
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CURRENT APPLICATION NUMBER: US/09/996,634
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
                                                                        NUMBER OF SEQ ID NOS: 169
                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 61258
                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences TITLE OF INVENTION: immunostimulatory Peptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09997182
o. US20030049263A1
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nilarity 25.2%;
Conservative
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701 Fifth Avenue

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RESULT 10
US-10-193-002-199
; Sequence 199, Application No. US20030;
; Publication No. US20030;
; GENERAL INFORMATION;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. SEQ ID NO 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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PRIOR FILING DATE: 1995-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/447/135
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 61257
CURRENT APPLICATION NUMBER: US/09/997,181
CURRENT FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 94
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mycobacterium tuberculosis
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                                                       APPLICANT: Reed, Steven G.
                                                                                                                                                                                                     379 LAN 381
                                                                                                                                                                                                                                    125 LVN 127
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                                                                                                                                                                                                                                                                                                                                                                      SGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSG 74
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                                                                                        Application US/10193002 o. US20030135026A1
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                    Skeiky, Yasir A.W.
Dillon, Davin C.
     Campos-Neto, Antonia
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Pred. No. 7.5;
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Matches
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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mes 31; Conserv
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APPLICATION NUMBER: US/10/193,002

FILING DATE: 10-Jul-2002

CLASSIFICATION: «Unknown»

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/072,596 FILING DATE: 05-MAY-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 199:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                272 LAN 274
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                                                                                                                                                                                                                                                                                                                                                                    YGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD---ITVGQY------GGNNAA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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ZIP: 98104-7092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDRESSEE: SEED and BERRY LLP
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                             Houghton, Raymond
Vedvick, Thomas S.
                                                              Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
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Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Twardzik, Daniel R.
Lodes, Michael J.
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                                                 Raymond
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                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                               Sequence 16, Application US/09996194 Patent No. US20020151696A1
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Best Local (
              APPLICANT: Bandaru, Rajasehkar
TITLE OF INVENTION: 84242, 8035, 55304, 52999, and 21999,
TITLE OF INVENTION: No. US20020151696A1el Human Proteins and Methods of Use Thereof
FILE REPERENCE: 35800/240590
CURRENT APPLICATION NUMBER: US/09/996,194
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 60/250,348
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/250,073
PRIOR APPLICATION NUMBER: 60/253,878
PRIOR APPLICATION NUMBER: 60/253,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                             272 LAN 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 FGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSNTGGFNMGQYNTGYLNSGNYNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 SGTGNVGI----GNSGTGNWGIGNSGNSYN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 SGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSG
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Similarity 25.2%;
31; Conservative
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STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/084,843 FILING DATE: 25-Feb-2002
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STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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DATE:
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                                                                                                                                                                                     RESULT 14
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NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 873
TYPE: PRT
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; OTHER INFORMATION: Pfam consensus
US-09-996-194-16
                                                                                                                                                                                                                                                                                                                                        US-10-238-075-1549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Moraxella catarrhalis US-09-952-267-13
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                                                                 Sequence 1549, Application US/10238075

Publication No. US20030148324A1

GENERAL INFORMATION:

APPLICANT: I.N.S.E.R.M.

APPLICANT: I.N.S.E.R.M.

TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolar TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides and of these polynucleotides are polynucleotides and the polynucleotides are polynucleotides and the polynucleotides are polynucleotides and the polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotides are polynucleotid
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PRIOR FILING DATE: 2000-11-30
NUMBER OF SEO ID NOS: 22
SOFTWARE: FASTSEO for Windows Version 4.0
SEO ID NO 16
LENGTH: 65
TYPE: PRT
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Publication No. US20030032772A1
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Best Local Similarity
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APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HANSEN, ERIC J. APPLICANT: AEBI, CHRISTOE
                                  FILE REFERENCE: BLANDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/336,447 PRIOR FILING DATE: 1999-06-21
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CURRENT APPLICATION NUMBER: US/09/952,267
CURRENT FILING DATE: 2001-09-12
CURRENT APPLICATION NUMBER: US/10/238,075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 THEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 GRPAVGVI-----NIPAANITSRNHYDQLVTRVVTHEIAHAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLIVGILGMATTASAQQTIARQ--GKGMHSIIGGGNDNEANGDYSTVSGGDYNE-----
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COPE, LESLIE D.
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24.8%; Pred. No. 7.7;
7ative 20; Mismatches
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47.7%;
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RESULT 15

US-09-820-843A-21

US-09-820-843A-21

Requence 21, Application US/09820843A

Publication No. US20030039963A1

Publication No. US20030039963A1

PAPLICANT: Council of Scientific and Industrial Research

TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI

TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES

FILE REFERENCE: 063915

CURRENT APPLICATION UNMEBER: US/09/820,843A

CURRENT APPLICATION UNMEBER: US/09/820,843A

CURRENT FILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 118

SOFTMARE: PatentIn version 3.0

SEQ ID NO 21

LENGTH: 354

TYPE: PRT

ORGANISM: M. tuberculosis
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PRIOR APPLICATION NUMBER: 0003145
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1549
LENGTH: 182
TYPE: PRT
ORGANISM: Escherichia coli
US-10-238-075-1549
Search completed: March 11, 2004, 19:18:37 Job time: 25.6 secs
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NAME/KBY: misc feature
OTHER INFORMATION: PPE
NAME/KBY: misc feature
OTHER INFORMATION: gi|1781260
US-09-820-843A-21
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Best Local Similarity 25.2%;
Matches 31; Conservative 1
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                                                                                                                                 147
                                                                                       132 TAN 134
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                                                                                                                                                                             82 NIGIGLTGDG---QIGIGGLNSGSGNIGFGNSGTGNVGLFNSGTGN---
                                                                                                                                                                                                                    87 NSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNA 146
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                                                                                                                                 TAN 149
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                                                                                                                                                                                                                                                                -SNNIGFGNTGSGNFGFGNTGNN
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Maximum Match 10
Listing first 45
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Perfect score:
           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: pir1:*
2: pir2:*
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IGNMENTS

fimbrin protein agfA precursor - Salmonella enteritidis

text_change 08-0 seer, P.A.; Kay, seer, P.A.; Kay, sing thin, aggrega 497 ing thin, aggrega 1497 idue 44 as Ile i.J.; Kay, W.W. aggregative fimb 357 eimbriae iimbriae iissue plasminoge	prote Oy	HEO OF TO DE		Cispecies: Salmonella enteritidis C;Species: Salmonella enteritidis C;Date: 31-Dec-1996 #sequence revision 31-Dec-1996 #text_change 08-Oct-1999 C;Accession: JC6039; PC6015; A44898 R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W. J. Bacteriol. 178, 662-667, 1996 A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae. A;Reference number: JC6039; MUID:96146512; PMID:8550497 A;Accession: JC6039 A;Molecule type: DNA A;Residues: 1-151 <col/> A;Accession: PC6015 A;Accession: PC6015 A;Accession: PC6015 A;Accession: PC6015 A;Accession: PC6015 A;Accession: PC6015
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A;Cross-references: EMBL:X90754; NID:gl147558; PIDN:CAA62282.1; PID:gl147564
A;Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence submitted to the EMBL Data Library, August 1995
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G64846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change C;Accession: S70788; G64846; S31202; S34560; S34559 R;Hammarr, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S. Mol. Microbiol. 18, 661-670, 1995 Mol. Microbiol. 18, 661-670, 1995 A;Title: Expression of two csg operons is required for production A;Reference number: S70783; MUID:96414468; PMID:8817489
     A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74126.1; A;Experimental source: strain K-12, substrain MG1655 R;Olsen, A.; Arnqvist, A.; Hammar, M.; Sukupolvi, S.; Normark, S. Mol. Microbiol. 7, 523-536, 1993
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Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K. A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero A;Reference number: AB0502; MUID:21334947; PMID:11677608

A;Accession: A10635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        major curlin
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A;Residues: 1-151 <PAR>
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                                                                                                                     Molecule type: DNA
                                                                                                                                                   Status: nucleic
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been called Salmonella typhi
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Pred. No. 9.7e-53;
3; Mismatches 11
                                                                                                                                              shown; translation not
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e, N.; Farrar,
                                                                         PID:g1787279
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RiHayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Hayashi, T.; Yokoyama, K.; Hattori, M.; Shinagawa, H. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001

A,Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7

A;Reference number: A99829; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Escherichia
C;Date: 18-Jul-2001 #se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and H-kininogen; in the absence of CsgA, CsgB can sel F;1-20/Domain: signal sequence #status predicted <SIG>F;21-151/Product: curlin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: major component of wild-type curli; interaction between CsgA and CsgB tr A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Olsen, A.N.; Arnqvist, A.M. submitted to the EMBL Data Library, A;Reference number: S34559
                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-152 <HAY>
                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A99629; A; Accession: D90806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              curlin major subunit CsgA [imported] -
C;Species: Escherichia coli
                                                                                                                                                                                                                                                        A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: D90806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: csgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-133, 'RQRDSGWLW' < OLS3 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S34559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type:
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A;Cross-references: EMBL:L04979
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A; Residues: 1-6,
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                                                                                                                                                                                                                                 Experimental source:
                                                                                                                                                                                                                                                                                                                             Status: preliminary
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                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
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MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAL
                           MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHAL
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                                                                                                                                                                                                                                    GB:BA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154
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                                                                                                             64.3%;
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68.9%;
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                                                                                                               Score 501.5;
Pred. No. 2.
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Pred. No. 3.1e-38;
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                                                                                           Mismatches
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                                                                                                                  .3e-36;
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QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG 119

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A; Molecule type: DNA
A; Residues: 1-1748 <TAY>
A; Cross-references: EMBL:L03710; NID:g161751; PID:g161752
A; Cross-references: EMBL:L03710; NID:g161751; PID:g161752
R; Taylor, F.M.; Martindale, D.W.
Nucleic Acids Res. 21, 4610-4614, 1993
Nucleic Acids Res. 21, 4610-4614, 1993
A; Title: Retroviral-type zinc fingers and glycine-rich repeats
A; Reference number: S42135; MUID:94051569; PMID:8233798
A; Accession: S42135
             A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-
A;Cross references: EMBL:L03710
R;Martindale, D.W.; Taylor, F.M.
Nucleic Acids Res. 16, 2189-2201, 1988
Nucleic Acids Res. 16, 2189-2201, 1988
A;Title: Multiple introns in a conjugation-specific gene from Tetrahymena thermophila.
A;Reference number: S03650; MUID:88189811; PMID:3357771
A;Accession: S03650
A;Molecule type: DNA
A;Residues: 236-250,'I',252-255,'N',257-773 <MAR>
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: H85665
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: H8565 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, October 1992
A;Reference number: S42136
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A; Residues: 1-152 <S'
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Nature 409, 529-533, 2001
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Best Local S
Matches 102
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Molecule type: DNA
;Residues: 236-250,'I',252-255,'N',257-773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: S42136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.3%; Score 501.5; DB 2; 67.1%; Pred. No. 2.3e-36; tive 21; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-Jul-1997 #text_change 07-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151
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Potamousis,
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                                                                                                                                                                                                                                                                                                                protein
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K.; Aj
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A;Cross-references: EMBL:
C;Genetics:
A;Genetic code: SGC5
A;Genetic code: SGC5
A;Introns: 85/3; 136/1; 1
C;Keywords: zinc finger
F;1164-1450/Region: zinc
F;1451-1464/Region: zinc
                                                                                                                                                                                                       F;1478-1491/Region: z
F;1501-1514/Region: z
F;1530-1543/Region: z
F;1555-1568/Region: z
F;1579-1592/Region: z
F;1602-1615/Region: z
F;1602-1615/Region: g
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                                                                                                                                                     Matches
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                                                                                                                                                                    Local
                         142 FGNNATAN
                                                                          82 GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVG 141
                                                                                                                             25 QWGGGGNHNGG---GNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADV 81
                                                                                                                                                      39;
                                                                                                                                                                  Similarity
                                                -SGSGNQ----TGGGWGSN---DNQQQQNENTGGGGWGSSNS---NQTNNESS--
WGSNNOAS
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                             zinc
                                                                                                                                                                                                       zinc finger
glycine-rich
                                                                                                                                                                                                                                zinc
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                                                                                                                                                                                                                                                                                     zinc
                                                                                                                                                                                                                                                                                                 zinc
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                                                                                                                                                                                                                    finger CCHC
                                                                                                                                                                  14.6%;
                                                                                                                                                      22;
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Pred.
                                                                                                                                                                                                                      motiff
motiff
motiff
motiff
                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                     290/2; 327/3; 499/1; 573/2; 607/3; 708/3;
                                                                                                                                                                 114; DB 2
No. 0.11;
                                                                                                   ----CQSNVQES-TTTSSGGWGS----
                                                                                                                                                                               2
                                                                                                                                                      27;
                                                                                                                                                                             Length 1748;
                                                                                                                                                      Indels
                                                                                                                                                      40;
                                                                                                     1680
                                                                                                                                                      8
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curlin nucleator protein csgB precursor - Escherichia coli (strain K-12) N;Alternate names: csgB protein; curlin nucleation component; minor curlin C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01-Mar-2002 C;Accession: S70787; F64846

A;Description: minor component of wild-type curli; interaction between CsgA and CsgB A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli th and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-21/Domain: signal sequence #status predicted <SIG> F;2-151/Product: minor curlin chain #status predicted <MAT> A;Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62281.1; PID:g1147563
A;Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence as submitted to the EMBL Data Library, Augus
R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; R.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997 A; Gene: csgB A; Map position: 23.15 C; Function: A;Residues: 1-151 <BLAT> A;Cross-references: GB:AE000205; GB:U000096; NID:g1787265; PIDN:AAC74125.1; PID:g1787278, A;Experimental source: strain K-12, substrain MG1655 C;Genetics: A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: F64846 A;Status: nucleic acid sequence not shown; translation not R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S. Mol. Microbiol. 18, 661-670, 1995
Mol. Microbiol. 18, 661-670, 1995
A;Tille: Expression of two csg operons is required for production A;Reference number: S70783; MUID:96414468; PMID:8817489 A; Molecule type: DNA A; Residues: 1-151 < HAM> A; Molecule type: DNA A;Status: nucleic acid sequence not A; Accession: S70787 shown; translation not shown shown; translation not shown of fibronectin- and August ŭ ŏ

Score

107.5;

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2:

Length 151;

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RESULT 9
G85665
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A;Cross-references: GB:AE005174; NID:g12514573; PIDN:AAG55787.1; GSPDB:GN00145; UWGP:Z1
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                          A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: G85665
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A; Molecule type: DNA
A; Residues: 1-151 <HAY>
A; Residues: 1-151 <HAY>
A; Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:g13360879; GSPDB:GN00154
A; Cross-references: Strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                   R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glassiller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     curlin minor chain precursor, CsgA homolog [imported] - Escherichia coli (strain
                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                      iller, L.; Grotbeck, E.J.; Davis, Nature 409, 529-533, 2001
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C90806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Hayashi, T.
gasawara, N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         minor curlin subunit precursor CsgB [imported] - Escherichia coli (strain 0157:H7, C;Species: Escherichia coli (C;Pate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
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                                                                                                                                Query Match
Best Local :
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;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001;Accession: G85665
                                                                                                                                                                                                                                                                                                Molecule type: DNA
                                                                                                              Matches
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Best Local
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                              49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70
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                                                                                                                                Similarity
                       IGQAGTNNSAQLRQGGSKLLAVVAQEGSSNRAKIDQTGDYNL-AYIDQAGSANDASISQG
                                                              ITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASDSSVMVRQVGFGNNATANQY
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                                                                                                            Conservative
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                                                                                                        Score 107.5; DB Pred. No. 0.024; 9; Mismatches
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Pred. No. 0.024;
9; Mismatches
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9; Mismatches
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lanta, E.;
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Potamousis,
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K.; Aj
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Nature 413, 848-852, 2001

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero'

A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleation component of curlin monomers [imported] - Salmonella enterica su C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AH0635
                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-151 < PAR >
                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher th, T.; Connecton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
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                                                                                                                                                                                                            A; Gene:
                                                                                                                                                                                                                                                                                                               A;Status: preliminary
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A;Cross-references: GB:U43280; NID:g1184712;
A;Experimental source: strain 276755-3b
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C;Function:
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R;Collinson, S.K.; Clouthier, S.C
J. Bacteriol. 178, 662-667, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fimbrin protein agfB precursor - Salmonella enteritidis
C;Species: Salmonella enteritidis
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                                                                                                                             Matches
                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                              Cross-references: GB:AL513382; PIDN:CAD08267.1; PID:g16502314; GSPDB:GN00176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 MAHALQSDARKSE----TTITQSGYGNGADVGQ-GADNST-----IBLTQNGFR 98
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                                       IATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQEGEN
                                                                              MAHALQSDARKSE-----TTITQSGYGNGADVGQ-GADNST-----IELTQNGFR
NNATIDQWNAKNSDIT-VGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                           Conservative
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                                                                                                                         17;
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                                                                                                                       Score 106.5; DB Pred. No. 0.029; 7; Mismatches
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Pred. No. 0.0
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                                                                                                                         43;
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A;Residues: 1-145 <KUR>
A;Residues: 1-145 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL45562.1;
A;Experimental source: strain C58 (Dupont)
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                                                                                                                                                                                                                                                                                    A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                     R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quro. A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein AGR_L 228 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, I
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Best Local S
Matches 39
                                                                                                                                                                                                    Cross-references:
                                                                                                                                                                                                                        ;Molecule type: DNA
;Residues: 1-145 <K
                                                                                                                                                                                                                                                      Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                         Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002 Accession: H98144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: AD3143
                                                                                                                 Query Match
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position:
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                                                                                                                                   n: linear chromosome
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                                                 LLKVAAFAAIVVSGSALAGVVP-----
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                                                                                                                                                                                                    GB:AE007870; PIDN:AAK88682.1;
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                                                                                                 12.2%;
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Pred. No. 0.25
22; Mismatches
                                                                                                 Score 95.5;
Pred. No. 0.
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                                                                                   57;
                                                                                                                                                                                                    PID:g15158413; GSPDB:GN00170
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                   60
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; Markelz, B.;
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                                                                                                                                                                                                                                                         Science 294,
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                                                                                                                                                    A;Status:
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Query Match
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A; October 1 DNA
A; Molecule type: DNA
A; Residues: 1-141 < KUR>
A; Cross-references: GB: AE008689; PIDN: AA145560.1;
A; Cross-references: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003
C;Accession: F70675
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                                            A; Gene: Atu4766
A; Map position:
                                                                                           A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                          A; Authors: Yoo, ster, E.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                         A;Title: The Genome of the Natural Genetic Engineer Agrobacterium A;Reference number: AB2577; MUID:21608550; PMID:11743193
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Experimental source: strain |
                                     position:
                                                                                                                                                                                                                                                                                                                                                      P.; Romero, P.; Zhang, 294, 2317-2323, 2001
                                                                                                                                                                                                          preliminary
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                                                                                                                                                                                                                                                                                                                                   Y.; Biddle,
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27.1%;
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Pred. No. 1
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  93;
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                                                                                                                                          PID:g17743275; GSPDB:GN00187
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    141;
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McClell
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Best Lo	Best Local Similarity 26.0%; Pred. No. 0.39; Matches 39; Conservative 22; Mismatches 63; Indels 26; Gaps 6;	
Qy	PQWGGGGNHNGG	
Вb		
γQ	53 HEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD 112	
Вb	57RAYSLYRNFKDANIKQLGRGNAAGIAQNGGGNLGFIRQRGNGHSATLQQ-NGNNNA 111	
Qy	113 ITVGQYGGNNAALVNQTASDSSVMVRQVGF 142	
Db	112 YGIFQYGRNTGTNVVQDGDNGSGLTFSYGW 141	
Search con Job time	Search completed: March 11, 2004, 18:42:09 Job time : 11.3 secs	

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: March 11, 2004, 18:14:48; Search time 6.3 Seconds (without alignments) 1248.031 Million cell updates/sec

Title: Perfect score: Sequence: US-09-543-407-18
780
1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151

Scoring table:

Searched: BLOSUM62 Gapop 10.0 , Gapext 0.5 141681 seqs, 52070155 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

141681

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Regult No.	Score	Query Match	Length	BB	ID	Description
1	691	88.6	151	ㅂ	CSGA SALTY	P55225 galmonella
N	523	7.	151	_		escherich
w	501.5	64.3	152	-	CSGA_ECO57	93u24 escherichi
4	97.	13.8	151	_	CSGB_ECOLI	escherichi
v	106.5	•	151	μ		
0	106.5	13.7	151	1	CSGB_SALTY	•
7	92	٠	401	μ	YKO3_CAEEL	P34291 caenorhabdi
œ	92	•	1656	_	OMPB_RICJA	
9	91.5	٠	590	_	GP63_LEIDO	1e
10	91	11.7	1093	,_	PER_DROWI	Q03297 drosophila
11	90	11.5	602	_	GP63_LEIMA	w
12	90	11.5	906	μ	GLR1_HUMAN	P42261 homo sapien
13	88.5	11.3	1655	μ	OMPB_RICCN	Q9kka3 r outer mem
14	88	11.3	599	μ	GP63_LEICH	P15706 leishmania
15	87.5	11.2	1028	μ	OVO_DROME	P51521 drosophila
16	87.5	11.2	1567	μ	ICEN_XANCT	
17	96	11.0	485	1	Y136_TREPA	treponema
18	86	٠	493	۳	GATA_RHIME	7 7
19	84	10.8	646	٢	GP63_LEIME	P43150 leishmania
20	84		907	_	GLR1_MOUSE	P23818 mus musculu
21	84		907	۲	GLR1_RAT	
22	83	•	720	1	KRE6_YEAST	P32486 saccharomyc
23	83	10.6	947	<u>, , </u>	SECA_STRCO	P55021 streptomyce
24	82	10.5	342	μ	OMPC_RAHAQ	-
25	۲	10.4	424	_	COAA_BPFD	P03661 bacteriopha
26	۲	10.4	424	_	COAA_BPM13	
27	81.5	10.4	493	۲	GATA_AGRTS	Q8ufs8 agrobacteri
28	81	10.4	365	۲	ROA1_DROME	
29	81	10.4	576	_	DEAF_DROME	Q24180 drosophila
30	81	10.4	678	_	YF48 MYCTU	
31	18	10.4	1034	Н	ICEN PANAN	
32	80.5	10.3	641	H	IMD_ARTGO	N
33		10.3	1185	H	MAPX_DROME	P23226 drosophila

4 5	44	43	42	41	40	39	38	37	36	35	34	
78	78	78	78	78.5	78.5	79	79	79.5	79.5	79.5	80	
10.0	10.0	10.0	10.0	10.1	10.1	10.1	10.1	10.2	10.2	10.2	10.3	
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YDBA_ECOLI	ICEN ERWHE	CAR7_CANAL	YB47 MYCPN	MLE_DROME	LIPM NEIMA	YM96_YEAST	AC22_TENMO	OMPB_RICRI	120K_RICRI	SECA_STRGR	MSA2_PLAF2	
						Q04893 sacc	P26968 tene	Q53047 r ou	P14914 rick	P95759 stre	Q03646 plas	
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ALIGNMENTS

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SEQUENCE FROM N.A. SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931; SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931; MEDLINE=22531367; PubMed=12644504; MEDLINE=22531367; PlubKett G. III, Mayhew G.F., Rose D.J., Deng W., Liou SR., PlubKett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;	SEQUENCE FROM N.A. SPECIES=S.typhi; STRAIN=CT18; MEDLINE=21534947; PubMed=11677608; MEDLINE=21534947; PubMed=11677608; Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bencley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Cronin A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18."; Nature 413:848-852 (2001).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SPECIES=S.typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720; SPECIES=S.typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677809; MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan B., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2."; Nature 413:852-856(2001).	Salmonella typhi, and Salmonella typhi, and Salmonella enteritidis. Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella. NCBI_TaxID=602, 601, 592; [1]	JIT 1 A SALTY CSGA_SALTY STANDARD; PRT; 151 AA. P5525; 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Major curlin subunit precursor (Fimbrin SEFI7). CSGA OR AGFA OR STM1144 OR STY1181 OR T1776. Salmonella typhimurium,

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Query Match
Best Local S
Matches 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol. 173:4773-4781(1991).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.
-COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
FIBRONECTIN.
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                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Doran J.L., Collinson S.K., Burian J., Sarlos G., Todd E.C. Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.; "DNA-based diagnostic tests for Salmonella species targetin the structural gene for thin, aggregative fimbriae."; J. Clin. Microbiol. 31:2263-2273(1993).
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MEDLINE=94013373; PubMed=8104955
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Collinson S.K., Cl
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Mori H., Seki Y.,
Sampei G., Seki Y.,
Sampei G., Seki Y.,
                 Salmonella enteritidis."
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Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
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Riley M., Collado-Vides J., Glasner J.D.,
Gregor J., Davis N.W., Kirkpatrick H.A.,
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MEDLINE=96414468; PubMed=8817489;
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STRAIN=K12 / W3110;
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A., Goeden M.A., Rose D.J.,
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                 App1.
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MEDLINE=21218556; PubMed=11319125;
Uhlich G.A., Keen J.E., Elder R.O.;
"Mutations in the csgD promoter associated with variations expression in certain strains of Escherichia coli 0157:H7."
Appl. Environ. Microbiol. 67:2367-2370(2001).
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Major curlin subunit precursor.
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PINCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURCILIED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN.
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SEQUENCE FROM N
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O1-OCT-1996 (Rel. 34, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Minor curlin subunit precursor.
CSGB OR B1041 OR 21675 OR ECS1419.
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Hammar M., Arnqvist A., Bian Z., Olsen A., "Expression of two csg operons is required fibronectin- and congo red-binding curli po
                                                                                                                                          SEQUENCE FROM N. STRAIN=K12 / MC4
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This SWISS-PROT entry is copyright. It is produce the Swiss Institute of Bioinformatics the European Bioinformatics that European Bioinformatics that it is non-profit institutions as long as is modified and this statement is not removed. Use entities requires a license agreement (See http.
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Mol. Microbiol. 13:1021-1032(1994).

-i- FUNCTION: CURLIN IS THE STRÜCTURAL SUBUNIT OF THE CURLI. CU COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT G TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21156231; PubMed=11259796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyi Hayashi T., Makino E., Ohnishi M., Kurokawa T., Tanaka M., Tobe Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Oshima T., Aiba H., Baba T., Fujita K., Kanai K., Kashimoto K.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Mocomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

Perna N.T. Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95157246; PubMed=7854117;
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of enterohaemorrhagic Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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                                                                            J. Bacteriol. 185:2330-2337 (2003).

-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.
-COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONE
                                                                                                                                                                                                                                                 Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Ieather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.", Nature 413:848-852(2001).
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28-FEB-2003 (Rel. 41, Created,
28-FEB-2003 (Rel. 41, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Minor curlin subunit precursor.
                                                                                                                                            MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi st
and CT18.";
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 SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation suropean Bioinformatics Institute. There are no restrictions on its
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Best Local S
Matches 35
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P55226;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SPECIES=S. typhimurium; STRAIN=SR-11;

MEDLINE=98117058; PubMed=9457880;

Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;

"Curli fibers are highly conserved between Salmonella typhimurium

Escherichia coli with respect to operon structure and regulation."

J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                                                                        McClelland M., Sanderson K.E., Spieth J., Courtney L., Porwollik S., Ali J., Dane L. Leonard S., Nguyen C., Scott K., Holmes A. Ryan E., Sun H., Florea L., Miller W., St. Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEF17
CSGB OR AGFB OR STM1143
Salmonella typhimurium, and
Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by arentities requires a license agreement (See http://www.isborsend an email to license@ibb-sib.ch).
                                                                                                                     MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P
"Salmonella enteritidis agfBAC operon encoding thin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Finbria; Signal; Complete proteome.
SIGNAL 21 PINTIAL.
CHAIN 22 151 MINOR CURLIN SUBUNIT.
SEQUENCE 151 AA; 16254 MW; 161C54326E573495 CRC64;
                                                                                         J. Bacteriol. 178:662-667(1996).
                                                                                                                                                                                                  Nature 413:852-856(2001).
[3]
                                                                                                                                                                                                                                                                                                                                     SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720; MBELLINE-21534948; PubMed-11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacteriaceae; Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                   SPECIES=S.enteritidis; STRAIN=27655-3B;
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             'Complete
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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            FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF CURLIN MONOMERS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35;
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30.7%;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                          Dante M., Du F., Ho
olmes A., Grewal N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
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                                                                                                                                                                                                                                                                           Stoneking T.,
                                                                                                                                                                                                                                              enterica serovar Typhimurium
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M., Du F., Hou S., Layman D.,
Grewal N., Mulvaney E.,
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CSGA/CSGB

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Matches 46; Conserv
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between
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                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                             Durbin R.; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6239
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EMBL; AE008749; AAL20073.1; -.
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                                                                                       Hypothetical SEQUENCE 4
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                                                                                                                              WormPep;
                                                                                                                                                       PIR; C88571; C88571
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101 AA; 4
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protein C05B5.3 in chromosome
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Matches 45
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Trigream; S-layer; C
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_RICJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000
30-MAY-2000
16-OCT-2001
                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Alphaproteobacteria;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rickettsia japonica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequencing of the gene encoding japonica.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=35790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 006653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OMPB
                                                                                                                                                                                                                                                    InterPro; IPR005546; Autotransporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ubmitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY. PLAY A ROLE AS A RICKETSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity)
FUNCTION: THE (By similar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       layer with hexagonal symmetry.
SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Cell wall.
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                                                                                                                                                                                                      PF03797; Autotransporter; 1.
Ws; TIGR01414; autotrans_barl;
                                                                                                                                                                                                                                                                                                      AB003681; BAA20138.1;
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                          Similarity
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                                                                                                                                                                                                                                                                              IPR006315; Autotransport
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  Conservative
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    19;
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Score 92; DB 1;
Pred. No. 4;
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                                                                                                               32 kDa BETA PEPTIDE. POLY-GLY.
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  52;
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                                           Length 1656;
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MBL outstation -
  56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Webb J.R., Button L.L., McMaster R.W "Heterogeneity of the genes encoding of Leishmania donovani.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GP63
                                                                                                                                                                                                                                     EMBL; M60048; AAA29244.1; HSSP; P08148; 1LML.
                                                                                                                                                                                                                                                                           entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                              PRINTS; PR00782; LSHMANOLYSIN. PROSITE; PS00142; ZINC_PROTEAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
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10-OCT-2003
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                                                                                                                                     Zymogen;
                                                                                                                                                  Hydrolase;
                                                                                                                                                                                                 InterPro; IPR006025; Pept M Zn
InterPro; IPR001577; Peptidase
                                                                                                                                                                                                                           MEROPS; M08.001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=5661;
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COPACTOR: Binds 1 zinc ion per subunit (By simi
SUBCELLULAR LOCARION: Attached to the membrane
SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Biochem. Parasitol. 48:173-184(1991). FUNCTION: Has an integral role during in the mammalian host.
                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: Preference for hydrophobic P1' and basic residues at P2 and P3'. A model r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEIDO
                                                                                                                                                                                     PF01457; Peptidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anolysin precursor (EC surface glycoprotein)
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                                                                                                                                     Signal;
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                                                                                                                                     Metalloprotease; Glycoprotein; Metal-binding;
ignal; Cell adhesion; GPI-anchor; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        donovani.
Euglenozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 20, Created)
(Rel. 20, Last sequence update)
(Rel. 42, Last annotation update)
sin precursor (EC 3.4.24.36) (Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=1762629;
L.L., McMaster R.W.;
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565
590
251
252
252
253
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321
129
217
                                                                                                                                                              PROTEASE; 1.
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POTENTIAL.
ACTIVATION PEPTIDE.
LEISHMANOLYSIN.
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(See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     major
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membrane by a GPI-anchor.
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- outstation
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Best Local S
Matches 43
     period length of circadian and ultradian rhythms; an increase in PER dosage leads to shortened circadian rhythms and a decrease leads to lengthened circadian rhythms. Essential for the circadian rhythms component of the male courtship song that originates in the thoracic nervous system. The biological cycle depends on the rhythmic formation and nuclear localization of the TIM-PER complex. Light induces the degradation of TIM, which promotes elimination of PER. Nuclear sativity of the heterodimer coordinatively regulates PER and TIM transcription through a negative feedback loop. Behaves as a negative element in circadian transcriptional loop. Does not appear to bind DNA, suggesting indirect transcriptional inhibition (By similarity); the complex then promote with timeless (TIM); the complex then
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DISULFID
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CARBOHYD
                                                                                                                                                                                                                              SEQUENCE OF 579-646 FROM N.A.
MEDLINE=93196482; PubMed=8450754;
Peixoto A.A., Campesan S., Costa R.H., Kyriacou C.P.;
"Molecular evolution of a repetitive region within the
                                                                                                                                                                                                                                                                                   [2].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PER_DROWI STANDARD; PRT; 1093 AA.

Q03297; O18421; O18422; P91721; P91722;

Q1-QCT-1993 (Rel. 27, Created)

15-JUL-1998 (Rel. 36, Last sequence update)

16-QCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                               Gleason J.M., Powell J.R.; "Interspecific comparisons of the period locus "Interspecific and intraspecific comparisons of the period locus the Drosophila willistoni sibling species."; Mol. Biol. Evol. 14:741-753(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIGIJ
                                                                                                                                                                                                                    Drosophila."
                                                                                                                                                                                                                                                                                                                                                STRAIN=Various strains;
MEDLINE=97357421; PubMed=9214747;
                                                                                                                                                                                                                                                                                                                                                                                                  Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7260;
                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila willistoni (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGFYQADFS-KAEEMPWGRNA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YDOLVTRVVTHEMAHALGESVVFFRDARILESISNVRHKDFDVPVINSSTAVAKAREQYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TA---SDSSVMVRQVGFGNNA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTLEYLEMEDQGGAGSAGSHIKM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGA-----DVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQ
                                                                                                                                                                                                       . Evol. 10:127-139(1993).
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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-i- SUBCELLULAR LOCATION: Nuclear at specific periods of the day.
First accumulates in the perinuclear region about one hour before
translocation into the nucleus. Interaction with Tim is required
for nuclear localization (By similarity)
-i- pTM: PHOSPHORYLATED WITH A CIRCADIAN RHYTHMICITY, PROBABLY BY THE
DOUBLE-TIME ROOTEIN (DBT). PHOSPHORYLATION COULD BE IMPLICATED IN
THE STABILITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAIN ATLIXCO. SIMILARITY: Contains 2 PAS (PER-ARNY-SIM) dimerization domains SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PER-TIM (BY SIMILARITY).
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domains

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EMBL; U51055; EMBL; U51056; EMBL; U51057; EMBL; U51069; EMBL; U51060; EMBL; U51061; EMBL; U51063; EMBL; U51066; EMBL; U51066; EMBL; U51066; EMBL; U51066; EMBL; U51066; EMBL; U51066; EMBL; U51066; EMBL; U51066; EMBL; U51066; EMBL; U51066; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EM
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                                                                            VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50112;
                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00989; PAS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rhythms;
                                                                                                                                                                                                                                                                                                                                                          618
718
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759
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617
622
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730
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AAB41366 1;
AAB41366 1;
AAB41366 1;
AAB41367 1;
AAB41369 1;
AAB41370 1;
AAB41370 1;
AAB41371 1;
AAB41372 1;
AAB41373 1;
AAB41373 1;
AAB41375 1;
AAB41375 1;
AAB41376 1;
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AAB41362.1;
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                                                                                             POLY-LYS.
POLY-GLY.
POLY-GLY.
POLY-SER.
POLY-ALA.
T -> A (IN
S -> F (IN)
G -> V (IN)
G -> V (IN)
G -> S (IN)
MISSING (I)
MISSING (I)
MISSING (I)
MISSING (I)
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  PORTO
                    MISSING
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                                                                                                               A (IN STRAIN 0811.4).
F (IN STRAIN 0811.4).
V (IN STRAIN GUANA).
A (IN STRAIN SANTA MARIA).
S (IN STRAIN SANTA MARIA).
S (IN STRAIN PORTO ALEGRE 3
ING (IN STRAIN PORTO ALEGRE 3
ING (IN STRAIN PORTO ALEGRE 4
ALEGRE 2,
                                     (IN STRAINS LIMA B, L'HAB
40 MORA).
(IN STRAIN PORTO ALEGRE 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCALIZATION SIGNAL (POTENTIAL)
                  (IN STRAINS
AINS GUADELOUPE, MAI
PORTO ALEGRE 1 AND
                                                                              L'HABITATUE
                                                                                                                    GRE 3).
GRE 4).
AND MANAUS
                      MANAUS
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STATAT

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Query Match
Best Local S
Matches 24
                                                        X-RAY CRYSTALLOGRAPHY (1.86 ANGSTROMS).
MEDLINE=98416698; PubMed=9739094;
Schlagenhauf E., Etges R., Metcalf P.;
"The crystal structure of the Leishmani."
                                          leishmanolysin.";
Structure 6:1035-1046(1998)
                                                                                                                                                         Homans S.W., Bordier C.; "Structure of the glycosyl-phosphatidylinositol membrane anchor of the Leishmania major promastigote surface protease."; J. Biol. Chem. 265:16955-16964(1990).
                                                                                                                                                                             MEDLIND---
Schneider P., Ferynn
S.W., Bordier C.
                                                                                                                     Schlagenhauf E., Etges R., Metcalf P., "Crystallization and preliminary X-ray
                                                                                                                                      MEDLINE=95406217;
                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE MEDITIME=88154764; PubMedd=3346625; Button L.I., McMaster W.R.; "Molecular cloning of the major s J., Exp. Med. 167:724-729(1988).
                                                                                                Proteins 22:58-66(1995).
                                                                                                                                                                                                                                  Button L.L.,
                                                                                                                eishmanolysin,
                                                                                                                                                                                                                                           REVISIONS.
                                                                                                                                                                                                                                                                                                     Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida;
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                       u1-AUG-1988 (Rel. 08, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell
(Major surface glycoprotein) (GP63 protein) (Pendomepridase)
                                                                                                                                                                                                                                                                                                                                                                          GP63_LEIMA
P08148; P15906;
01-AUG-1988 (Re
                                                                                                                                                                                                                                                                                                                                                                                                  LEIMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT
VARIANT
VARIANT
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                     endopeptidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                           Exp.
FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

CAPALYTIC ACTIVITY: Preference for hydrophobic residues at P1 and P1' and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.
                                                                                                                                                                                                                                                                                                                                                                                                                                               87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            NSTIELTQNGFRNNATIDQWNAKNSDITVGQY 118
                                                                                                                                                                                                                                                                                                                                                                                                                              -----SCSGLGGNGNVGSGNGNNSQPSTNQY 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGGGGGGGGGGGLPLFL-----DVTHTSSSSQNKGPTGVAAGGAGGGVGGGG-- 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  886
1093
                                                                                                                                                                                                                        McMaster W.R.;
171:589-589(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 747
764
                                                                                                                the major
                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                        PubMed=2145267;
guson M.A.J., McConville M.J., Mehlert
                                                                                                                                     PubMed=7675788;
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766
886
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26.1%;
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                                                                                                                surface
                                                        Metcalf P.;
the Leishmania major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Mismatches
                                                                                                                                                                                                                                                                                                                                         3 4.24.36) (Cell surface protease) (Gp63 protein) (Promastigote surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 91; DB
Pred. No. 3.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISSING (IN STRAINS MANAUS 4,
ALEGRE 1 AND PORTO ALEGRE 2).
S -> A (IN STRAINS GUADELOUPE
MISSING (IN STRAIN MANAUS 3).
A -> T (IN STRAIN 0811.4).
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                      ဝှု
                                                                                                              metalloproteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB6DE050267EC187 CRC64;
                                                                                                                                                                                                                                                                                      101-123
                                                                                                                                                                                                                                                                                                                                                                                        602
                                                                                                                    diffraction studies of
                                                                                                                                                                                                                                                                                                          Trypanosomatidae; Leishmania
                                                                                                                                                                                                                                                              antigen of leishmania.";
                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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                                                         surface
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EMBL; Y00647; CAA68673.1; -.

PIR; PL0221; PL0221.

PDB; 11ML; 17-SEP-97.

MEROPS; M08.001; -.

InterPro; IPR006025; Pept M Zn BS.

InterPro; IPR001577; PeptIdase M8; 1.

PRINTS; PR00187; ESHMANOLYSIN.

PRINTS; PR00782; LISHMANOLYSIN.
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COFACTOR: Binds 1 zinc ion per subunit.
SUBCELULIAR LOCATION: Attached to the membrane by a GPI-anchor.
PTM: THE PHOSPHATIDYLINOSITOL MOIETY OF THE GPI-ANCHOR CONTAINS
FULLY SATURATED, UNBRANCHED 1-O-ALKYL CHAIN (MAINLY C24:0) AND J.
MIXTURE OF FULLY SATURATED UNBRANCHED 2-O-ACYL CHAINS (C12:0,
C14:0, C16:0, AND C18:0). ×

SIMILARITY: Belongs to peptidase family M8.

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PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Zymogen; Signal; Cell adhesion; GPI-anchor; 3D-structure; Lipo 3D-structure; Lipoprotein.

ACTIVATION PEPTIDE. LEISHMANOLYSIN. REMOVED IN MATURE FOI ZINC (CATALYTIC). POTENTIAL.

(CATALYTIC)

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33.3%;
                       63953 MW;
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               Score 90; DB 1; Length 602;
Pred. No. 1.9;
6; Mismatches 16; Indels
                       982EF3245D87C43E CRC64;
          -SDAR----
          -KSETTITQSGYGNG
               Gaps
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          78
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GIRI_HUMAN STANDARD; PRT; 906 AA.
P42261;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Glutamate receptor 1 precursor (GluR-1) (GluR-A) (GluR-K1) (Glutamate receptor 1 precursor (GluR-1) (GluR-A) (GluR-K1) (GluTamate receptor 1 precursor (GluR-1) (GluR-A) (GluR-K1) (GluTamate receptor 1 precursor (GluR-1) (GluR-A) (GluTamate receptor 1 precursor (GluR-A) (GluR-A) (GluTamate receptor 1 precursor (GluR-A) (GluR-A) (GluTamate receptor 1 precursor (GluR-A) (GluTamate receptor 1 precursor (GluR-A) (GluTamate receptor 1 precursor (GluR-A) (GluTamate receptor 1 precursor (GluR-A) (GluTamate receptor 1 precursor (GluR-A) (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluT
                                                                                                         EMBL; M81886; AAA58395.1; -.
EMBL; X58633; CAA41491.1; -.
EMBL; M64752; AAA58613.1; -.
PIR; A40222; A40222.
PIR; $25852; $25852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as modified and this statement is not removed. I
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-- SIMILARITY: Belongs to the ligand-gated ionic channel family.
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"Molecular cloning and chromosomal localization of glutamate receptor genes.";

Proc. Natl. Acad. Sci. U.S.A. 88:7557-7561(1991).

-!- FUNCTION: L-glutamate acts as an excitatory new
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"The human glutamate receptor cDNA GluR1: cloning,
expression and localization to chromosome 5.";
DNA Seq. 2:211-218(1992).
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Sun W., Ferrer-Montiel A.V., Schinder A.F., McPherson J.P.,
Evans G.A., Montal M.;
"Molecular cloning, chromosomal mapping, and functional exp
human brain glutamate receptors.";
Proc. Natl. Acad. Sci. U.S.A. 89:1443-1447(1992).
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MEDLINE=92329975; PubMed=1320959;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91352027; PubMed=1652753;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P42261-2; Sequence=VSP_000092, VSP_000093, VSP_000094, VSP_000095, VSP_000096; TISSUE SPECIFICITY: Widely expressed in brain.
MISCELLANEOUS: This receptor binds AWPA(quisqualate) > glutama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: L-glutamate acts as an excitatory neurotransmitter at many synapses in the central nervous system. The postsynaptic actions of Glu are mediated by a variety of receptors that are named according to their selective agonists.

SUBCELLULAR LOCATION: Integral membrane protein.

ALTERNATIVE PRODUCTS:
; A40222; A40222.
; S25852; S25852.
P; P19491; 1GR2.
ew; HGNC:4571; GRIJ
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpb)
(Surface protein antigen) (Cell surface-exposed protein (Surface protein ompb); 32 kDa beta peptide)
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Pfam; PF01094; ANF_receptor; 1.
Pfam; PF00060; lig_chan; 1.
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GO:0008066; F:glutamate receptor activity; TAS.
GO:0015277; F:kainate selective glutamate receptor activity; TAS.
GO:0007165; P:signal transduction; TAS.
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-I- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By Similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Samson D., Raoult D.,
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CHAIN
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EMBL; AF123721; AAF34124.1; --
EMBL; AF123726; AAF34129.1; --
EMBL; AF149110; AAD39533.1; --
PIR; E97835; E97835.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (By similarity).
-!- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered layer with hexagonal symmetry (By similarity).
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 33-1649 FROM N.A. STRAIN-Indian tick typhus, and Malish MEDLINE-20393643; PubMed=10939649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
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"The rickettsial outer membrane protein A and of the rickettsia of the most divergent rickettsia of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the recent of the re
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Ogata H., Audic S., Renesto-Audiffren
Samson D., Roux V., Cossart P., Weisse
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Matches 41
          MEROPS; MOB.001; -.
InterPro; IPRO06025; P
InterPro; IPRO01577; P
Pfam; PF01457; Peptida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GP63 LEICH
P15706;
01-APR-1990
                                                                              EMBL; M80672; AAA29238.1; -.
EMBL; M28527; AAA29235.1; -.
PIR; A44951; A44951.
                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                      "Three distinct RNAs for the surface protease gp63 a expressed during development of Leishmania donovani promastigotes to an infectious form.";
J. Biol. Chem. 267:1888-1895(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90205976; PubMed=2320059;
Miller R.A., Reed S.G., Parsons M.;
"Leishmania gp63 molecule implicated in cellular adhesion lacks
Arg-Gly-Asp sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEICH
                                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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NCBI_TaxID=44271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92112918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leishmanolysin precursor (EC 3.4.24 (Major surface glycoprotein)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ramamoorthy R., Donelson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endopeptidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eishmania chagasi.
                                                                                                                                                                                                                                                                                                liol. Chem. 267:11000-1101.

PUNCTION: Has an integral role during the intercal in the mammalian host.

In the mammalian host.

CATALYTIC ACTIVITY: Preference for hydrophobic residues at CATALYTIC ACTIVITY: and P3'. A model nonapeptide
                                                                                                                                                                                                                                                 P1' and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyr-|-Leu-Lys-Lys-
COPACTOR: Binds 1 zinc ion per subunit (By similarity).
SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the El
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                                                                    P08148;
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(Rel. 14, Last sequence update)
(Rel. 42, Last annotation update)
sin precursor (EC 3.4.24.36) (Cell surface protease)
sin precursor (EC 3.4.24.36) (Promastigote surface
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        06025; Pept M_Zn_BS.
01577; Peptidase_M8.
Peptidase_M8; 1.
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LSHMANOLYSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=1370484;
onelson J.E., Paetz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.3%;
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Pred.
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Matches 21
                                                                                                    SEQUENCE FROM N.A.
STRAIN=cregon-R;
MEDLINE=91293102; PubMed=1712294;
MEDLINE=91293102; PubMed=1712294;
Meyel-Ninio M.T.M., Terracol R., Kafat
"The ovo gene of Drosophila encodes a
for female germ line development.";
EMBO J. 10:2259-2266(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ULT 15
DROME
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ACT SITE
METAL
                                                                                                                                                                                                                       TISSUE-Ovary;

MEDLINE=95021209; PubMed=7935398;

GARTINKE M.D., Wang J., Liang Y., Mahowald A.P.;

GARTINKEL M.D., Wang J., Liang Y., Mahowald A.P.;

"Multiple products from the shavenbaby-ovo gene region of Drosophila

"Multiple products from the genetic complexity.";
                                                                                                                                                                                                                                                                                                                                                                                                              OVO_DROME STANDARD; PRT; 10
P51521; Q9XZU4;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID CARBOHYD
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                      -!- FUNCTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF I
LINE CELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION.
-!- SUBCELLULAR LOCATION: Nuclear (Potential)
-!- DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND
ACCUMULATES IN NURSE CELLS DURING OOGENESIS. STORED IN 1
BUT IS RAPIDLY LOST IN THE EMERYOS EXCEPT FOR ITS CONTIN
                                                                                                                                                                                                             melanogaster:
Mol. Cell. Bi
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Zymogen; Signal
                                                                                                                                                                                                                                                                                                                  Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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             PRESENCE
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ignal; Cell adhes
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             IN THE GERM LINE PRECURSOR POLE CELLS
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 Contains
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46.7%;
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Pred. No. 2.8;
3; Mismatches
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EMBL; X59772; CABB6921.1; ALT_SEQ.
PIR; A56038; A56038.
HSSP; P07248; 2ADR.
TRANSFAC; T00669; --
P1yBase; FBgn0003028; ovo.
InterPro; IPR007087; Znf C2H2.
Pfam; PF00096; zf-C2H2; 3.
SMART; SM00335; ZnF C2H2; 3.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.
Zinc_finger; Metal-binding; DNA-binding; Re
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                                                                                                                                                                                                                    ---GGGPSANSGGGGGGGGGGYINCGGVGGPNNSLDGNNLLNFASVSNYNESNSKFHNH 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1028;
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Title:
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Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1017041 seqs, 315518202 residues
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_archea:*
sp_bacteria:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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sp_rodent:*
sp_virus:*
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sp_unclassified:*
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SUMMARIES

16	15	14	13	12	11	10	9	8	7	σ	_U	4.	w	N		Result No.
105.5	106.5	107.5	107.5	107.5	108	110.5	113	114	122	303	428.5	498.5	550	593.5	682	Score
13.5	13.7	13.8	13.8	13.8	13.8	14.2	14.5	14.6	15.6	38.8	54.9	63.9	70.5	76.1	87.4	Query Match
91	1209	160	160	151	171	151	502	1748	29	76	150	152	149	150	152	Query Match Length DB
N			16			N	16		N					N	2	B
Q9S3J8	Q89CK5	Q83RU7	Q8CW64	Q7UCZ1	Q89JI3	Q7X244	Q8EIH4	Q94821	Q9S3J5	Q54069	Q7X237	Q8CW63	Q7X240	Q7X243	033802	ID
Q9s3j8 escherichia	Q89ck5 bradyrhizob	Q83ru7 shigella fl	Q8cw64 escherichia	Q7ucz1 shigella fl	Q89ji3 bradyrhizob	Q7x244 citrobacter	Q8eih4 shewanella	Q94821 tetrahymena	Q9s3j5 escherichia	Q54069 salmonella	Q7x237 enterobacte	Q8cw63 escherichia	Q7x240 citrobacter	Q7x243 citrobacter	O33802 salmonella	Description

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93 92	93.5	93.5	93.5	93.5	93.5	94	94.5	94.5	95.5	95.5	95.5	95.5	96	96.5	97	97	97	97	97.5	97.5	98	98	98	99	100	101	101.5
11.9	12.0	12.0	12.0	12.0	12.0	12.1	12.1	٠	12.2	12.2	12.2	12.2		12.4	12.4	12.4	12.4			12.5	12.6	12.6	12.6			12.9	13.0
141 353	1615	582	582	287	139	480	348	153	3552	3501	1613	145	490	1765	2039	2035	1422	368	152	151	3659	362	157	130	179	262	154
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Q8U6P1 Q8EV92	Q9KKA8	Q7TW98	P71868	Q9VIX6	Q8EIH3	Q89EV2	093397	Q89JI6	Q8XSD6	901XBD	Q9KKB2	Q8U6N9	Q8EYY9	Q7V8S5	Q8ZN57	Q9XCJ4	Q8EFU3	Q8EWD6	Q7X241	Q7X238	Q98LN6	Q8EV84	Q88HG0	Q89JI4	033801	Q9VIX5	210680
Q8u6p1 agrobacteri Q8ev92 mycoplasma	Q9kka8 rickettsia	Q7tw98 mycobacteri	P71868 mycobacteri	Q9vix6 drosophila	Q8eih3 shewanella			Q89ji6 bradyrhizob		Q8y106 ralstonia s		Q8u6n9 agrobacteri		Q7v8s5 prochloroco	7	Q9xcj4 salmonella		Q8ewd6 mycoplasma	Q7x241 citrobacter	Q7x238 enterobacte	Q98ln6 rhizobium l		Q88hg0 pseudomonas	Q89ji4 bradyrhizob	O33801 salmonella	Q9vix5 drosophila	Q89ji5 bradyrhizob

ALIGNMENTS

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121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151	61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120	61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120	1 MKLLKVAAFAAIVVSGSAVAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ 60	Query Match 87.4%; Score 682; DB 2; Length 152; Best Local Similarity 89.4%; Pred. No. 1.7e-46; Matches 135; Conservative 4; Mismatches 12; Indels 0; Gaps 0;	E 152 AA;	MBL; AU00514; CAA04151.1; *. NON TER 152 152	Immun. 6	saimoneila typnimulium sk-ii with mouse smail intestinai epitheilai cella.":	notes inter		MEDLINE=98053981; PubMed=9393832; Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z., Pfeifer J.D.,	SEQUENCE FROM N.A.	NCB1_18X1U=602;	Enterobacteriaceae; Salmonella.	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	Salmonella typhimurium.	AgfA protein (Fragment). AGFA.	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	-1998 (TrEMBLrel. 05, Creat		033802 PRELIMINARY; PRT; 152 AA.	RESULT 1

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RESULT 3
Q7X240
ID Q7X2
AC Q7X2
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                                                                                                                                                                                                                     EMBL; AJS
SEQUENCE
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"Production of Cellulose and Curli Fimbriae by Members of the Fami Enterobacteriaceae Isolated from the Human Gastrointestinal Tract. Infect. Immun. 72:4151-4158 (2003).
EMBL; AJ515701; CAD56675.1; -...
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EMBL; AJ515700; CAD56672.1; -. SEQUIENCE
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Q7X243;
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Bacteria; Proteobacteria;
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15016 MW; 1D7141B8D6973DC6 CRC64;
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72.2%;
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                                                                                          Score 550; DB
Pred. No. 4.5e
20; Mismatches
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Last annotation updat
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Pred. No. 1.7e-39;
4; Mismatches 18
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Q8CW63;
01-MAR-2003
    STRAIN=Fec39;
Zogaj X., Bok
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                                          SEQUENCE FROM N.A.
                                                                               NCBI_TaxID=28141;
                                                                                                      Enterobacteriaceae;
                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                               Enterobacter sakazakii
                                                                                                                                                                    CSGA.
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MEDLINE=22388234; PubMed=12471157;
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NCBI_TaxID=217992;
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67.1%;
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    Nimtz
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                                                                                                                         Gammaproteobacteria;
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  Romling
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                                                                                                                         Enterobacteriales;
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01-MAY-2000 (TrEMBLrel. 1:
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Curlin subunit monomer (E-
CSGA.
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Q54069;
01-NOV-1996
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Q9S3J5;
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Bacteria; Proteobacteria; Gamma
Enterobacteriaceae; Salmonella
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EMBL; AJ515702; CAD56678.1; -.
SEQUENCE 150 AA; 15112 MW; 5D8BB2D872DF15F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cox J.M., Eglezos S., Woolcock J.B.; "Virulence of Salmonella entertitidis in chickens correlates colony morphology and expression of SEF17 fimbriae."; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
Enterobacteriaceae;
                                            Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                      Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                          GNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNST
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                                                                                                                                                                                                                                                                                                                           IELTQNGFRNNATIDQ 105
                                                                                                                                                                                                                                                                                                                                                                                  GNHXGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QWNSKDSVMNVSQYGGLNGALVDQTASNSTVNVTQIGFGNHATAHQY
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                      Proteobacteria;
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76 AA;
                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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7704 MW;
  Escherichia
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                                                                                 (Fragment)
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19,
19,
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13, Last sequence up
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                      Gammaproteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 303; LB
Pred. No. 6.6e-
3; Mismatches
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Pred. No. 1.8e
?1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2FD5411241A7BCB1 CRC64;
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                                                                                                                                                                                           PRT;
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                                                                                                                                           Query Match
Best Local S
Matches 39
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Best Local S
Matches 26
                                                                                                                                                                                                                          PROSITE;
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            "Retroviral type zinc fingers and glycine-rich repeats encoded by cnjB, a Tetrahymena gene active during meios: Nucleic Acids Res. 21:4610-4614(1993).

EMBL; X06462; CAB37323:1; -.

EMBL; L03710; AAC37171.1; -.

PIR; S42136; S42136.
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Q94821; P92146; P92145;
01-FEB-1997 (TrEMBLrel.
01-FEB-1997 (TrEMBLrel.
                                                                                                                                                                                                                                                                  PRINTS; PR00939; C2HCZNFINGER.
SMART; SM00343; ZnF C2HC; 7.
PROSITE; PSS0158; ZF CCHC; 7.
CONFLICT 251 251 M
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MEDLINE=88189811; PubMed=3357771;
Martindale D.W., Taylor F.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora;
Tetrahymenina; Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNJB protein.
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MEDLINE-99314153; PubMed-10386375;
La Ragione R.M., Collighan R.J., Woodward M.J.;
La Ragione to Collighan R.J., Woodward M.J.;
"Non-curliation of Escherichia coli 078:K80 isol
IS1 inserti on in csgB and reduced persistence i
FEMS Microbiol. Lett. 175:247-253(1999).
EMBL; AJ131756; CAB45380.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P05888; 1AAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Taylor F.M., Martindale D.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=94051569; PubMed=8233798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5911;
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                                                                                                                                                                                                                                                                                                                                                  fam; PF00098; zf-CCHC;
                       82
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                                                                                                                                                                Similarity
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GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVG
                                                             QFGGGGNSNGGQSWGTSSGSDWN------CQSNVQES-TTTSSGGWGS----
                                                                                               QWGGGGNHNGG---GNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADV
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1748 AA;
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                                                                                                                                                                                                                              199624 MW;
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02, Created)
02, Last sequence update
25, Last annotation upda
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Pred. No. 0.00
1; Mismatches
                                                                                                                                                                Pred.
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RESULT 10
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                                          Bacteria; Proteobacteria; Gammag
Enterobacteriaceae; Citrobacter
              SEQUENCE FROM N.A.
                                NCBI_TaxID=213763;
                                                                  Citrobacter
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                                                                                                                                           Q7X244
                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequences:";
Shewanella oneidensis.";
Shewanella oneidensis.";
1123 (2002).
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                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Complete proteome.
SEQUENCE 502 AA; 52441 MW; D08CA23D6C46B62D CRC64;
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EMBL; AE015532; AAN53941.1;
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Alteromonadaceae; Shewanella.
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                   Shigella flexneri.
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Enterobacteriaceae;
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Proteobacteria;

Gammaproteobacteria;

Enterobacteriales;

Shigella.

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Q89JI3;
01-JUN-2003
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiun Sasamto S., Watanabe A., Idesawa K., Iriguchi M., Kaw Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada Tabata S.;
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Bacteria; Proteobacteria;
Bradyrhizobiaceae; Bradyrh
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CSGA OR BLL5300.
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"Production of Cellulose and Curli Fimbriae by Members
Enterobacteriaceae Isolated from the Human Gastrointest
Infect. Immun. 72:4151-4158(2003).
EMBL; AJ515700; CAD56671.1;
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                                                                                                                                                                       171 AA; · 17448 MW;
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Bradyrhizobium.
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"Extensive mosaic structure revealed by the complete genome of uropathogenic Escherichia coli.";
proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
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STRAIN-06:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=2388234; PubMed=12488234;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome. SEQUENCE 160 AA;
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Enterobacteriaceae; Escherichia.
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EMBL; AE016981; AAP16542.1; -.
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15868 MW; 5D5D266B964014A0 CRC64;
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Last annotation updat
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Pred. No. 0.45;
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SEQUENCE
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchium Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kaw Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada Tabata S.;
                                                                                                                                                                                                                         "Complete genomic sequence of nitrogen-fixing Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bradyrhizobiaceae;
NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bradyrhizobium japonicum.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
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Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Li
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Ch
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., H
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Bacteria, Proteobacteria,
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YGNVTVTGSTGATTIAL ---
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nilarity 25.0%;
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Bradyrhizobium.
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Shigella.
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Pred. No. 0.4
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Pred. No. 5.
-GNGNDTIDASG--YGNVITLGNGNDIVHPGDGASQTTAG
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113	111	1 1 1	3 1	123	132	153	378	450	504	504	523	528	574	597	606	609	611	619	622	662	684	689	689	709	774	Score	
	10.9	10.0			7		48.8	٠	65.1	65.1	67.6	68.2	74.2	77.1	78.3	78.7	•	80.0	80.4	85.5	88.4	89.0	89.0	91.6	100.0	Query Match	æ
4.7) K	2 0	J (23	22	45	122	142	120	120	151	151	151	151	151	151	151	151	151	151	151	151	151	151	151	Length	
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TEO ZONOA		AABSOS CO	36536944	AAB36321	AAB36318	AAB36316	AAR52663	AAR52664	AAW23569	AAR62761	ABR82651	AAB36343	AAB36348	AAB36355	AAB36352	AAB36347	AAB36346	AAB36351	AAB36349	AAB36354	AAW23570	AAB36341	AAR74625	AAB36353	AAB36350	ID	
בשרסבסזי ה. נכדו נ	Satuoner		e colmone		Aab36318 Salmonell	Aab36316 Salmonell		Aar52664 Fibronect	9		Abr82651 E. coli C	Aab36343 Escherich	Aab36348 AgfA::PT3	Aab36355 AgfA::PT3		::	AgfA::	::	AgfA::	Aab36354 AgfA::PT3	Aaw23570 Salmonell	Aab36341 Salmonell	Aar74625 AgfA sequ	Aab36353 AgfA::PT3	0 AgfA::P	Description	

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriacese for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinant gene into the chromosome of the homologous species; (3) directing recombinantion of a recombinant gene back into the chromosome of the homologous species, replacing the native

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 137; 139pp; English.

Aag29727 Arabidops	3 AAG29727	468	11.6	89.5	45
Aag29728 Arabidops	3 AAG29728	447	11.6	89.5	44
Abg07164 Novel hum	4 ABG07164	423	11.6	89.5	43
Abr82642 E. coli	7 ABR82642	24		90	42
Abg04318 Novel hum	4 ABG04318	677	11.7	90.5	41
Aaw32312 Leishmani	2 AAW32312	502		91	40
Abu21488 Protein e	6 ABU21488	186		91	39
Aab36331 Escheri	3 AAB36331	23		92	38
Abr82647 E. coli	7 ABR82647	24	12.3	95	37
Aab36328 Salmonel	3 AAB36328	19		96	36
Aab36336 Salmonell	3 AAB36336	19		96	ω 5
Aab36323 Salmonell	3 AAB36323	19		96	34 4
Aab36344 Escherich		151		96.5	33
Abr82649 E. coli	7 ABR82649	26	13.2	102	32
Aab36319 Salmonel		23		109	31
Aab36324 Salmonel		23	14.1	109	30
Aab36340 Salmonel		23	14.1	109	29
Aab36337 Salmonel	3 AAB36337	22		111	28
Aab36327 Salmonel	3 AAB36327	22	14.3	111	27
Aab36322 Salmonel	3 AAB36322	22	14.3	111	26

ALIGNMENTS

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RESULT 1
AAB36350
ID AAB3
WPI; 2000-672631/65.
N-PSDB; AAC64626.
                                                                                                                                                                 05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                   Salmonella enteritidis
                                                                                                                                                                                                                                vaccine; immune response; immunogen.
                                                                                                                                                                                                                                      Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                               26-FEB-2001
                                                                                                                                                                                                                                                                            AAB36350;
                                                                                                                                                                                                                                                                                        AAB36350 standard;
                                                                                                                                                    05-APR-1999;
                                                                                                                                                                             12-OCT-2000.
                                                                                                                                                                                          WO200060102-A2
                                                                                                                                                                                                                                                  AgfA::PT3#5 amino acid sequence SEQ ID NO:20
                                                                                                                                        (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                              Escherichia coli.
                                                                                                                           Doran JL,
                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                     99US-0127888P
                                                                                                                                                                                                                                                                                        protein;
                                                                                                                            Collison
                                                                                                                                                                                                                                                                                        151
                                                                                                                            SK,
                                                                                                                                                                                                                                                                                        ₽
                                                                                                                            Kay WW;
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RESULT 2
AAB36353
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Best Local
Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                WPI; 2000-672631/65.
N-PSDB; AAC64629.
                                                                                                                                                                                                 White AP,
                                                                                                                                                                                                                                                                                                               05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella;
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                                                                                                                                                                                                                                                        (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                              Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid sequence SEQ ID NO:26.
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Pred. No. 8.8e-71;
Mismatches 0;
                                                                                                                                                                                                 Kay WW
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Disclosure; Page 138; 139pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign ppitope or antigen. Also described are: (I) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the ccopy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or CC enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for cliting an immune response in an animal. In a fimbrial presentation consistent the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin proteins are usually strong communogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong communogens, which may be important for directing an immune response cagainst the inserted epitope, and hybrid fimbriae are easy and consequence in an invention consequence is given in the exemplification of the present invention
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Matches 1
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                                                                                                                                                                                                                                                                                                                       25-MAR-2003
26-JUN-1995
                                                                                                                                                                                                                  Salmonella.
                                                                                                                                                                                                                                                    Salmonella; AgfA; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                            AAR74625 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 151
                      (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP (KING/) KING J.
                                                                         26-APR-1993;
                                                                                                            26-APR-1994;
                                                                                                                                               10-NOV-1994
                                                                                                                                                                                                                                                                                      AgfA sequence
                                                                                                                                                                                WO9425598-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                         93US-00054452
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Pred. No. 3.7e-64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GQGADNSTIELTQNGFRNNATIDQWNAKNSD
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RESULT 4
AAB36341
ID AAB3
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Best Local Similarity 90.7
Matches 137; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described
                                                                                Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB36341 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ87467.
                                                                                                                                         WPI; 2000-672631/65.
N-PSDB; AAC64617.
                                                                                                                                                                                                                                    05-APR-1999;
                                                                                                                                                                                                                                                               05-APR-2000; 2000WO-CA000356
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                                                                                                                                                                                                                                                                                                                                                                                        Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                              26-FEB-2001
                                                       Disclosure; Page 135; 139pp; English
                                                                                                                                                                                                           (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                           vaccine; immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Collinson
                                                                                                                                                                                 Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                    99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                         response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95pp; English.
                                                                                                                                                                                 Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clouthier SC,
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Pred. No. 4.1e-62;
                                                                                                                                                                                 SK,
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                                                                                                                                                                                 Kay
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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    are:
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RESULT 5
AAW23570
ID AAW2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong
Collinson SK,
                                                                                                                                          03-JUN-1997
                                                                                                                                                                                                                                                                                   Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                      Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
                                                                                                                                                                                                                                                                                                                                                         Salmonella
                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW23570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW23570 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 151 AA;
                                                                                                         26-APR-1994;
                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                                    (UYVI-) UNIV VICTORIA INNOVATION &
                                                                      26-APR-1993;
                                                                                                                                                                             US5635617-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDARKYDQLYTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                         enteritidis 27655-3b agfA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
Kay
                                                                      93US-00054452
                                                                                                         94US-00233788
                                                                                                                                                                                                                                 Location/Qualifiers 123
                                                                                                                                                                                                             /note= "Encoded by GCC"
WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.0%;
   Doran
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 689; DB 3;
Pred. No. 4.1e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                      VED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 136; Conserv
Recombinant agfA gene which encodes foreign
                                            N-PSDB; AAC64630.
                                                         WPI; 2000-672631/65.
                                                                                     White AP,
                                                                                                                (UYVI-) UNIV VICTORIA
                                                                                                                                           05-APR-1999;
                                                                                                                                                                    05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                   12-OCT-2000
                                                                                                                                                                                                                             WO200060102-A2
                                                                                                                                                                                                                                                                                   Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                       Escherichia
                                                                                                                                                                                                                                                                                                                               Salmonella;
                                                                                                                                                                                                                                                                                                                                                          AgfA::PT3#9
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB36354 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents agfA encoded by the full derived from Salmonella enteritidis 27655-3b. The nucleio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 7; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-309886/28.
N-PSDB; AAT74142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNPALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDARKYDQLVTRVVTHEMAHAGQGADNSTIBLTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDARKSETTITOSGYGNGADVGQGADNSTIELTONGFRNNATIDOWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                  Doran JL,
                                                                                                                                                                                                                                                                                                                            agfA;
                                                                                                                                                                                                                                                                                                                                                        amino acid sequence
                                                                                                                                                                                                                                                                       COLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                           99US-0127888P
                                                                                                                                                                                                                                                                                                               response;
                                                                                                                                                                                                                                                                                                                           chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.4%;
90.1%;
having a segment replaced by a foreign DNA sequence epitope or antigen, expresses recombinant AgfA
                                                                                    Collison
                                                                                                                                                                                                                                                                                                               immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ω
••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 684; DB 2; Length 151; Pred. No. 1.3e-61; Mismatches 12; Indels
                                                                                    SK,
                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO:28
                                                                                 Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  he full agfA gene
nucleic acid can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT 7
AAB36349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) CC directing recombination of a recombination of a recombination of a recombination of a recombination of a recombination of copy of that gene; (3) directing recombination of a recombinative CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the CC useful for the expression of recombinant AgfA protein which is useful for celliting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to SO,000 copies/cell), the hybrid fimbria protein which is useful for immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong CC immunogens, which may be important for directing an immune response CC against the inserted epitope, and hybrid fimbriae are easy and CC inexpensive to purify in large amount. The present sequence is given in txx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 136
               05-APR-2000; 2000WO-CA000356
                                                                                                                           Synthetic
                                                                                                                                                                Salmonella enteritidis.
                                                                                                                                                                                                                     Salmonella; agfA;
                                                                                                                                                                                                                                                                                                                                                                    AAB36349 standard; protein; 151
                                                    12-OCT-2000
                                                                                       WO200060102-A2
                                                                                                                                                                                                   vaccine;
                                                                                                                                                                                                                                                         AgfA::PT3#4
                                                                                                                                                                                                                                                                                              26-FEB-2001
                                                                                                                                                                                                                                                                                                                                   AAB36349;
                                                                                                                                       Escherichia colı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                               106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                   immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.5%; ilarity 81.9%; Conservative
                                                                                                                                                                                                                                                       amino acid sequence SEQ ID NO:18.
                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                 response;
                                                                                                                                                                                                                   chromosomal gene replacement; fimbrin;
                                                                                                                                                                                                 ımmunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 662; DB Pred. No. 2.3e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·YDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQ
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ches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                   epitope;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105
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99US-0127888P

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RESULT 8
AAB36351
ID AAB3
XX
AC AAB3
XX
OT 26-F
XX
DE Agf!
XX
KW Salt
KW Vac:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant Agfa protein containing a replacement segment or segments of foreign amino
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                      Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                              AgfA::PT3#6 amino acid sequence SEQ ID NO:22
                                                                                                        26-FEB-2001
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vaccine; immune response; immunogen
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                                                                                                                                                                                                                                                                                                                                                                                     43 ----YDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF
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Pred. No. 2.8e-55;
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Best Local
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                                                                                                                                                                                                                                                                                                                                  Sequence 151
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N-PSDB; AAC64627.
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104
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                                  99 NNATIDOWNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                       Similarity
                                                                                                                          SDARK----
                                                                                                                                                                                                        MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                               MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSI YQYGSANAALALQ
                                                                                SDARKSETTI TQSGYGNGADVGQGADNYDQLVTRVVTHEMAHA
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                                                                                                                                                                                                                                               Score 619; DB
Pred. No. 5.6e
0; Mismatches
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RESULT 9

98 60 60

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103

AAB36346 standard; protein; 151

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The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) CC directing recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene CC comprising separating an amino acid polymer comprising a recombinant AgfA cromptising separating an amino acid polymer comprising a recombinant AgfA cromptising sequences grown on a Salmonella, E. coli or CC polymer into the animal in conjunction with a carrier or diluent. (I) is cuseful for the expression of recombinant AgfA protein which is useful for cell for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to System the heterologous antigens are presented in high numbers (up to company the heterologous antigens are presented in high numbers (up to company the heterologous antigens are presented in high numbers (up to company the heterologous antigens are presented in high numbers (up to company the heterologous antigens are presented in high numbers (up to company the heterologous antigens are presented in high numbers (up to company the presented protein possesses both the immune response against the inserted epitope, and hybrid fimbriae are easy and consense to the present invention of the present invention
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Best Local Similarity
Matches 122; Conserv
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                                                                                                                                                       Sequence
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Pred.
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                                                                                                611; DB 3;
No. 3.7e-54;
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       The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC assembly system of strains of Salmonella, Becherichia coli and CC Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal. CC comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an explacement segment or segments of foreign amino cc acid sequence or sequences grown on a Salmonella, E. coli or continuous continuous call, from the host cell and introducing the compositing an immune response in an animal. In a fimbrial presentation continuent response in an animal. In a fimbrial presentation continuent response in an animal. In a fimbrial presentation continuous copies/cell), the hybrid fimbrin protein which is useful for continuous copies/cell), the hybrid fimbrin protein possesses both the immune response in an animal. In a fimbrial strong immune response in the heterologous antigens are presented in high numbers (up to composite the linearing and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong cimmunogens, which may be important for directing an immune response in a part of the contribution and animal and the contribution and contribution and contribution in the contribution and contribution and contribution in the contribution and contribution in the contribution in the contributio
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Escherichia coli.
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Best Local
The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriacese for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombination of the homologous species; (3) directing recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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N-PSDB; AAC64628.
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N-PSDB; AAC64631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.3%;
82.1%;
                                                                                                                                                                                  Collison
                                                                                                                                                                                                                                                                                                                                                                                                                   ımmunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 606; DB 3;
Pred. No. 1.2e-53;
                                                                                                                                                                                  SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                  Kay
                                                                                                                                                                                   £
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 151;
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The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign DI sequence which encodes a foreign epitope or antigen. Also describe

foreign DNA so described

Recombinant agfA gene having a segment replaced by a foreign which encodes foreign epitope or antigen, expresses recombina protein useful for eliciting immune response in animal.

- ~y a roreign DNA sequence expresses recombinant AgfA se in animal.

Disclosure; Page 139; 139pp; English

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RESULT 13
AAB36348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant CR Agfa, CsgA and Agfa-homologue fimbria subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the CR homologous species; (3) directing recombinant gene into the chromosome of the back into the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant Agfa protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC Enterobacteriaceae host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant Agfa protein which is useful for CC eliciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to CC immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit protein possesses both the CC immunogens, which may be important for directing an immune response CC inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
WPI; 2000-672631/65
                                                     White AP,
                                                                                                                                                                 05-APR-1999;
                                                                                                                                                                                                                 05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                          12-OCT-2000
                                                                                                                                                                                                                                                                                                                             WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella; agfA; chromoso vaccine; immune response;
                                                                                                           (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AgfA::PT3#3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB36348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB36348 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonalla Bookselette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNNNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDARKSETTI TOSGYGNGADVGQGADNSTI ELTONGFRNNA TYDOLVTRVVTHEMAHAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                   Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                              99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acid sequence SEQ ID NO:16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.1%;
81.5%;
                                                     Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 597; DB Pred. No. 9.8e-5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                   SK,
                                                   Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3;
.8e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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밁 Ś 밁 á 밁 S

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AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively (2)
Cd directing recombination of a recombination for the chromosome of the homologous species; (3) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for sequence of sequences antigens are presented in high numbers (up to 100 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the heterologues are insurant for an efficient live vaccine, the high may be important for firefrican immune response
             Query Match
Best Local S
Matches 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                     Sequence 151
                                                                                                                                                                                               against the inserted epitope, and hybrid inexpensive to purify in large amount. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAC64624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 136; 139pp; English
                                                                                                                                                              inst the inserted epitope, and hybrid fimbriae are easy and
xpensive to purify in large amount. The present sequence is
exemplification of the present invention
                                           Similarity
                                                                                                                                                                                                                                                   which may be important for
                                                                                                                        B
                                   74.2%;
80.8%;
             Score 574; DB
Pred. No. 2.2e
6; Mismatches
DB 5,
2.2e-50;
23;
                                                                                                                                                                                                                                                directing an immune response
                                                              Length 151;
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121
                              121
                                                                                                                                                                                                  122;
                                                                 61
                                                                                               61
                   NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                               SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                        SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                               MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                6;
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                0;
                                                                                                                                                                                                Gaps
                                                                 120
                                                                                                                                60
                                                                                                 120
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AAB36343 standard; protein; 151 AA

닭 Ś 밁 Ś В Ś

Escherichia coli CsgA amino acid sequence SEQ ID NO:7.

26-FEB-2001

(first entry)

Salmonella; agfA; vaccine; immune response; chromosomal gene replacement; fimbrin; epitope; immunogen.

Escherichia coli

WO200060102-A2

12-OCT-2000

X P X P X S X X X X D X P X A X X

05-APR-2000;

2000WO-CA000356

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RESULT 15
ABR82651
ID ABR82
XX ABR82
AC ABR82
XX O4-DE
XX O4-DE
XX X C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC segment of the gene has been replaced by a segment of a foreign DNA

CC sequence which encodes a foreign epitope or antigen. Also described are:

(1) use of thin aggregative fimbriae (SEP17/TAF) nucleation depended

CC assembly system of strains of Salmonella, Escherichia coli and

CC Enterobacteriaceae for the production of fimbriae comprising recombinant

CC AgfA, CegA and AgfA-homologue fimbrian subunits, respectively; (2)

CC directing recombination of a recombinant gene into the chromosome of the

CC back into the chromosome of the homologus species, replacing the native

CC comprising separating an amino acid polymer comprising a recombinant AgfA

CC comprising separating a replacement segment or segments of foreign amino

CC acid sequence or sequences grown on a Salmonella, E coli or

CC protein containing a replacement segment or segments of foreign amino

CC protein containing a replacement segment or segments of foreign amino

CC protein containing a replacement segment or segments of foreign amino

CC protein the animal in conjunction with a carrier or diluent. (I) is

CC useful for the expression of recombinant AgfA protein which is useful for

CC useful for the expression of recombinant in a fimbrial presentation

CC solonous antigens are presented in high numbers (up to

SOLO,000 copies/cell), the hybrid fimbrin protein possesses both the

communogenicity and adhesion properties relevant for an efficient live

communogens, which may be important for directing an immune response

CC adainst the inserted entrone and hybrid fimbriae are assy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 104
                  E. coli CsgA subunit 15 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                           04-DEC-2003
                                                                                                 ABR82651
                                                                                                                                    ABR82651 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYVI-) UNIV VICTORIA
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                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104;
                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                           μ
                                                                                                                                                                                                                                                                                                                                                                                                                                 μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 68.9
04; Conservative
                                                                                                                                                                                                                                                        NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                          SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                    GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                                                                                                                                                                                             TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
                                                                                                                                                                                                                                                                                                                                                                                           MKLLKVAAIAAIVFSGSALAGVVPQYGGGGHHGGGGNNSGFNSELNIYQYGGGNSALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention describes a recombinant agfA gene he dene has been replaced by a segment of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 135; 139pp; English.
                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0127888P
                                                                                                                                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                      151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 528; DB 3;
Pred. No. 1.1e-45;
0; Mismatches 27
                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kay WW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Search completed: March 11, Job time: 45.9 secs

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Best Local S
Matches 103
                                                                                                                                                                                                                                                            The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABR02642, ABR026449. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Bsoherichia coli, Salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli 15 kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmor or Shigella infections.
                                                                                                                                                                                                                                     Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 41-42; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bjoerck L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JAN-2002; 2002GB-00002275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2003; 2003WO-EP000943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasma protein; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003064446-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HANS-) HANSA MEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-646136/61.
121
                                                          61
                                                                                                                                                                              103;
                                                                                                                    ш
                                                                                                                                      1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACF36153
                                                       TDARNSDITITQHGGGNGADVGQSSDDSSIDLTQRGFGNSATLDQWNGKNSEWTVKQFGG
                                                                          MXLLKVEAIAAIVESGSALAGVVPQYGGGGNHGGGGNNGGPNSELNIYQYGGGNSALALQ
 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
                             NNAALVNOTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                           67.6%; ilarity 68.2%; Conservative 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olsen A,
                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wikstroem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      response; antibacterial; vaccine; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                           Score 523; DB 7;
Pred. No. 3.4e-45;
0; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herwald
   151
                                                                                                                                                                              28;
                                                                                                                                                                                                        Length 151;
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US-09-498-520A-18
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Sequence 59, Appl Sequence 27661, A Sequence 27661, A Sequence 27661, A Sequence 4764, Appli Sequence 4764, Appli Sequence 2, Appli Sequence 2, Appli Sequence 26, Appli Sequence 26, Appli Sequence 214, Appli Sequence 204, Appli Sequence 2131, Appli Sequence 2131, Appli Sequence 2132, Appli Sequence 2133, Appli Sequence 214, Appli Sequence 2167, Appli Sequence 217, Appli Sequence 117, Appli Sequence 117, Appli Sequence 118, Appli Sequence 23, Appli Sequence 23, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, Appli Sequence 218, A
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Query Match 88.4%; Best Local Similarity 90.1%; Matches 136; Conservative

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Score 684; DB 1; I Pred. No. 5.5e-66; 3; Mismatches 12;

Length 151; Indels

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DB 1; Leng 5.5e-66;	US-08-233-788A-59 IS Sequence 59, Application US/08233788A Patent No. 5635617 GENERAL INFORMATION: APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. AUMBER OF SEQUENCES: 61 CORESSPONDENCE ADDRESS: ADDRESSEE: Seed and Berry STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle CITY: Seattle COMPUTER: Hashington COUNTRY: U.S.A. ZIP: 98104-7092 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/233,788A FILING DATE: 26-APR-1994 CLASSIFICATION NUMBER: US/08/233,788A FILING DATE: 26-APR-1994 ATTORNEY/AGENT INFORMATION: AREFERINCE/DOCKET NUMBER: 920043.403C2 TELEFONNE: (206) 622-4900 TELEFONNE: (206) 622-4900 TELEFONE: CHARACTERISTICS: LENGTH: 151 amino acidd TOPOLOGY: 11near MOLECULE TYPE: parotein US-08-233-788A-59	ALIGNMENTS	28 74.5 9.6 304 1 US-07-851-976B-8 29 74.5 9.6 304 1 US-08-291-609-8 30 74.5 9.6 304 1 US-08-291-609-8 31 74.5 9.6 304 3 US-08-850-554-8 31 74.5 9.5 211 1 US-08-133-011-16 32 73.5 9.5 211 1 US-08-133-011-16 34 73.5 9.5 211 1 US-08-322-76-852-34 37 73.5 9.5 211 1 US-08-399-575-34 37 73.5 9.5 211 1 US-08-899-575-34 38 73.5 9.5 211 1 US-08-899-575-34 39 73.5 9.5 211 2 US-08-899-575-34 39 73.5 9.5 211 2 US-08-899-575-34 40 73.5 9.5 211 3 US-08-999-7739-16 41 73.5 9.5 211 3 US-08-907-739-16 42 73.5 9.5 211 5 PCT-US93-08364-16 42 73.5 9.5 211 5 PCT-US93-08364-16 43 73.5 9.5 211 5 PCT-US93-08364-16 44 73.5 9.5 211 5 PCT-US95-08743-34 45 73.5 9.5 264 US-09-495-880A-26 45 73.5 9.5 269 3 US-08-438-745-4
th 151;	DETECTION		Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 16, Appli Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 34, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 26, Appl Sequence 27, Appl Sequence 26, Appl

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             Sequence 27661, Application US/09252991A Patent No. 6551795
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
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APPLICANT:
                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Seed and Berry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 92
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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William W.
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Pred. No. 9.2e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6001592
GENERAL INFORMATION:
APPLICANT: Kunio
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SEQ ID NO 27661
LENGTH: 208
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                                                                                                                                                                 APPLICATION NUMBER: JP 8-1844
FILING DATE: 15-July-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
REFERENCE/DOCKET NUMBER: F-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR EILING DATE: 1998-07-27
                                                                                TELEPHONE: (212)986-2340
TELEFAX: (212)953-7733
INFORMATION FOR SEQ ID NO: 3
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                               CURRENT AFFICATION NUMBER: US/08/854,00 FILING DATE: May 28, 1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
100 8-184459
                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette, 3.50 inch, COMPUTER: IBM Compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,038A
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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TITLE OF INVENTION:
                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: JAPAN
ZIP: 514-01
TOPOLOGY:
                    TYPE:
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                                      LENGTH:
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5. 6001592
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               amino acid
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KANION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
VENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
VENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
VENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
VENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
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US-09-498-520A-18
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Matches
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LENGTH: 321
TYPE: PRT
ORGANISM: Caulobacter crescentus
                                    Sequence 4764, Application US/09328352 Patent No. 6562958 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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CURRENT FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rock, Charles O APPLICANT: Heath, Richard
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
ORGANISM: Pin
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LOCATION:
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                                                                                                                                                                                                                                                          84 GADNSTIEL-TONG----FRNNATIDOWNAKNSDITV---
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                                                                                                                                                          LDAAKSCFAMGQSAGG
                                                                                                                                                                                         QTASDSSVMVRQVGFG 143
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Pred. No. 1.
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Pred. No. 2;
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US-08-458-023B-6
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                                                                      US-08-458-023B-6
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Query Match
Best Local Similarity
Matches 35; Conserv
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SEQ ID NO 4764
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Best Local Similarity
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, VI
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/458,023B
FILING DATE: 01-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS FILE REFERENCE: GTC99-03PA CURRENT APPLICATION NUMBER: US/09/328,352 CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                         TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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APPLICANT:
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                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                      MOLECULE TYPE:
                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Boominathan, Karuppan C. IITLE OF INVENTION: ASPERGILLUS EXPRESSION NUMBER OF SEQUENCES: 16
                                                                                                  TYPE: ami
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ZIP: 101
                                                                                                                                                                                                                                                          NAME: Lowney Dr., Karen A. REGISTRATION NUMBER: 31,27
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                                                                                                                                       LENGTH:
                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 NISGNSFTLIGNSSSSSVNTAPTTTSNTVNDNDTID--NGNSGGTGSGSGNGSGDGLLNG 391
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 10.1%;
ilarity 30.7%;
Conservative 1:
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                   Score 78;
Pred. No.
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Pred. No. 8;
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                                   Length 363;
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Mismatches

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RESULT 9
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US-08-331-515A-2
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US-08-331-515A-2
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Sequence 2, Application US/09168406A
PATENT NO. 6258769
GENERAL INFORMATION:
APPLICANT: Welinder, Karen G.
APPLICANT: Andersen, Morten B.
TITLE OF INVENTION: Peroxidase Variants With Improved
TITLE OF INVENTION: Hydrogen Peroxidase Stability
                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Patent No. 5851811
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Harrington, James J. REGISTRATION NUMBER: 38,711 REFERENCE/DOCKET NUMBER: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/331,515A
FILING DATE: 01-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                        YQ-GS-----KCESPVRK----ILRIVFHDAIGFSPALTAAGQFGGGADGSII 101
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Andersen, Morten B
FENTION: PEROXIDASE VARIANTS WITH IMPROVED
VENTION: HYDROGEN PEROXIDE STABILITY
                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Pred. No. 3.8;
13; Mismatches
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US-09-128-450-26
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; NAME/KEY: VARIANT
; LOCATION: (1)...(435)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-168-406A-2
                                                                                                                                                                                            Best Loc
Matches
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CURRENT FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 08/331,51
PRIOR FILLING DATE: 1994-11-01
PRIOR APPLICATION NUMBER: PCT/DK93/
PRIOR FILLING DATE: 1993-06-01
PRIOR FILLING DATE: 1993-06-01
PRIOR FILLING DATE: 1992-06-01
NUMBER: 0F92/92
PRIOR FILLING DATE: 1992-06-01
NUMBER: 0F92/92
PRIOR FILLING DATE: 1992-06-01
NUMBER: 0F92/92
PRIOR FILLING DATE: 1992-06-01
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Best Local (
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LENGTH: 435
TYPE: PRI
ORGANISM: Coprinus cinereus
                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 50121
CURRENT APPLICATION NUMBER: US/09/128,450
CURRENT FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chesebro,
                                                                                                                                                                                                                                                                       LENGTH: 254
TYPE: PRT
ORGANISM: Hamster sp.
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                                                                                                                                                                                                            Local
 205
                            135 VMVRQV 140
                                                           145 WEDRYYRENMARYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDIK 204
                                                                                      85 ADNSTIELTQNGFRNNA----TIDQWNAKNS-----DITVGQYGGNNAAL-VNQTASDSS 134
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                                                                                                                                                     26 WG-GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQG 84
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35; Conserv
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IMERVV 210
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Chabry, Joelle
Priola
                                                                                                                        WGQGGGTHNQWNKPSKPKTNMK--HMAGAAAAGAVVGGLGGY--MLGSAMSRPMMHFGND 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FastSEQ for Windows Version
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                                                                                                                                                                                                          Score 77.5;
Pred. No. 2;
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Pred. No. 3.8;
13; Mismatches
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US-07-792-259-17
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SEQ ID NO 26
LENGTH: 254
TYPE: PRT
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Best Local (
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Patent No. 635561
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APPLICANT: Chabry, Joelle
APPLICANT: Priola, Susette
TITLE OF INVENTION: Inhibitors of Formation of Protease Resistant Prion
TITLE OF INVENTION: Protein
FILE REFERENCE: 50121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PILE REFERENCE: 50121
CURRENT APPLICATION NUMBER: US/09/823,494
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/128,450
PRIOR FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 29
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                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tent No.
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ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1615 L. STREET, N.W.
ATTORNEY/AGENT INFORMATION: NAME: SCOTT, WATSON T.
                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                          TITLE OF
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                                 APPLICATION NUMBER: FILING DATE: 199111 CLASSIFICATION: 43:
                                                                                                                                                                                                                                                CITY: WASHINGTON
                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 VMVRQV 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32; Conservative
                                                                                                                                                                                          20036
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Similarity 25.4%;
                                                                                                                                                                                                                                                                                                      I: SUMIDA, MOTOO
INVENTION: PEROXIDE GENE OF MICROBIAL ORIGIN
F SEQUENCES: 17
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                                                                                                                                                                                                                               D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/07792259
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HATANAKA, HARUYO
SHIBANO, YUJI
AMACHI, TERUO
NAKAYAMA, TORU
                                                                                                                                                                                                               USA
                                                    19911115
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                                                                   US/07/792,259
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Pred. No. 2;
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                                                                    US-09-056-556-204
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Query Match 9.9
Best Local Similarity 26.3
Matches 37; Conservative
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                     SEQUENCE CHARACTERISTICS
LENGTH: 943 amino aci
                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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STREET: Seattle
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                                                                                    STRANDEDNESS
TOPOLOGY: 1:
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: 202-822-0944
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                                                                                                                                                                                           TELEFAX:
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                                                                                                                                                                                         (206) 682-6031
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                                                                                    linear
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9.9%; Score 77; DB
26.2%; Pred. No. 14;
tive 14; Mismatches
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                                  DB 4;
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                                  Length 943;
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   Indels .
   24;
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   Gaps
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US-09-072-596-199
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                                                                                                                                                                  Query Match
Best Local Similarity
Matches 37; Conserv
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                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206) 682-60: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                      RADME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION: (206) 622-4900
TELEPHONE: (206) 622-490
                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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129 TASDSSVMVRQVGFGNNATAN 149
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                                                               RVVTHEMAHAGQGADNSTIELT---QNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQ 128
                                  NTGNNNIGFANTGNNNIGIGLSGDNQQFN---IASGWNSGTGNSGLFNSGTNNVGIFNA 573
                                                                                                 GSGNIGVFNVGSGSLGNYNIGSGN-----LGIYNIGFGNVGDYNVGFGNAGDFNQGFA 516
                                                                                                                                   GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAA--LALQSDARKYDQLVT
                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
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6300 Columbia Center,
                                                                                                                                                                         9.9%; Score 77; DB ilarity 26.2%; Pred. No. 14; Conservative 14; Mismatches
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Hendrickson, Ronald C.
HENDRICKSON: COMPOUNDS AND METHODS FOR DIAGNOSIS
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Vedvick, Thomas S.
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                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                        DB 4;
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                                                                                                                                                                                                        Length 943;
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Search completed: March 11, Job time: 12.4 secs
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US-09-477-135A-131
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SEQ ID NO 131
LENGTH: 943
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Best Local Similarity
Matches 37; Conserv
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PRIOR FILING DATE: 1997-12-
PRIOR FILING DATE: 1996-06-
PRIOR FILING DATE: 1996-06-
PRIOR APPLICATION NUMBER: 1
PRIOR FILING DATE: 1995-06-
PRIOR FILING DATE: 1995-06-
PRIOR FILING DATE: 1995-06-
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CURRENT FILING DATE: 2000-01-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nano, Francis
ITITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
ITITLE OF INVENTION: immunostimulatory Peptides
                                                                     681 GTGN---
                                                                                                                                                                                                            571 GSGNIGVFNVGSGSLGNYNIGSGN-----LGIYNIGFGNVGDYNVGFGNAGDFNQGFA 623
                                                                                                     129 TASDSSVMVRQVGFGNNATAN 149
                                                                                                                                        624 NTGNNNIGFANTGNNNIGIGLSGDNOOGFN---IASGWNSGTGNSGLFNSGTNNVGIFNA 680
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                                                                                                                                                                        72 RVVTHEMAHAGQGADNSTIELT---QNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQ 128
                                                                                                                                                                                                                                              16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAA--LALQSDARKYDQLVT 71
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                                                                   -VGIANSGTGN
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               2004, 18:44:51
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                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                    Score 77;
Pred. No.
                                                                   694
                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                      DB 4;
14;
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd

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Title:
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Maximum Match 100%
Listing first 45 summaries
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     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications AA:*

1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep:*

6: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pep:*

10: /cgn2_6/prodata/1/pubpaa/US09E_PUBCOMB.pep:*

11: /cgn2_6/prodata/1/pubpaa/US09E_PUBCOMB.pep:*

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13: /cgn2_6/prodata/1/pubpaa/US09E_PUBCOMB.pep:*

14: /cgn2_6/prodata/1/pubpaa/US09E_PUBCOMB.pep:*

15: /cgn2_6/prodata/1/pubpaa/US10E_PUBCOMB.pep:*

16: /cgn2_6/prodata/1/pubpaa/US10E_PUBCOMB.pep:*

17: /cgn2_6/prodata/1/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/prodata/1/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep:*

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Match
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Gapop 10.0 , Gapext 0.5
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774
1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
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     13.1
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     445
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 9 US-09-810-264-28

9 US-09-793-306-146

14 US-10-128-714-3213

14 US-10-128-714-8213

14 US-10-238-075-1119

14 US-10-238-075-1119

15 US-09-996-194-16

16 US-09-996-194-16

17 US-09-820-843A-21

18 US-10-369-493-20619

19 US-10-369-493-3641

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10 US-10-3369-493-3641
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US-10-156-761-9343
US-10-238-075-749
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Sequence 20638, A
Sequence 343, App
Sequence 749, Appl
Sequence 28, Appl
Sequence 3213, Ap
Sequence 8213, Ap
Sequence 8213, Ap
Sequence 1119, Ap
Sequence 16, Appl
Sequence 16, Appl
Sequence 21, Appl
Sequence 20619, A
Sequence 30619, A
Sequence 3641, Ap
Sequence 3641, Ap
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73.5	73.5	73.5		74	74	74	74	74	75	75	75	75.5	•	75.5	•	75.5	76	76	76	76.5	77	77	77	77	77	77.5	78	78	78.5
9.5		9.5				9.6		9.6	9.7	9.7		9.8		9.8		9.8	9.8	9.8	9.8	9.9	9.9	9.9	9.9		9.9	10.0	10.1	10.1	10.1
219	219	211	211	402	400	350	284	253	358	254	250	2893	552	482	254	254	2122	892	252	254	943	943	943	943	943	254	594	545	271
9	9	15	14	9	14	14	14	10	14	10	8	10	15	14	15	14	9	10	14	14	14	14	10	10	9	15	14	15	14
US-09-809-517A-27	US-09-809-517A-24	US-10-273-973-16	US-10-016-986-34	US-09-712-363-147	US-10-009-823A-10	US-10-156-761-13168	-10-156-761-	US-09-880-748-2098	US-10-156-761-9634	US-09-880-748-1186	US-08-779-457-49	-09-882-227-	US-10-369-493-3745	US-10-156-761-8763	US-10-410-907A-7	US-10-304-630-23	US-09-813-214A-9	US-09-952-267-5	US-10-304-630-32	US-10-301-488A-26	US-10-084-843-204	US-10-193-002-199	US-09-997-181-131	US-09-997-182-131	US-09-996-634-131	US-10-410-907A-5	US-10-156-761-13173	US-10-369-493-18473	US-10-156-761-11721
Sequence 27, Appl	24,	16	e 34	147	e 10	e 13	8340,	2098,		e 118	49, Ap	522, 1	3745,	87	7,	Sequence 23, Appl	9 A	v	w	N	N	199,	131,	e 131,	131	Sequence 5, Appli	13		Sequence 11721, A

ALIGNMENTS

RESULT 1 US-10-369-493-20638

Qу 51	Db 19	φ	Query Match Best Local Matches 4	; NAME/KEY: unsure ; LOCATION: (1)(; OTHER INFORMATIO US-10-369-493-20638	; TYPE: PRT; ORGANISM: FEATURE:	; SEQ ID NO 20638 ; LENGTH: 445	; PRIOR APPI ; PRIOR FILI ; NUMBER OF	; CURRENT AF	; TITLE OF I	; APPLICANT:	APPLICANT:	, APPLICANT:	; FUDITICATION NO. USZU ; GENERAL INFORMATION:	; Sequence 20638, A
GSANAALALQSDARKYDQLYTRVVTHEMAHAGQGADNSTIELTQNGFRNNATID 104	19 AAFAADSNTVYLNQTGNDQQANITQSGNGNSVGAFNGNSGFLQENGTLSGA-NLLTVKQS 77	7 AAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQY 50	Query Match 13.1%; Score 101.5; DB 15; Length 445; Best Local Similarity 26.0%; Pred. No. 0.046; Matches 45; Conservative 20; Mismatches 55; Indels 53; Gaps	NAME/KEY: unsure LOCATION: (1)(445) OTHER INFORMATION: unsure at all Xaa locations 0-369-493-20638	TYPE: PRT ORGANISM: Rhodopseudomonas palustris FEATURE:	0638 45	PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2002-02-21 NUMBER OF SEO ID NOS: 47374	CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28	TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B	TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS	Slater, Steven C.	APPLICANT: Cao, Yongwei	ORMATION:	Sequence 20638, Application US/10369493
ARKYDQLVTRVVT ;	NOTGNDQQANITO	VVSGSALAGVVPQ	13.1%; Score 26.0%; Pred. ive 20; Mi	ure at all Xa	onas palustri		R: US 60/360, -02-21 7374	BER: US/10/36 003-02-28	ANTS WITH IMP 2052)B	eng RESSION OF MI	yen C.	4	336/5A1	ion_US/103694
HEMAHAGQGA	SGNGNSVGAFNGN	WGGGGNHN	101.5; DB 1 No. 0.046; smatches 55	a locations	co:		039	9,493	ROVED PROPERT	CROBIAL PROTE				93
DNSTIELTQ	ISGFLQENGTLSG	IGGGNSSG	.5; Length 4							INS IN PLANTS				
NGFRNNATID	A-NLLTVKOS	PDSTLSIYQY	45; 53; Gaps							S FOR PRODUCTION OF				
104	77	50	7;							CTION OF				

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; ORGANISM: Escherichia coli
US-10-238-075-749
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                                                                                     NUMBER OF SEQ ID NOS: 1576
SOFTWARE: PatentIn version 3.1
SEQ ID NO 749
LENGTH: 1778
TYPE: PRT
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                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Streptomyces avermitilis US-10-156-761-9343
                                                                                                                                                                                                                                                                                                                      Sequence 749, Application US/10238075
Publication No. US20030148324A1
GENERAL INFORMATION:
                                                                                                                                                                 FILE REFERENCE: BLANDINE
CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 0003145
PRIOR FILING DATE: 2000-03-10
                                                                                                                                                                                                                                 APPLICANT: I.N.S.E.R.M.
TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ś
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9343
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APPLICANT: IKEDA,
APPLICANT: ISHIEZ,
APPLICANT: HORIK;
APPLICANT: SHIBA,
APPLICANT: SAKAK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9343, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITILB OF INVENTION: NOVEL POLYNUCLEOTIDES
TILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                             113 TGALLPWDAKNFD----KIGGKD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 NATIDOWNAKNSDITVGOYGGNN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 GWWTYDPGVFNKITQDSSSNGŠKVSVÍQDGKNNVFSIKQGNTGNŠTSVNQIG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKVLÓPELDKFEEQTGIKVKLEVVPWSDLLNKILT--ATTSĠĠĠPĎVLNÍGNTWSASLQA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---LOSDARKYDQ-----LVTRVVTHEMAHAGQGADNSTIELTQN-GFRN 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MRSIRAĀĀVGĀVTMSLALAĀSĀC----GĞĞSSTĞĞĞSNDSÞ-KTLT-YWASNQGĀSIAVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNSNS-----VGRDIQGKQSGAGNSAAIFQEGTGSDVELQQTGTSNGAVPS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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               10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.2%;
       Score 84.5;
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Pred. No. 0.24;
27; Mismatches
DB 14; Length 1778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46; Indels 33;
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US-09-793-306-146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT; ORGANISM: Triticum aestivum US-09-810-264-28
                                                                                                                                                                        GENERAL
                                                                                                                                                                               Sequence 146, Application US/09793306
Patent No. US20020098200A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 20.8.
37; Conservative
APPLICANT: Skeiky, Yasir
APPLICANT: Ovendale, Pamela
APPLICANT: Jen, Shylan
APPLICANT: Lodes, Michael
APPLICANT: Lodes, Michael
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
FILE REFERENCE: 014058-008740US
FILE REFERENCE: 014058-008740US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-810-264-28
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APPLICANT: Skeiky, Yasir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 278
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APPLICANT: Lu, Guihua
APPLICANT: Zhang, Lingyu
TITLE OF INVENTION: WRKY Transcription Factors and Methods
TITLE OF INVENTION: 0f Use
FILE REPERENCE: 1183
FILE REPERENCE: 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28, Application US/09810264
Patent No. US20020076775A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/810,264 CURRENT FILING DATE: 2001-03-16 PRIOR APPLICATION NUMBER: US 60/190,467 PRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Crane, APPLICANT: Famod
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                                                                                                                                                                     INFORMATION
                                                                                                                                                                                                                                                               179 CTTVGCPVRKHVERASHDNRÁVÍTTYEGRHŚHDVPVGRGAGASRÁLPTSSSSDSSVVV 236
                                                                                                                                                                                                                                                                                                                            120 -HGDNEGSSGGTGACVKPVREPRLVVQTLSDÍÐILDDGFRWRKYGQKVVKGNÞNÞRSYYK 178
                                                                                                                                                                                                                                                                                                                   99
                                                                                                                                                                                                                                                                                                                                                                75 TH---EMAHAGOGA-----DNSTIELTQNGFR----
                                                                                                                                                                                                                                                                                                                                                                                                                         15 SGSALAGVVÞQWGGGGNHNGGGNSSGÞDSTLSIYQYGSANAALALQSDARKYDQLVTRVV 74
                                                                                                                                                                                                                                                                                                                                                                                            71 NSSGCAAVIAE-----DHTNGSEHSGPTPENSSVTFGDDEADNGAEDETKRRKE----- 119
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                                                                                                                                                                                                                                                                                            5 KVAAFAAIVVSGSALAGVVPQW----GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL- 59
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lu, Omolayo O.
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Pred. No. 1.8;
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1; Mismatches
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RESULT 6
US-10-128-714-3213
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                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version
SEQ ID NO 3213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3213, Application US/10128714 Publication No. US20030119013A1
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SEQ ID NO 146
LENGTH: 597
TYPE: PRT
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Best Local Similarity
                                                                             Matches
                                                                                                                Query Match
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PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus
TITLE OF INVENTION: Methods of Use
TITLE OF INVENTION: Methods of Use
TITLE REFERENCE: 1018-2018-999
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NUMBER OF SEQ ID NOS: 164
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PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 60/223,821
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
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                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-06-05
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                                    13 VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQL---
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                                                                                               Similarity
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VLTGHKGSVTCVRWGGTGKI----YTSSHDRTIKIWNAQNGSLLQTLSAHAHRVNHLALS
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                                                                                             Pred.
                                                                                             Score 82.5;
Pred. No. 4;
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US-10-238-075-1119
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Sequence 1119, Application US/10238075
Publication No. US20030148324A1
GENERAL INFORMATION:
APPLICANT: I.N.S.E.R.M.
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LENGTH: 515
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Publication No. US20030119013A1
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APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT FILLING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/303,899
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SOFTWARE: PatentIn ver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          274
                                                                                                                                                                                                                                         108 AKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNN 145
                                                                                                                                                                                                                                                                                           330 TDFALRTAYHD--HTGKVPGSDTEKVAVAKKRFEQAAMVNNKIVEKLVSASDDFTMYLWD
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Tishkoff, Daniel
Zamudio, Carlos
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                                                                                                                                                                                               PENSTKPIARLLGHQKEVNHVTFSPDMAYIASAGFDNH
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Pred. No. 5;
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TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolal TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of the: FILE REFERENCE: BLANDING CURRENT APPLICATION NUMBER: US/10/238,075 CURRENT FILING DATE: 2002-09-10 PRIOR APPLICATION NUMBER: 0003145

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                                               NAME/KEY: misc feature
LOCATION: (1158). (1158)
OTHER INFORMATION: The 'Xaa' at lo
NAME/KEY: misc feature
LOCATION: (1159). (1159)
OTHER INFORMATION: The 'Xaa' at lo
NAME/KEY: misc feature
LOCATION: (1168). (1168)
OTHER INFORMATION: The 'Xaa' at lo
NAME/KEY: misc feature
LOCATION: (1270). (1270)
OTHER INFORMATION: The 'Xaa' at lc
NAME/KEY: misc feature
LOCATION: (13480). (13480)
OTHER INFORMATION: (13480)
OTHER INFORMATION: (131038)
OTHER INFORMATION: Unsure
LOCATION: (31038). (31038)
OTHER INFORMATION: Unsure
NAME/KEY: misc feature
LOCATION: (31038). (31038)
OTHER INFORMATION: Unsure
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SEQ ID NO 252
LENGTH: 2834
TYPE: PRT
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NUMBER OF SEQ ID NOS: 1576
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1119
LENGTH: 2732
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Welch, Rodney A.
APPLICANT: Burland, Valerie D.
TITLE OF INVENTION: NO. US20030165870A1e1
FILE REFERENCE: 960296.97648
CURRENT APPLICATION NUMBER: US/10/085,959
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/242,412
PRIOR FILING DATE: 2000-10-19
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OTHER INFORMATION: Unsure
                    NAME/KEY: misc feat LOCATION: (31042)..
                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature LOCATION: (493) . (493) OTHER INFORMATION: The 'Xaa' at location 493 stands for Asn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 ASGRLTVNNSLATGAVTAKGOGVTLTGDHKAGGNLSVSSRRDIVLS---NGTLNSDKDLS 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 AFAAIVVSGSALAGVVPQWGGG:---GNHNGGGN---SSGPDSTLSIYQYGSANA--ALA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGNNAALVNOTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTAGGRITQQ-----NEKLTAGRDVTLAAKNITQD-----TASQINAARDIVTV--- 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/10085959
o. US20030165870A1
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                    feature
(2)..(31042)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -ASDTLTTQGQITAGQNLTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.7%; Score 82.5;
27.8%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                     at location 1168 stands
                                                                                                                                                                          location 1270 stands for Thr,
                                                                                                                                                                                                                                                                                               location 1159 stands
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RESULT 11 US-09-820-843A-21

Sequence 21, Application US/09820843A

Publication No. US2003003963A1

GENERAL INFORMATION:

APPLICANT: Council of Scientific and Industrial Research

TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTE

TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES

FILE REFERENCE: Q63915

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US-09-996-194-16
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                                                              Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 16
LENGTH: 65
TYPE: PRT
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Patent No. US20
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PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/250,073
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/253,878
PRIOR FILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 35800/240590
CURRENT APPLICATION NUMBER: US/09/996,194
CURRENT FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bandaru, Rajasehkar
TITLE OF INVENTION: 84242, 8035, 55304, 52999,
TITLE OF INVENTION: No. US20020151696A1e1 Huma
                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE:
                                                                                                                                                                            FEATURE:
                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Unsure NAME/KEY: misc feature LOCATION: (31799)..(31799) OTHER INFORMATION: Unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (44922)...(44922)
OTHER INFORMATION: Unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/250,338
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 22
                               51 GSANAALALQSDARKYDQLVTRVVTHEMAHA 81
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GVINIPAANITSRNHYDQLVTRVVTHEIAHA 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09996194
                                                                   10.6%;
ilarity 58.1%;
Conservative
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27.8%;
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                                                                  Mismatches
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Pred. No. 45;
L6; Mismatches
                                                                                  Score 82; I
Pred. No. 0.
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SEQ ID NO 20619
LENGTH: 486
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CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.0
SEQ ID NO 21
LENGTH: 354
                                                                                                                                                                                                                       Query Match
Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                                                                       .10-369-493-20619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)8
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
OTHER INFORMATION: PPE
NAME/KEY: misc_feature
OTHER INFORMATION: gi|1781260
                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
LOCATION: (1)..(486)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                       PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Rhodopseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                          145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 TAN 149
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                                                                                                                                                              11 AIVVSGS----ALAGVVPQWGGGGNHNGGGNSSGP-----DSTLSIYQYGSANAAL
                                                                                                                                                                                                                       Similarity
                                                                                ALQSDARKYDQLVTRVVTHEMAHAG--QGADNSTIELTQNG---FRNNATIDQWNAKNSD 112
                                                                                                                      SVVVAGTDYRDIVAGVLPSLGGVKKAYAIGDGSGPFAPFKDLASDTPFSAPEFGAADGF- 144
                                                                                                                                                                                                      Conservative
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    QYGGNNAALVNQTASDSSVM 136
                                                                                                                                                                                                                     10.4%; Score 80.5; DB 15; 23.5%; Pred. No. 7.5;
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                                          -VIIHTAAVGGRPRGA-----LISQGNLLIAQSSLVDAWRLTEAD
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Pred. No. 3.5;
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US-10-156-761-13039
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Best Local Sim
Matches 53;
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LENGTH: 562
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         Sequence 3641, Application US/10369493 Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OMURA,
APPLICANT: IKEDA,
APPLICANT: ISHIKA
APPLICANT: HORIKA
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Publication No. US20030119018A1
SEQ ID NO 3641
LENGTH: 276
                                                         APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10 (52052)B
CURRENT FILLNG DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                             APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory
APPLICANT: Slater, Steven C
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR PPLICATION NUMBER: UP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 249-262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICANT: SHIBA, TADAYOSHI
PPLICANT: SAKAKI, YOSHIYUKI
PPLICANT: HATTORI, MASAHIRA
ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 NITSGDYAGONTALRIGGNNTVNKDVLLSISSDMONSGRRWGFRAN 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 DITVGQYGGNNAAL-----VNQ----TASDSSVMVRQVGFGNN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 VHGHWELEVADATGÁLQGRLEIPFIDQSKLSNAVDTTTÍGIAWTNIRTN--LADFSIRAQ 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 IRHFMMRSDAKTMQAFYIPVQTSNKKGGYDATTRDPLSTGVSWKPVVWQGAHYEANDHGS 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 SGSPSYASLPKGIAGRSENAGLIIGSSYIGGDDDGTGTDSTGRLNLYSYQRANVGSFGEN 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 VNLGMLPLFHVTGLGLMLTLQQAGGASVI 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 -----VTHEMAH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 SGSALAGVVPQWGGGGNHNGG---GNS-----SGPDST--LSIYQYGSANA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 10.3%; Score 79.5; I
Similarity 23.5%; Pred. No. 11;
53; Conservative 20; Mismatches
                                                                                                                                                                                                                      Goldman, Barry S.
Chen, Xiarfor
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HORIKAWA, HIROSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----AGQG------ADNSTIELTQNGFRNNATIDQWNAKNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 562;
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                                                                                                                                                                                                      FOR PRODUCTION
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APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 7876
LENGTH: 688
TYPE: PRT
ORGANISM: Candida albicans
US-10-032-585-7876
Search completed: March 11, 2004, 19:18:38 Job time: 25.6 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-10-032-585-7876
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Best Local Similarity 23.5
Matches 42; Conservative
                                                                                                                                                                                                                                                                       Query Match 10.2%; Score 79; DB 14; Length 688; Best Local Similarity 22.7%; Pred. No. 17; Matches 27; Conservative 24; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7876, Application US/10032585 Publication No. US20030180953A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 WTETYRTNVASIYEMTSAFLPLLQASTERHPGWSGTVVNISSISGQVKSAQHHFSYNAS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 WNAKNS------DITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNAT 147
                                                                                                                                                                                   488 GNNNGSGNSSGTTNNSNNYN----NKSISKKNEIDDGDDLNPTSITNNTGLTNNNNSKSP 543
                                                                                          544 AKSKKKSNFDNNSNSALNNLDKSKLKINT---NEITNISETTSNSSSPVINLNHGGRSS 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                       30 GNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGADNST 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 DARKYDQ---LVTRVVTHE-----MAHAGQGADNSTI-----ELTQNGFRN-NATIDQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 LAGVVPQWGGGGNHNG-----
                                                                                                                                   90 IE-LTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNAT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVTKKEDIAALVKEIESREKCLCILVNNAGISSSSVTTEASDPKELKHNLFDNENATFDD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAGRVALVTGGGTGIGLMATQALAVNGAKVYIAGRNKEKLDKVVEIYNKDVEGEIIALQA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GGNSSGPDSTLSIYQYGSANAALALQS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69; Indels 50;
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ALIGNMENTS

ated the codon ACG for residue 44 as I L.; Muller, K.H.; Trust, T.J.; Kay, W. Ehtracterization of thin, aggregative characterization consecution residue 44 as Ile t, T.J.; Kay, W.W. in, aggregative fimbriae 1677357 CBIP:45936) CBIP:45936 CBIP	(EC Qy 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151	1 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQNNAKNSDITVGQYGG 120	Oy 61 SDARKYDOLYRVYTHEMAHAGGANSTIELTQNGFRNARTIDGWAKNSDLTVGQYGG 120	•	antig Db 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ	ase r Oy 1 MKLLKVAAPAATVVSGSALAGVVPQWGGGGNRNGGGNSNGSPDSTLSTVQYGSANAALALQ 60	Matches 137; Conservative 3; Mismatches	n (EC Best Local Similarity 90.7%; Pred. No. 3.1e-	Onors, Match													chain A;Accession: A44898		A; Reference number: A44898; MUID:91310586; PMID:1677357	A; Title: Purification and characterization of thi	J. Bacteriol. 173, 4773-4781, 1991	B: Collingon of a smooth for the color and t	1. Note: the authors translated the codon ACG for residue 44 as Ile	
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121

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A;Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August R;Blattner, F.R.; Plunkett III, G,; Bloch, C.A.; Perna, N.T.; Burland, V.; Rile A; Rose, D.J.; Mau, B; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74126.1; A;Experimental source: strain K-12, substrain MG1655 R;Oleen, A.; Arnqvist, A.; Hammar, M.; Sukupolvi, S.; Normark, S. Mol. Microbiol. 7, 523-536, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 12-Reb-1998 #sequence revision 20-Reb-1998 #text_change 01 C;Accession: S70788; G64846; S31202; S34569, S34559 R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S. Mol. Microbiol. 18, 661-670, 1995
Mol. Microbiol. 18, 661-670, 1995
Mol. Expression of two csg operons is required for production A;Reference number: S70783; MUID:96414468; PMID:8817489
A;Accession: S70788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
$70788
curlin protein csgA precursor - Escherichia coli (strain N;Alternate_names: csgA protein; major curlin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     th, T.; COMMENCE, O'GAORA, P.
, S.; Moule, S.; O'GAORA, P.
Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Authors: Complete genome sequence of a multiple drug resistant
A;Title: Complete genome sequence of a multiple drug resistant
A;Title: Complete genome sequence of Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amilian Amil
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                                                                                                                                                                                                                                                        A; Accession: G64846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-151 < HAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: nucleic acid sequence not shown; translation not
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A; Residues: 1-151 < PAR>
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R;Parkhill, J.; Dougan, G.; Jam
                                                                                                                                              Residues: 1-151 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62282.1; PID:g1147564
                                                                                                                                                                                 Molecule type: DNA
                                                                                                                                                                                                                 Status: nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 137; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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secies has also been called Salmonella typhi
2001 #sequence_revision 09-Nov-2001 #text_c
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                                                                                                                                                                                                              acid sequence
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in, A.;
                                                                                                                                                                                                      not shown; translation not shown
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Pred. No. 3.1e~51;
3; Mismatches 11
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Davis,
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    Salmonella enterica subsp.

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ies, R.M.; Dowd, L.;
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C;Accession: D90806
C;Accession: D90806
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, A.; Lunca, R;Hayashi, T.; Makino, K.; Kuhara, S.; Shiba, T.; Hattori, M.; Shii gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shii DNA Res. 8, 11-22, 2001
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia
A;Title: Complete genome sequence of enterohemorrhagic Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                       curlin major subunit CsgA [imported]
C;Species: Escherichia coli
C;Date: 18-Jul-2001 4--
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                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-152 <HAY>
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D90806
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A; Residues: 21-42;44-50 <OLS2>
R; Olsen, A.W.; Armqvist, A.M.
submitted to the EMBL Data Library,
A; Reference number: 834559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: major component of wild-type curli; interaction between CsgA and A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia cc and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;21-151/Product: curlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-133,'RQRDSGWLW' <OLS3>
A;Cross-references: EMBL:L04979; NID:g290424;
A;Experimental source: strain K-12, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: The RpoS sigma factor relieves H-NS-mediated transcriptional repression A;Reference number: S31202; MUID:93211294; PMID:8459772
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Best Local Similarity
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                                                                        ; Score 506.5; DB 2; 
; Pred. No. 7.7e-36; 
21; Mismatches 28;
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Pred. No. 1.2e-37;
0; Mismatches 27
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QSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG

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hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain EDL9: C;Species: Escherichia coli (c;Species: Escherichia coli (c;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: H85665 (c;Accession: H856
                                                                                                             A;Residues: 1-145 <KUR>
A;Crose-references: GB:AE008689; PIDN:AAL45562.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu4768
A;Map position: linear chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Authors: Yoo, H.; ster, E.W.
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A; Cross-references: GB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y.; Biddle, P.; Jung, M.; Krespan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.4%;
                         13.6%;
                                                                                                                                                                                                                                                                                                                                                                                            Natural Genetic Engineer Agrobacterium tumefaciens C58 MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
Score 105.5; DB Pred. No. 0.049; 7; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 506.5; DB 2
Pred. No. 7.7e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151
                                                                                                                                                                                                                                        PID:g17743277;
   61;
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                                                        Length
      Indels
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T.; Levy, R.; Li, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152;
                                                              145;
                                                                                                                                                                                                                                           GSPDB:GN00187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSPDB:GN00145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119
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F3F19.21 protein - Arabidopsis thaliana
G;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
C;Accession: C86266
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conm, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Hultzar, L.
Nature 408, 816-820, 2000
A,Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Waiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A,Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A,Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A,Feference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C86266
A,Status: preliminary
A,Molecule type: DNA
A;Genetics: GB:AE005172; NID:94850402; PIDN:AAD31072.1; GSPDB:GN00141
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein AGR L_228 [imported] - Agrobact; Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 C;Accession: H98144
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A; Residues: 1-145 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 ALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 IVGHQ----YGR-----HNLSAVGQEGHDNYGSTTQNGNRNVAGI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVGHQ----
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A97359; MUID:21608551; PMID:11743194
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C.; Allinger,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S.; Miller, N.; Blanchard, M.; Qurollo, M.; Doughty, D.; Scott, C.; Lappas, C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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Markelz,
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rkelz, B.
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$70787

curlin nucleator protein csgB precursor - Escherichia coli (strain K-12)
curlin nucleator protein csgB protein; curlin nucleation component; minor curl
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 01-Mar-2
C;Accession: $70787; F64846
C;Accession: $70787; F64846
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C;Accession: $70787; F64846
C;Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X90754; NID:gl147558; PIDN:CAA62281.1; PID:gl147563 A;Experimental source: strain K12, substrain W3110 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Augu. R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; R.A.; Rose, D.J.; Mau, B.; Shao, Y.
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A;Title: Expression of two csg operons is required for production of A;Reference number: S70783; MUID:96414468; PMID:8817489

A;Accession: S70787
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A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F64846
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;Residues: 1-151 <BLAT>
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                                                                                                                                                                                                                                                                                                                               SSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGF
                                                                                                                        SNRAKIDQTGDYNL-AYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                               AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
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V.; Riley, M.;
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A; Residues: 1-151 <STO>
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A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                iller, L.; Grotbeck, E.J.
Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                R;Perna, N.T.; Plunkett III, G.; Burland, V.; iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, J
                                                                                                                                                                                                                                                                                                                                                                                                                        curlin minor chain precursor, C; Species: Escherichia coli
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gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                         A; Status: preliminary
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                                                                                                                                                                                                                                                                                              A; Reference number: A85480;
                                                                                                                                                                                                                                                                                                               A; Title: Genome sequence
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A;Accession: C90806
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                                                                                        Similarity
 AAGYDLANSEYNF---
                                  SSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGF
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80; MUID:21074935; PMI
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hypothetical glycine-rich protein [imported] - Sinorhizobium mel C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change C;Accession: E95965 C;Accession: E95965 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001 A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid

pSymB megaplasmid from the

N2-fixing

P.; Vorholter, 30-Sep-2001

Herna endo

Sinorhizobium meliloti (strain

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RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY SNRAKIDQTGDYNL-AYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY

129 151

E95965 RESULT

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RESULT 13
S11672
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Mol. Gen. Genet. 223, 163-166, 1990
A; Title: Conserved repetition in the ice nucleation gene inaX A; Reference number: S11672; MUID:91080859; PMID:2259339
A; Accession: S11672
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A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; L hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Reference number: A96039; MUID:21368234; PMID:11474104
RESULT
S07053
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A;Accession: E95965
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-1567 <ZHA>
A;Cross-references: EMBL:X52970; NID:g48531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Statue: preliminary
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A;Cross-references: GB:AL591985; PIDN:CAC49389.1; PID:g15140875; GSPDB:GN00167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ce nucleation protein - Xanthomonas campestris
;Species: Xanthomonas campestris
;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                                                                  ;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: DNA
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIVVSGSALAGVVPQ--WGGGGNHNGGGNSSGPDSTLSIYQYGS-----ANAA----
                                                                                STQTARKGSDITAG-YGSTGTAGSDSALIAGYGSTQTAGSESSLT--AGYGSTQTARK 374
                                                                                                                      -DOWNAKUSDITVGQYG-----GUNAALV-----NOTASDSSVMVRQVGFGUNATANQ 150
                                                                                                                                                                  STLTAGYGSTQTAQEGSRLTSGYGSTATSGSDSAVI ----SGYGSTQTAGSESSLTAGYG
                                                                                                                                                                                                                                                VYGSTLTGADQSRLVAGYGSTETAGDHSDLIAGYGSTGTAGSDSSI-LAGYGSTQTAAGR 263
                                                                                                                                                                                                                                                                                         VSGSALAG-----VVPQWGG----GGNHN------GGGNSSGPDSTLSIYQYGSANAALAL
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                                                                                                                                                                                                                                                                                                                                  27;
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Pred. No. 8.9;
27; Mismatches
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A;Molecule type: DNA R;Bouvier, C.; Vogel, H.; Reichelt, R.; Etges, R. R;Bouvier, J.; Bordier, C.; Vogel, H.; Reichelt, R.; Etges, R. Mol. Biochem. Parasitol. 37, 235-246, 1989
A;Title: Characterization of the promastigote surface protease A;Reference number: A60648; MUID:90114330; PMID:2608099
A;Accession: A60648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-602 <BUT>
A;Cross-references: GS:Y00647; NID:g9554; PIDN:CAA68673.1;
A;Note: this is a revision to the sequence from reference A
R;Button, L.L.; McMaster, W.R.
J. Exp. Med. 167, 724-729, 1988
A;Title: Molecular cloning of the major surface antigen of
A;Reference number: A27598; MUID:88154764; PMID:3346625
A;Accession: A27598
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C;Date: 16-Sep-1992 #sequence_revision
C;Accession: PL0221; A27598; A60648
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A;Status: not compared with conceptual translation A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-1322 <ABE>
A;Cross-references: GB:X17316; NID:g296095; PIDN:CAA35194.1; C;Superfamily: ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ice nucleation protein inaA - Erwinia ananas C;Species: Erwinia ananas C;Species: Erwinia ananas C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change C;Accession: S07053 R;Abe, K.; Watabe, S.; Emori, Y.; Watanabe, M.; Arai, S. FEBS Lett. 258, 297-300, 1989
                                                                                 C;Complex: homodimer
C;Function:
                                                                                                                                submitted to the Brookhaven Protein Data Bank, A;Reference number: A68135; PDB:LLML A;Contente: annotation; X-ray crystallography, A;Note: strain LRC-L119
                                                                                                                                                                                                                                          A;Experimental source: strain LEM513 R;Schlagenhauf, E.; Etges, R.; Metcalf, P.
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A; Note: the activated C; Superfamily: leishma
                      A; Description: catalyzes the hydrolysis of peptide bonds between two hydrophobic residue \tilde{A}_i; Note: the activated form can activate the proenzyme form
                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 101, 'E', 103-118, 'SV', 121-123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leishmanolysin (EC 3.4.24.36) precursor [validated] - Leishmania major
N;Alternate names: promastigote surface proteinase; surface endopeptidase glycoprotein
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     leishmanolysin
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                                                                                                                                                            X-ray crystallography, 1.86 angstroms,
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A27598
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Maximum Match 100%
Listing first 45 summaries
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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MEDLINE-91310586; PubMed-1677357;
Collinson S.K., Emcedy L., Mueller K.-M., Training and characterization of thin,
salmonella enteritidis.";
J. Bacteriol. 173:4773-4781(1991).
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P28307;
01-DEC-1992
01-OCT-1996
28-FEB-2003
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                                    Salmonella enteritidis.";
J. Bacteriol. 173:4773-4781(1991).
-!- FUNCTION: CURLIN IS THE STRUCT
                                                                                                                                                                                                                                            Yano M., Horiucni T.; "A 718-kb DNA sequence of the Escherichia corresponding to the 12.7-28.0 min region DNA Res. 3:137-155(1996).
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STRAIN-K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhaw
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                                                                         SEQUENCE OF 21-31.
MEDLINE=91310586; PubMed=1677357;
Collinson S.K. Emoedy L., Trust T.J.,
"Purification and characterization of t
                                                                                                                                            Arnqvist A., Olsen A., Pfeifer J., "The Crl protein activates cryptic fibronectin binding in Escherichia Mol. Microbiol. 6:2443-2452(1992).
                                                                                                                                                                                                                                       DNA
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"The RpoS sigma factor relieves repression of csgA, the subunit Escherichia coli.";
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MEDLINE=96414468; PubMed=8817489;
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STRAIN=K12 / M
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MEDLINE=93023873; PubMed=1357528;
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         FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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28-FEB-2003
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28-FEB-2003
      SEQUENCE FROM N.A.

STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."
                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Major curlin subunit precursor.
CSGA OR Z1676 OR ECS1420.
Escherichia coli O157:H7.
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STRAIN=0157:H7 / ATCC 43895;
STRAIN=0157:H7 / ATCC 43895;
MEDLINE=21218556; PubMed=11319125;
Uhlich G.A., Keen J.E., Elder R.O.;
"Mutations in the csgD promoter associated with variations expression in certain strains of Escherichia coli 0157:H7."
Appl. Environ. Microbiol. 67:2367-2370(2001).
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EMBL; X90754; CAA62282.1; -.
EMBL; AE000205; AAC74126.1; -
EMBL; D90741; BAA35832.1; -.
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NCBI_TaxID=83334;
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28-FEB-2003 (Rel. 41, Last annotation updi
Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
Escherichia coli, and
Escherichia coli 0157:H7.
Bacteria, Proteobacteria; Gammaproteobacteria; Escherichia.
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino K., Ohnishi M., Murata T., Tanaka M., Tobe T Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Complete genome sequence of enterohemorrhagic Escherichia coli o157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
-IPONCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI OT TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
SEQUENCE FROM N.A.
STRAIN-KI2 / MC4100;
MEDLINE-96414468; PubMed-8817489;
Hammar M., Arngvist A., Bian Z., Olsen A.,
"Expression of two csg operons is required fibronectin- and congo red-binding curli po
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EMBL; AE005315; AAG55788.1; -.
EMBL; AP002554; BAB34843.1; -.
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                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                     Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoy: Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe I Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunac Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Oshima T., Aiba H., Baba T., Fujita K., Kanai K., Kashimoto K.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Mishimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., May
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Roman B., Shao Y.;
MBU B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    corresponding to the 12.7 DNA Res. 3:137-155(1996).
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Yano M., Horiuchi T.;
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MEDLINE=21156231; PubMed=11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Perna N.T., Plunkett G. III, Burla
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STRAIN=0157:H7
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Mol. Microbiol.
                                                                                                                                            SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY
                                                                                                                                                              CURLIN MONOMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
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on the linkage map.";
                                      . Usage by http://www.
                                                                  its content
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                                                                                  restrictions
                                        isb-sib.
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M., Tobe T.,
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CAA62281.1;

InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 81.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION;

Ice_nucleatn.
ucleation; 81.

57.

EMBL; X52970; HSSP; P06620;

lina. CAA37140.1; or send an email to license@isb-sib.ch).

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Best Local S
Matches 32
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PIR; G85665; G85665. PIR; G85665, G85665. PIR; S70787; S70787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P18127;
01-NOV-1990
01-NOV-1990
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                  CTYSTALLIZATION IN SUPERCOOLED WATER.

1. SUBCELLULAR LOCATION: Outer membrane (By similarity).

1. DOMAIN: CONVENINS 153 IMPERFECT REPRAITS OF THE CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.

1. MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT C.

2. SIMILARITY: Belongs to the bacterial ice nucleation protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Conserved repetition in the ice nu
Xanthomonas campestris pv. transluc
Mol. Gen. Genet. 223:163-166(1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=90092494; PubMed=2599095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PANAN
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                                                                                                                                                 Ice nucleation; Repeat; Outer membrane.

DOMAIN 162 1281 OCTAPEPTIDE PERIODICITY
SEQUENCE 1322 AA; 131094 MW; 89B0EE24AA837039 CR
                                                                                                                                                                                                                                                                                                                                 EMBL; X17316; CAA35194.1; -. PIR; S07053; S07053. HSSP; P06620; 1INA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Abe K., Watabe S., Emori Y., Watanabe M., Arai S.; "An ice nucleation active gene of Erwinia ananas. Se to those of Pseudomonas species and regions required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1991
                                                                                                                                                                                                                                                     InterPro; IPR000258; Ice nucleatn Pfam; PF00818; Ice nucleation; 69 PRINTS; PR00327; ICENUCLEATN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleation activity.";
FEBS Lett. 258:297-300(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pantoea ananas (Erwinia uredovora).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTYSTAILIZATION IN SUPERCOOLED WATER.
SUBCELLULAR LOCATION: OUTER membrane (By similarity).
DOMAIN: CONTAINS MANY IMPERFECT REPEATS OF THE CONSENSUS
OCTAPEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleation
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                                                                               Similarity
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     GGGNSSGPDSTLSI YQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTI ELT
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(Rel. 17, Last sequence update)
(Rel. 40, Last annotation updat
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                                                                                                                                                                                                           MEDLINE=98416698; PubMed=9739094;
Schlagenhauf E., Etges R., Metcalf P.;
"The crystal structure of the Leishmania major surface proteinase
                                                                                                                                                                                                                                                                                                                      Schlagenhauf E., Etges R., Metcalf P., "Crystallization and preliminary X-ray
                                                                                                                                                                                                                                                                                                                                                                                                                Schneider P., Ferguson M.A.J., McConville M.J., Homans S.W., Bordier C.; "Structure of the glycosyl-phosphatidylinositol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell
(Major surface glycoprotein) (GP63 protein) (F
                                                                                                                                                                                       Structure
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Eukaryota; Euglenozoa;
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J. Biol. Chem. 265:16955-16964(1990).
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                                                                                                                                                                                                  eishmanolysin.";
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                                                 FUNCTION: Has an integral role during the infection of macrophag in the mammalian host.

CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 and p1 and basic residues at P2 and P3'. A model nonapeptide is p1 and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyr-1-Leu-Lys-Lys-

COEACTOR: Binds 1 zinc ion per subunit.

COEACTOR: Binds 1 zinc ion per subunit

SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. PM: THE PHOSPHATIDYLINOSITOL MOIETY OF THE GPI-ANCHOR CONTAINS FULLY SATURATED UNBRANCHED 1-O-ALKYL CHAIN (MAINLY C24:0) AND A MIXTURE OF FULLY SATURATED UNBRANCHED 2-O-ACYL CHAINS (C12:0)
                        SIMILARITY: Belongs to peptidase family
                                        MIXTURE OF FU
C14:0, C16:0,
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167:724-729(1988).
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171:589-589(1990)
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PIR; PL0221; PL0221.

PDB; 1LML; 17-SEP-97.

MEROPS; MO8.001; -.

InterPro; IPR006025; Pept M Zn BS.

InterPro; IPR001577; Peptidase M8.

PRANTS; PR01457; Peptidase M8.

PRANTS; PR00782; LSHMANOLYSIN.
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Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc;
Zymogen; Signal; Cell adhesion; GPI-anchor; 3D-structure; Lipoprotein.
SIGNAL 1 39 POTENTIAL.
PROPEP 40 100 ACTIVATION PEPTIDE.
CHAIN 101 577 LEISHMANDLYSIN
PROPEP 578 602 REMOVED IN MATURE FORM.
METAL 264 264 ZINC (CATALYTIC).
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(Rel. 41, Created)
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain , Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                            CHAIN
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MEDLINE=2253136-7. pbMed=12644504;
MEDLINE=2253136-7. plunkeet G. III, Mayhew G.F.,
Deng W., Liou S.-R., Plunkeet G. III, Mayhew G.F.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner
"Comparative genomics of Salmonella enterica serova
                                                                                                                                                                                                                                                                                             SEQUENCE
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SEQUENCE FROM N.A.
SPECIES=S.typhimurium; STRAIN=SR-
SPECIES=98117058; PubMed=9457880;
MEDLINE=98117058; PubMed=9817880;
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EMBL; AE008749; AAL20073.1; -.
EMBL; U43280; AAC43598.1; -.
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Collinson S.K., Clouthier S.C., Doran
"Salmonella enteritidis agfBAC operon
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Mol. Blochem. Parasitol. 48:173-184(1991).
                                                              CARBOHYD
                                                                                                                                                                      METAL
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-!- SIMILARITY: Belongs to peptidase family M8.
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Eukaryota; Euglenozoa;
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                                                                                                                                                                                                                                                                  Hydrolase;
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                                                                                                                                                                                                                                                                                                                             MEROPS; M08.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Webb J.R., Button
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endopeptidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Biochem. Parasitol. 48:173-184(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92107220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leishmanolysin
(Major surface
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 Local Similarity
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                                                                                                                                                                                           SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COFACTOR: Binds 1 zinc ion per subunit (By similar SUBCELLULAR LOCATION: Attached to the membrane by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in the mammalian host. CATALYTIC ACTIVITY: Pr
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ignal; Cell adhesi
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Rel. 20, Last se
Rel. 42, Last an
n precursor (EC:
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                                                  PubMed=1762629;
L.L., McMaster R.W.;
                                62950 MW;
                                                                                                                                                                                                                                                                                                                                                                                license agreement
11.4%;
89.5%;
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Last seq
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t annotation update)
(EC 3.4.24.36) (Cell (in) (GP63 protein) (P)
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Score
Pred.
                                        GPI-anchor amidated similarity)
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(Promastigote surfa
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ХВ)
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                                                (POTENTIAL)
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                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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01-APR-1990
                                                                                 PRINTS; PR00782; LSDUING PROTEASE; 1.

PROSITE; PS00142; ZINC_PROTEASE; 1.

Hydrolase, Metalloprotease; Glycoprotein; Me
Hydrolase, Metalloprotease; GPI-anchor;
                                                                                                                                                                                                                EMBL; M80672; AAA29238.1; -. EMBL; M28527; AAA29235.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed during development of Leishmania promastigotes to an infectious form."; J. Biol. Chem. 267:1888-1895(1992).
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InterPro; IPR001577; Peptidase_M8.
Pfam; PF01457; Peptidase_M8; 1.
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MEDLINE=92112918; PubMed=1370484;
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Eukaryota; Euglenozoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wilson M.E.
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10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surfa
                                                                                                                                                                                                                                                                                                                                                               COFACTOR: Binds 1 zinc ion per subunit (By simi SUBCELLULAR LOCATION: Attached to the membrane
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donovani chagasi
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embrane by a GPI-anchor.
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RESULT 12
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Matches 17
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STRAIN=MNYC/BZ/62/M379;

MEDLINE=93149206; PubMed=8426614;

Medina-Acosta E., Karess R.E., Russell D.G.

"Structurally distinct genes for the surfi
"Structurally distinct genes for the surfi
mexicana are developmentally regulated.";

Mol. Biochem. Parasitol. 57:31-46(1993).

-!- FUNCTION: Has an integral role during
in the mammalian host.
EMBL; X64394; CAA45733.1; -.
PIR; S19916; S19916.
HSSP; P08148; ILML.
MEROPS; MO8.001; -.
GlycoSuiteDB; P43150; -.
GlycoSuiteDB; P43150; -.
InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001577; Peptidase M8.
Pfam; PF01457; Peptidase M8; 1.
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01-NOV-1995 (Rel. 32, Last septence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin C1 precursor (EC 3.4.24.36) (Cell surface I (Major surface glycoprotein) (GP63 protein) (Promastigote
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Eukaryota; Euglenozoa;
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SIMILARITY: Belongs to
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Matches
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28-FEB-2003
28-FEB-2003
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Zymogen; S
           This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are use by non-profit institutions as long as its condified and this statement is not removed. Usage entities requires a license agreement (See http://worsend an email to license@isb-sib.ch).
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STRAIN=969A45;
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PROSTIE; PS00142; ZINC PROTEASE;
Hydrolase; Metalloprotease; Glyco
Zymogen; Signal; Cell adhesion; I
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1764;
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SIMILARITY: Belongs to the
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no protein 3 precursor (
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ZINC (CATALYTIC) (BY BY SIMILARITY ENGLARITY E
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m DNA sequences
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STRAIN-06:H1 / CFT073 / ATCC 700928;

STRAIN-06:H1 / CFT073 / PubMed=12471157;

K MEDLINE=22388234; PubMed=12471157;

A Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P. Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Str. A Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., A Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome serof uropathogenic Escherichia coli.";

T of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

C -!- FUNCTION: Fimbriae (also called pili), polar filaments rad from the surface of the bacterium to a length of 0.5-1.5
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Best Local
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21-JUL-1986 (Rel. 01, Created,
21-JUL-1986 (Rel. 01, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
F7-2 fimbrial protein precursor (F7-2 pilin).
F7-2 OR PAPA OR C3592.
                                                                                                                                                                                             "DNA sequences of three coli strains: evidence c
                                                                                                                                                                                                                       Denich K., Bly O'Hanley P.D.;
                                                                                                                                                      SEQUENCE FROM N
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                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        van Die I., Bergmans H.;
"Nucleotide sequence of the gene encoding the
"nucleotide sequence of the gene encoding;
                                                                                                                                                                                                                                                                                                   a uropathogenic
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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NCBI_TaxID=562, 217992;
                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
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InterPro; IPR006059; SBP bac 1.
Pfam; PF01547; SBP bac 1; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                  Infect.
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HSSP; P06128; 1A54.
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                                                                                                                                                                            s of three papA genes from uropathogenic Escherichia evidence of structural and serological conservation . 59:3849-3858(1991).
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Pred. No. 2;
1; Mismatches
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PHOSPHATE BINDING PROTEIN 3.

PHOSPHATE SINDING PROTEIN 3.

N-palmitoyl cysteine (Fotent S-diacylglycerol cysteine (Fotent S-diacylglycerol cysteine)

CBOEAOAC10F463BC CRC64;
                                                                                                                                                                                                                                Braaten B.A., Hardy J., Low
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na N.T.,
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Q47879;
01-NOV-1997
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DISULFID
SEQUENCE
                                                                                                                                                  MEDLINE=94264407; PubMed=7764866; Michigami Y., Watabe S., Abe K., Obata H., Arai S.; "Cloning and sequencing of an ice nucleation active
             <u>:</u>
                                                                          Biosci.
                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Ga
Enterobacteriaceae; Pantoea.
                                                                                                                                                                                                                                                                                                           01-NOV-1997
16-OCT-2001
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                                                                                                                                         uredovora.";
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                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                               NCBI_TaxID=553;
                                                                                                                                                                                                                                                                     Pantoea ananas (Erwinia uredovora).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M12861; AAA23778.1; -.
EMBL; M68060; AAA24278.1; -.
EMBL; AE016766; AAN82040.1; F
EMBL; A03496; YQECF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         micrometers and numbering 100-300 per cell, enable bacteria to colonize the epithelium of specific host organs.
-i- SIMILARITY: BELONGS TO THE FIMA/PAPA FAMILY OF FIMERIA PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
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PERIODICITY IS SUPERIMPOSED.

MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED SIMILARITY: Belongs to the bacterial income.
                                                           sci. Biotechnol. Biochem. 58:762-764 (1994)
FUNCTION: Ice nucleation proteins enable
crystallization in supercooled water.
SUBCELLULAR LOCATION: Outer membrane.
DOMAIN: CONTAINS IMPERFECT REPEATS OF A C
A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE
                                                                                                                                                                                                                                                                                               nucleation protein
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Last annotation updat
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             bacterial ice nucleation
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Pfam; PF00818; Ice_nucleation; 51.

PRINTS; PR00327; ICENUCLEATUN.

PROSITE; PS00314; ICE_NUCLEATION; 34.

Ice_nucleation; Repeat; Outer_membrane.

DOMAIN 162 993 OCTAPEPTIDE PERIODICITY.

SEQUENCE 1034 AA; 103378 MW; FA222523D333EADD CRC64;
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                                                                               105 -QWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                      220 EESSQMAGYGSTQTGMKGSDLTAGYGSTGTAGDDSSL-IAGYGSTQTAGEDSSLTAGYGS
                                                                                                                                                                                                                                                            161 IATYGSTLSGTHQSQLIAGYGSTETAGDSSTLIAGYGSTGTAGSDSTL-VAGYGSTQTAG 219
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Q54069 salmonella
Q983j4 sescherichia
Q983j4 bradyrhizob
Q8elh3 shewanella
Q8elh3 shewanella
Q8elh4 shewanella
Q8esh4 shewanella
Q8esh5 garobacteri
Q89ji6 bradyrhizob
Q99saf2 arabidopsis
Q89ji5 bradyrhizob
Q7v885 prochloroco
Q88hg0 pseudomonas
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07x243 citrobacter
07x240 citrobacter
08cw63 escherichia
07x237 enterobacte
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45	44	43	42	41	40	39	38	37	36	35	34	3	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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Q8t986 drosophila	Q9ziy5 borrelia bu		Q8xsd6 ralstonia s	Q8y106 ralstonia s		Q8k6b1 streptococc	Q7u5x6 synechococc	Q8mny9 leishmania	Q25274 leishmania		7	Q89c73 bradyrhizob			Q7ulc5 mycobacteri	w	\vdash		Q9s3j8 escherichia	••		\vdash	Q82m56 streptomyce	Q8efu3 shewanella	-	Q83ru7 shigella fl		Q7uczl shigella fl

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61 SDARKYDQLYTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120	1 MKILKVAAFAAIVVSGSALAGVVÞQWGGGGNHNGGGNSSGÞÐSTLSIYQYGSANAALALQ 60 	Query Match 87.9%; Score 680; DB 2; Length 152; Best Local Similarity 89.4%; Pred. No. 2.3e-48; Matches 135; Conservative 4; Mismatches 12; Indels 0; Gaps 0;	NON TER 152 152 SEQÜENCE 152 AA; 15401 MW; 9DA7DADC2364B006 CRC64;	Immun. 65:5 J000514; CAJ	cells.";	"Expression of thin, aggregative fimbriae promotes interaction of Salmonella typhimurium SR-11 with mouse small intestinal epithelial	Normark S.J., Rhen M.;	Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z., Pfeifer J.D.,	SEQUENCE FROM N.A.	臣"	Enteropacteriaceae; Saimonelia. NCBI TaxID=602;	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	Salmonella typhimurium.		AgfA protein (Fragment).	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	05,	01-JAN-1998 (TrEMBLrel. 05, Created)		3800	

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RESULT 3
Q7X240
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EMBL, AJ518701; CAD56675.1; -...
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                                                                                                                                                                                                                                                                               NCBI_TaxID=546;
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Bacteria; Proteobacteria; Gammap
Enterobacteriaceae; Citrobacter.
NCBI_TaxID=213763;
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Best Local (
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Q7X237;
01-OCT-2003
STRAIN=Fec39
Zogaj X., Bol
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                              SEQUENCE FROM
                                                                                                                                                 01-OCT-2003
01-OCT-2003
                                                       NCBI_TaxID=28141;
                                                                          Enterobacteriaceae;
                                                                                      Bacteria;
                                                                                                       Enterobacter sakazakii.
                                                                                                                                   Curlin-csgA
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MEDLINE=22388234; PubMed=12471157;
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Q9S3J5;
Q1-MAY-2000
Q1-MAY-2000
Q1-MAR-2001
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"Virulence of Salmonella enteritidis in chickens correlates
colony morphology and expression of SEF17 fimbriae.";
Submitted (AFR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; US3207; AAA98671.1; -.
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EMBL; AJ515702; CAD56678.1; -
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7704 MW;
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15112 MW; SD8BB2D872DF15F3 CRC64;
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Salmonella.
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                                                                                                    (Fragment)
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                           Gammaproteobacteria;
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3; Mismatches
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7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                 "Complete genomic sequence of nitrogen-fixing Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
                                                                                                                                                                                                                                                                                                                                                                                               Sasamoto S., Watanabe Kohara M., Matsumoto Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
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MEDILINE=99314153; PubMed=10386375;
La Ragione R.M., Collighan R.J., Woodward M.J.;
La Ragione R.M., Collighan R.J., Woodward M.J.;
"Non-curliation of Escherichia coli O78:R80 isolates associated
"Non-curliation in csg8 and reduced persistence in poultry infect
IS1 inserti on in csg8 and reduced persistence in poultry infect
FEMS Microbiol. Lett. 175:247-253(1999).
ERBL, AJ131756; CAB45380.1; -.
                                                                                                                                                                                                                                                                                                         SEQUENCE 130 AA;
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bll5299 protein.
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41; Conservative
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Matanabe A., Shimpo
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89.7%;
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Pred. No. 0.04
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Pred. No. 0.00
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PRT;
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                                                                                                                                                      Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vanathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis."
      SEQUENCE
                                        Hypothetical
                                                                                                                               Nat. Biotechnol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22297686; PubMed=12368813;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shewanella oneidensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heidelberg J.F., Paulse
Read T.D., Eisen J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alteromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conserved hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8EIH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8EIH4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nat. Biotechnol. 20:1118-1123(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22297686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-MR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alteromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                             AE015532; AAN53941.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           curlin
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139 AA;
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   al protein;
502 AA; 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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AA;
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   n; Complete proteome.
52441 MW; D08CA23D6C46B62D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gammaproteobacteria;
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Pred. No. 0.13
18; Mismatches
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      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
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Matches 36
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Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                                 Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., WcChen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C. Kutyavin T., Levy R., Li M.-J., McClelland B., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Go Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Per. Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Doll Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002
01-JUN-2002
01-JUN-2003
                                                                                                      Hypothetical SEQUENCE 14
                                                                                                                               PIR;
                                                                                                                                          EMBL; AE009405; AAL45562.1; -.
EMBL; AE008209; AAK88682.1; -.
PIR; AD3143; AD3143.
                                                                                                                                                                                 Cielo C., Slater S., "Genome sequence of the plant Agrobacterium tumefaciens C58. Science 294:2323-2328(2001).
                                                                                                                                                                                                                                  Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Hapler C., Mullir Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=21608551; PubMed=11743194;
                                                                                                                                                                                                                                                                                                                                                                       "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein Atu4768. ATU4768 OR AGR_L_228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBU6N9;
                                                                                                                                                                                                                                                                                                                                             Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobiaceae; Rhiz
NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                               H98144; H98144
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                                                                Similarity
                                                                                                                                                                                                                                                                                                                                            294:2317-2323(2001).
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 MIRKSFIASALVALVGLSAAAPAMANDVRIEQYGWSNSAGGAQEGYGNRIRTYQNGGYNR
                        LLKVAAFAAIVVSGSALAGVVPQWGG------GGNHNGGGNSSGPDSTLSIYQYGSANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
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                                                                                                     l protein; Complete
145 AA; 14984 MW;
                                                                                                                                                                                                                                                                                                                                                                    of the natural genetic engineer
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                                                               13.6%;
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                                                 Score 105.5;
Pred. No. 0.32
27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last annotation
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Pred. No. 1.:
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                                                                                                                                                                                                           and biotechnology agent
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Best Local S
Matches 39
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Q9SAF2;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
73F19.21 protein (Hypothetical protein).
73F19.21 OR AT1G13190, F3F19.21 OR AT1G13190.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
   SEQUENCE FROM N.A.
STRAIN=cv. Columbia
Vysotskaia V.S., So
Liu S., Li J., Kren
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Q89J16;
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MEDLINE-22484998; PubMed-12597275;
MEDLINE-22484998; PubMed-12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Wada T., Yamada
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Bacteria; Proteobacteria;
Bradyrhizobiaceae; Bradyrh
NCBI_TaxID=375;
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Columbia;
V.S., Schwartz J.I
J., Kremenetskaia
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Bradyrhizobium.
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                                     J.R.,
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      N.A.
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AC007357; AAD31072.1; -. EMBL; AV062527; AAL32605.1; -. EMBL; BT002575; AAA000935.1; -. EMBL; BT002575; AAA000935.1; -. EMBL; C86266; C86266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Scker J., Theologis A., Davis R.W.,
                        Bradyrhizobium japonicum.
Bacteria; Proteobacteria;
Bradyrhizobiaceae; Bradyrh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0003676; F:nucleic acid binding; InterPro; IPR000504; RNA_rec_mot. Pfam; PF00076; rrm; 1. SMART; SM00360; RRM; 1. PROSITE; PS50102; RRM; 1. HYDOThatial Profile.
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Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn I
Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.,
"Arabidopsis thaliana chromosome, 1 BAC F3F19 sequence.";
                                                                                                          Bl15298 protein
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STRAIN=cv. Columbia;
NCBI_TaxID=375;
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573 AA; 6:
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                        cteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobium.
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Last annotation updat
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RESULT 15
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MEDLINB=22404998; PubMed=12597275;
MEDLINB=22404998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Kasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hemolysin-type calcium-binding region:RTX N-terminal domain.
                                                                                                                                                                                                                                            Complete
SEQUENCE
                                                                                                                                                                                                                                                                      MEDLINE-2282569; PubMed=12917642;
MEDLINE-2282569; PubMed=12917642;
Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb E.A., Zinser E.R., Chisholm S.W.;
"Genome divergence in two Prochlorococcus ecotypes reflects oceanic
niche differentiation.";
Nature 424:1042-1047(2003).
EMBL; BX572095; CAB20431.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prochlorococcus marinus (strain MIT 9313).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
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                                                                           52 SANAALAL--QSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATID-QWNA 108
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25; Conserv
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 SNSSINLG--SGNDSLLINASAN
                                                           KVAAFAA------IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYG 51
                            KNSDITVGOYGGNNAALVNOTAS 131
                                                                                                                                                                                                                                              1765 AA;
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                                                                                                                                                                                 12.6%; So ilarity 28.7%; Pi Conservative 21;
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Pred. No. 31;
21; Mismatches
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Search completed: March 11, Job time: 39.5 secs

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Database
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

. 22	A 6	2 2	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	_σ	4	ω	2	1	Result No.
113	115	115	115	132	146	371	443	497	497	516	521	567	600	601	602	604	609	619	657	677	682	682	712	776	Score
. d		•	4.	17.0	18.8	•	57.1	٠	64.0	66.5	•	73.1	77.3	77.4	77.6	•	78.5	•	84.7	•	•	87.9	•	8	Query
4) N	2 2	22	22	45	122	142	120	120	151	151	151	151	151	151	151	151	151	151	151	151	151	151	151	Length
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**************************************	AABSOSSO	AAB36339	AAB36325	AAB36318	AAB36316	AAR52663	AAR52664	AAW23569	AAR62761	ABR82651	AAB36343	AAB36348	AAB36349	AAB36353	AAB36347	AAB36346	AAB36352	AAB36350	AAB36355	AAW23570	AAB36341	AAR74625	AAB36354	В	ID
ADISZONN B. COII C	Salmoner	_	u	_		Aar52663 FNB curli	Aar52664 Fibronect	_	Aar62761 AgfA sequ	Abr82651 E. coli C	Aab36343 Escherich	Aab36348 AgfA::PT3	Aab36349 AgfA::PT3	Aab36353 AgfA::PT3	Aab36347 AgfA::PT3		Aab36352 AgfA::PT3	Aab36350 AgfA::PT3	Aab36355 AgfA::PT3	Aaw23570 Salmonell	Aab36341 Salmonell	Aar74625 AgfA sequ	Aab36354 AgfA::PT3	1 AgfA::P	Description

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombination of the homologous species; (3) directing recombination of a recombination of a recombination of the homologous species, replacing the native

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 137; 139pp; English.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
91	91	92.5	92.5	94.5	95	95.5	96	96	96	96	97.5	98	102	109	109	109	111	111	111
11.7	11.7	11.9	11.9	12.2	12.2	12.3	12.4	12.4	12.4	12.4	12.6	12.6	13.1	14.0	14.0	14.0	14.3	14.3	14.3
1751	1397	251	151	738	597	252	2309	19	19	19	520	26	26	23	23	23	22	22	22
ഗ	7	v	w	N	4	æ	4	w	ω	w	0	7	7	w	ω	w	w	ω	w
ABG91039	ADD42761	ABP45119	AAB36344	AAW56163	AAU08231	ADE83865	ABB66232	AAB36328	AAB36336	AAB36323	AA016497	ABR82645	ABR82649	AAB36319	AAB36324	AAB36340	AAB36337	AAB36327	AAB36322
Abg91039	Add42761	Abp45119	Aab36344	Aaw56163	Aau08231	Ade83865	Abb66232	Aab36328	Aab36336	Aab36323	Aao16497	Abr82645	Abr82649	Aab36319	Aab36324	Aab36340	Aab36337	Aab36327	Aab36322
Chlamydia	Chlamydia	Human BLy	Escherich	New DNA 8	Polypepti	Chemokine	Drosophil	Salmonell	Salmonell	Salmonell	Argiope t	E. coli c	E. coli V	Salmonell	Salmonell	Salmonell	Salmonell	Salmonell	Salmonell

ALIGNMENTS

RESULT 1

AAB36351 WPI; 2000-672631/65. N-PSDB; AAC64627. Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; White 05-APR-1999; 05-APR-2000; 2000WO-CA000356 12-OCT-2000. WO200060102-A2 Synthetic. Escherichia coli. Salmonella enteritidis. vaccine; immune response; immunogen. 26-FEB-2001 AAB36351; AAB36351 standard; AgfA::PT3#6 amino acid sequence SEQ ID NO:22 (UYVI-) UNIV VICTORIA. Doran JL, (first entry) 99US-0127888P protein; 151 Collison SK, ₿ Kay WW;

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RESULT 2
AAB36354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 151;
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Best Local :
Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Escherichia coli.
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Pred. No. 9.5e-68;
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Disclosure;

Page 138; 139pp; English

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RESULT 3
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CC directing recombination of a recombination of a recombination of the chromosome of the chomologous species; (3) directing recombination of a recombinant gene into the chromosome of the chomologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant Agfa (2) comprising separating an amino acid polymer comprising a recombinant Agfa (3) crotein containing a replacement segment or segments of foreign amino card sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the golymer into the animal in conjunction with a carrier or diluent. (1) is cuseful for the expression of recombinant Agfa protein which is useful for cellciting an immune response in an animal. In a fimbrial presentation consistency and adhesion properties relevant for an efficient live carcine, the carrier fimbrial subunit proteins are usually strong communogens, which may be important for directing an immune response consists the inserted epitope, and hybrid fimbriae are usually strong consists the inserted epitope, and hybrid fimbriae are easy and consists the inserted epitope, and hybrid fimbriae are sequence is given in the present threation of the present threation.
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Best Local !
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26-JUN-1995
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                                                                    26-APR-1993;
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                                                                                                                                                                                 WO9425598-A2
                                                                                                                                                                                                                    Salmonella.
                                                                                                                                                                                                                                                                                            AgfA sequence.
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               (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP
                                                                                                                                            10-NOV-1994.
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(first entry)
                                                                    93US-00054452
                                                                                                         94WO-IB000207
                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 151 AA
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Pred. No. 1.7e-61;
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RRESULT 4
AAB3631
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:
                                                                                                                                                                 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                 WPI; 2000-672631/65.
N-PSDB; AAC64617.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
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N-PSDB; AAQ87467.
                                                                                                                                                                                                                                                                                                                                                                  White AP,
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                                                                                                             Disclosure; Page 135; 139pp; English
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90.7%;
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Pred. No. 1.4e-58;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
Collinson SK,
                                                                                                                                                                                                                                                                                          US5635617-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella
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29-SEP-1997
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                                                                                                                                                                        26-APR-1994;
                                                                                                                                                                                                                                 03-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
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                                                         (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
                                                                                                                  26-APR-1993;
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(first entry)
Kay
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Pred. No. 1.4e-58;
2; Mismatches 12
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RESULT 6
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Best Local Similarity
Matches 136; Conserv
Recombinant agfA gene having a segment rewhich encodes foreign epitope or antigen,
                                           WPI; 2000-672631/65.
N-PSDB; AAC64631.
                                                                                     White
                                                                                                                                                                    05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                              12-OCT-2000
                                                                                                                                                                                                                         WO200060102-A2
                                                                                                                                                                                                                                                                Escherichia
                                                                                                                                                                                                                                                                             Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                       Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                          vaccine;
                                                                                                                                                                                                                                                                                                                                              AgfA::PT3#10 amino acid sequence SEQ ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                                                                               AAB36355 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated Salmonella gene agfa - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Fig 7; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-309886/28.
N-PSDB; AAT74142.
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                                                                                                                                                                                                                                                                                                         la; agfA;
immune re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                  Doran JL,
                                                                                                                                                                                                                                                                  coli.
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                                                                                                                                        99US-0127888P
                                                                                                                                                                                                                                                                                                      response;
                                                                                                                                                                                                                                                                                                                   chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.2%;
90.1%;
                                                                                   Collison
                                                                                                                                                                                                                                                                                                         immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 677; DB 2;
Pred. No. 4.4e-58;
2; Mismatches 13
            segment replaced by a foreign DNA sequence
                                                                                   SK,
                                                                                  Kay WW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 151
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expresses recombinant

05-APR-2000; 2000WO-CA000356

12-OCT-2000

WO200060102-A2

vaccine;

immune

response; immunogen

Salmonella enteritidis.

Synthetic. Escherichia coli. Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope

AgfA::PT3#5 amino acid sequence SEQ ID NO:20

26-FEB-2001 AAB36350;

(first entry)

AAB36350 standard; protein; 151

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RESULT 7
AAB36350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprising separating an amino acid polymer comprising a recombinant AgfA comprising sequence or sequence someth or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended
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                                                                                                                             106 WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                       Similarity 81.
                                                                                                                                                                                                                           SDARKSETTITQSGYGNGADVGQGADN------
                                                                                                                                                                                                                                                                                      MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                        SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 139; 139pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
A
                                                                                                                                                                                                                                                                                                                                                                                                              84.7%;
                                                                                         GGNNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                  Score 657; DB
Pred. No. 4e-5
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       0,:
                                                                                                                                                                                                                                                                                                                                                                                                            4e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length 151;
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ARBSULT 8
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ID AAB3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, cc comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino caid sequence or sequences grown on a Salmonella, E. coli or caid sequence or sequences grown on a Salmonella, E. coli or colymer into the animal in conjunction with a carrier or diluent. (1) is cc useful for the expression of recombinant AgfA protein which is useful for celiciting an immune response in an animal. In a finbrial presentation cc system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the cc simulation properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong c immunogenicity and adhesion properties relevant for an efficient live cagainst the inserted epitope, and hybrid fimbriae are easy and c inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                   Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEP17/TAF) nucleation depended assembly system of strains of Salmonella, Escharichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CegA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                           AgfA::PT3#7 amino acid sequence SEQ ID NO:24.
                                                                                                    26-FEB-2001
                                                                                                                                                                                   AAB36352 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              directing recombination of a recombinant gene into the chromosome of homologous species; (3) directing recombination of a recombinant gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA
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                                                                                                                                                                                                                                                                                                                               -----DQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                        SDARK----
                                                                                                                                                                                                                                                                                                                                                                                                            SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHA------
                                                                                                                                                                                                                                                                                       NNATI DQWNAKNSDI TVGQYGGNNAAL VNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                  (first entry)
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  response;
                                                                                                                                                                                protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 619; DB 3
Pred. No. 2e-52;
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                                                                                                                                                                                                                                                                                                                                                                      YDQLVTRVVTHEMAHAGQGADNSTIELTQNGFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for the system the heterologous antigens are presented in high numbers (up to $90,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 138; 139pp; English.
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121
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                                                           86
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                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGAD-----
                                                           HEMAHADQWNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                            MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                          GNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 609; DB 3;
Pred. No. 1.9e-51;
                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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RESULT

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                                                                                                                            Query Match
Best Local &
                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 135; 139pp; English.
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                                                                                                                                   Similarity
MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Doran JL,
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                                                                                                                                                                                                                                                                                 of the present invention
                                                                                                                         77.8%;
80.8%;
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                                                                                          DB 3; 1
5.9e-51;
les 23;
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MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ

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CC The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF17/TAP) nucleation depended CC Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue finbria subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant of a recombinant gene back into the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immune response in an animal. CC comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC strerobacteriaceae host cell, from the host cell and introducing the CC useful for the expression of recombinant AgfA protein which is useful for CC system the heterologous antigens are presented in high numbers (up to CC system the heterologous antigens are presented in high numbers (up to CC system the heterologous antigens are presented in high numbers (up to copies/cell), the hybrid fimbrin protein possesses both the carrier fimbrial subunit proteins are usually strong communogens, which may be important for directing an immune response cc against the inserted epitope, and hybrid fimbriae are easy and constructed in high numbers in a system the inserted epitope, and hybrid fimbriae are easy and constructed epitope, and hybrid fimbriae are easy and constructed epitope, and hybrid fimbriae are easy and constructed epitope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Best Local Similarity 81.5
Matches 123; Conservative
The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing an immune response in an animal, comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or
                                                                                                                                                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White AP,
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                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 138; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-2000; 2000WO-CA000356
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Pred. No. 9.3e-51;
5; Mismatches 23
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RESULT 12
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Matches 123;
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                                                                                                                                                                                                                                                           05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2001
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                                                                                                                                                                                                                                                                                                                 WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                           Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                          AgfA::PT3#4 amino acid sequence SEQ ID NO:18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB36349 standard;
                                                                                                                                                                                                      (UYVI-) UNIV VICTORIA
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                                                                                                                                    2000-672631/65.
DB; AAC64625.
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Pred. No. 1.2e-
4; Mismatches
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                                                                                                                                                                             SK,
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No. 1.2e-50;
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The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign D sequence which encodes a foreign epitope or antigen. Also describ

Also described

DNA

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

segment of the sequence which

Disclosure; Page 136; 139pp; English

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RESULT 13
AAB36348
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WPI; 2000-672631/65
                                                                  White AP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                              Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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81.5%;
                                                              Collison
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Pred. No. 1.5e
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                                                                  XS,
                                                           Kay WW
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.5e-50;
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RESULT 14 AAB36343 ID AAB3

AAB36343 standard; protein; 151

vaccine; Salmonella; agfA;

1mmune

response;

immunogen

chromosomal gene replacement; fimbrin; epitope;

Escherichia coli CsgA amino acid sequence SEQ ID NO:7

26-FEB-2001 (first entry)

AAB36343;

WO200060102-A2 Escherichia coli

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                                                                                                                                                                                                                                                                                                                                                                                        directing recombination of a recombinant gene into the chromosome of the chomologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid gequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for cellciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immune response
                                                                                                                                                                                                                                                                                            Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                         immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 136; 139pp; English
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                                             NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
NNAALVNOTASDSSVMVROVGFGNNATANOY
                                                                                           SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                         SDARKSETTITOSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
                                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVYDOLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 2.4e-47;
5; Mismatches 24
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05-APR-2000;

2000WO-CA000356

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CE Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA. CSGA and AgfA-homologue fimbrin subunits, respectively; (2) cc directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the coliviting an immune response in an asimal. In a fimbrial presentation CC sold sequence or sequences grown on a Salmonella, E. coli or SO,000 copies/cell), the hybrid fimbria protein which is useful for system the heterologous antigens are presented in high numbers (up to SO,000 copies/cell), the hybrid fimbria are usually strong constituted and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong constituted entrole and hybrid fimbriae are easy and
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Matches 105
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                    E. coli CsgA subunit 15 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                           04-DEC-2003
                                                                                                 ABR82651;
                                                                                                                                      ABR82651 standard; protein;
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                                                                                                                                                                                                                                                                                                                   TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                           (first entry)
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Pred. No. 7.5e-
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7.5e-43;
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                                                                                                                                                                                                                                          The invention relates to an isolated peptide capable of binding a mammal manufalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABR82642, ABR82648-49. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                         or Shigella infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmonella
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 41-42; 42pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2002; 2002GB-00002275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasma protein; immune response; antibacterial; vaccine; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
                                                                                                                                                                                                                                 15 kDa protein
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                                                                                    MKLLKVÄAFAAIVVSGSALAGVVPQWGGGGNHRGGGNSSGPDSTLSIYQYGSANAALALQ
                                                SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
   NNAALVNQTASDSSVMVRQVGFGNNATANQY
                            TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
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Search completed: March 11, Job time : 51.9 secs 2004, 18:33:44

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GNGAAVDQTASNSSVNVTQVGFGNNATAHQY

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seq length: 2000000000
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1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
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       Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Sequence 59, Appl Sequence 57, Appl Sequence 3, Appli Sequence 42, Appl Sequence 337, App Sequence 180, App Sequence 180, App Sequence 180, App Sequence 180, App Sequence 24717, A Sequence 24717, A Sequence 204, App Sequence 204, App Sequence 204, App Sequence 204, App Sequence 204, App Sequence 204, App Sequence 204, App Sequence 204, App Sequence 204, Appli Sequence 22, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 41, Appli
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIXQXGSANAALALQ

; TYPE: amino acid ; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-233-788A-59

Query Match 87.2%; Best Local Similarity 90.1%; Matches 136; Conservative

Score 677; DB 1; 1 Pred. No. 3.3e-59; 2; Mismatches 13;

Length 151;
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RESULT 1 US-08-233-788 Sequence 59 Fatent No. 59 FATENT OF TITLE OF FATILE OF FATILE OF FATILE OF FATILE OF FATILE OF FATILE OF FATILE OF FATILE OF FATILE OF FATILE OF FATILE OF FATILE OF FATILE FAT	2222 2222 2222 2322 2422 2422 2422 2422	
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TIONS FOR th Avenue	40-236-3401 34-000C-5130 25-619-32 37-716-2 36-447A-9 95-8048-26 52-991A-32096 53-991A-32096 36-447A-13 37-210A-4	
DETECTION	Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence	
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Sequence 3, Application US/08864038A Patent No. 6001592 GENERAL INFORMATION:
                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Dozan, Jan
APPLICANT: Kay, Will.
APPLICANT: Collinson
APPLICANT: Clouthier
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 3723836 SEEDANBERRY INFORMATION FOR SEQ ID NO: 57: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Seed and Berry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 92
                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.Ā.
ZIP: 98104-7092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/233,788A
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                                                                                                                                                                          VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
                                                                                                                                         GQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                              GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS
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KAY, William W.

Collinson, Karen S.

Clouthier, Sharon C.

VENTION: METHODS AND COMPOSITIONS FOR DETECTION

VENTION: OF SALMONELLA
                                                                                                                                                                                                                                               Conservative
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N: 435
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87.5%;
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Pred. No. 1.2e-41;
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RESULT 4
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ATTORNEY AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: '22,389
REFERENCE/DOCKET NUMBER: F-56
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION NUMBER: JP 8-184450
FILING DATE: MAY 28, 1997
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ORIGINAL SOURCE:
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CURRENT APPLICATION DATA:
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TTTY: Tsu-city
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10s 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: peptide
LOCATION: from 1 to 73
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Com
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                            ARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDI-TVGQYGGN 121
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OR SEQ ID NO:
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VENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR

VENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID

VENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING

VENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JAPAN
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from 1 to 738
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Sequence 5, Application US/09336447A Patent No. 6310190

GENERAL

INFORMATION:

APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.

MACIVER, ISOBEL

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CURRENT APPLICATION NUMBER: US/09/336,447A;
CURRENT FILING DATE: 1999-06-21;
NUMBER OF SEQ ID NOS: 98;
SOFTWARE: PatentIn Ver. 2.1;
SEQ ID NO 5;
LENGTH: 892;
TYPE: PRT
ORGANISM: Moraxella Catarrhalis
US-09-336-447A-5
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US-09-495-880A-42
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SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 42
LENGTH: 238
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Best Local 9
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Best Local (
                                                                                                                                                                                                                                                                                                                   -09-495-880A-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/495,880A CURRENT FILING DATE: 2000-02-01 PRIOR APPLICATION NUMBER: PCT/EP98/04836 PRIOR FILING DATE: 1998-08-03 PRIOR APPLICATION NUMBER: EP 97 11 3319.4 PRIOR FILING DATE: 1997-08-01 VINDER: EF 97 10 3319.4 PRIOR FILING DATE: 1997-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL METHOD AND PHAGE FOR THE IDENTIFICATION OF TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING MEMBERS OF A MUTTITLE OF INVENTION: (POLY) PEPTIDE COMPLEX FILE REFERENCE: MORPHO/9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: RUDERT, FRITZ
APPLICANT: GE, LIMING
APPLICANT: ILAG, VIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FISKE, MICHAEL J.

APPLICANT: FREDENBURG, ROSS A.

TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: AMCY:024
                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ompA-FLAG-peptide3-
OTHER INFORMATION: gene IIIs encoded by phage vector fpep3_1B-IR3seq (circular)
                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                               Local Similarity
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AKNSDI-----TVGQYG------GNNAALVNQTA-----SDSSVMVRQVGFGNNA 146
                                              ---GSGGGSEGGGSEGGGSEGG-GSGGGSGSGDFDYEKMANANKGAMTENADE-N 110
                                                                                      YQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWN 107
                                                                                                                                     KTAIAIAVALAGFATVAQADYKDVDCIVYHAHYLVAKCGGGGSEFNAGGGSGG-----
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                                                                                                                                                                                                                                               11.1%; Score 86.5; DB 4; Length 238; 24.3%; Pred. No. 0.69;
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US-09-598-419-337
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US-09-620-412C-337
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NUMBER OF SEQ ID NOS: 357

SOFTWARE: FastSEQ for Windows Version 3.0/4.0

SEQ ID NO 337

LENGTH: 585

TYPE: PRT
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Scholler, John
APPLICANT: Management of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the sta
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LENGTH: 585
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CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION FILE REFERENCE: 210121.469C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/598,419
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                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                  258 GLYTDKNLSITNITGIIEIANNKATDVGGGA-----YVKGTLTCENSHRLQFLKNSSDKQ 312
                                                                                                                                                                                                                                         206 LKAQASAG---NADAWASSSPQSGSGATTVSDSGDSSSGSDSDTSETVPVTAKGG---- 257
                                                                                                                                                       58 ALQSDARKSETTIT----QSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDIT 114
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31.6%; Pred. No. 2.
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Pred. No. 2.2;
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Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 180
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SOFTWARE: FastSEQ for
SEQ ID NO 180
LENGTH: 1752
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                                                                                                                                                                                                                                                                                                                                                APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 210121.469C7
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CURRENT APPLICATION NUMBER: US/09/556,877
CURRENT FILING DATE: 2000-04-19
                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Chlamydia
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
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ORGANISM: Chlamydia
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58 ALQSDARKSETTIT---QSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDIT 114
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                                                                              LKVAAFAAIVVSGSALAGVVPQWGGGGN--HNGGGNSSGPDS----TLSIYQYGSANAAL
                                                  LKAQASAG----NADAWASSSPQSGSGATTVSDSGDSSSGSDSDTSETVPVTAKGG----
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Skeiky, Yasir
Fling, Steve
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Pred. No. 9;
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PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 7849

LENGTH: 589

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-7849
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                                                                                                           Query Match
Best Local Similarity
Matches 32; Conservat
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Scholler, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C6
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Patent No. 6610836
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CURRENT APPLICATION NUMBER: US/09/489;039A

CURRENT FILING DATE: 2000-01-27
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CURRENT FILING DATE: 2000-06-20
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                                                                                                                      11.0%; Score 85.5; Dilarity 23.2%; Pred. No. 2.8; Conservative 17; Mismatches
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31.6%; Pred. No. 9;
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-4764
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SEQ ID NO 4764
LENGTH: 975
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GRIVENT: GATY L. Breton et al.

APPLICANT: GATY L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04
                                                                                     Matches
                                                                                                     Query Match
Best Local
                                                                                                                                                                                                         SEQ ID NO 24717
LENGTH: 461
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Best Local Similarity
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Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                             PRIOR FILING DATE: 1998-02-16
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION 1998-07-27
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE:
                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
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                                                6 VAAFAAIVVSG-SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANA---ALALQS
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                                                                                                     Similarity
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                  VAALPEVARSGPGAPSGTAPAGGGAA---GGKSPAGLGRLARRSSFPSSSATPPAATTYF 356
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1998-02-18
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Pred. No. 12;
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30710
LENGTH: 812
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SEQ ID NO 26658
LENGTH: 1034
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GENERAL INFORMATION:
APPLICANT: Marc J.
                                                                               Matches
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                                                                                                    Best
                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                               APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
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                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
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                                      14 VSGSALAGVVPQWGGGGNHNG-----GGNSSGPDSTLSIYQYGS-ANAALALQSDAR--
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VSDSSASGQV-EAGGAGNTGGLVGLSSGGEIFRSQASGSVYSKGGLATGGLIGKAEGNGM
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VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS VENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Search completed: March 11, 2004, 18:44:52 Job time : 13.4 secs	864 SVAHAISRGDVSGGFNS-LVGGLVGHNGGELVNVDASGRVSAAASASVGGLVGSNA 918	96 -VTHEMAHADQWNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNA 146	807 LGNLKASGSVTDQGGADLGGLVGNNSQSAIETAEATGKVSGGSNSRVGGLIGHNLGG 863	65KSETTITQSGYGNGADVGQGADNYDQLVTRV 95

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     Published_Applications_AA:*

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 15 US-10-369-493-20638

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9 US-09-841-132-445

9 US-09-841-132-594

10 US-09-880-748-1122

15 US-10-369-493-20619

10 US-09-881-132-180

10 US-09-881-132-180

10 US-09-880-748-2098

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10 US-09-880-748-1199
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Sequence 20638, A
Sequence 145, App
Sequence 445, App
Sequence 594, App
Sequence 5122, Ap
Sequence 50619, A
Sequence 5, Appli
Sequence 180, App
Sequence 180, App
Sequence 21, Appl
Sequence 21, Appl
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Sequence 1159, Ap
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ALIGNMENTS

US-10-369-493-20638

Sequence 20638, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:

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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PRICING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20638
LENGTH: 445
TYPE: PRT
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                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                    ORGANISM: Rhodopseudomonas palustris FEATURE: NAME/KEY: unsure LOCATION: (1)...(445)
OTHER INFORMATION: unsure at all Xaa locations
69 TITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQW-NAKNSDITVGQ---YGGN-NA 123
                                                                                                                        30 GNHNGGGNSS-----GPDSTLSIYQYGSANAA-----
                                                                                                                                                                                               Similarity
                                                                   GKQSGAGNSAAIFQEGTGSDVELQQTGTSNGAVPSGWNWTNDPGVFNKITQDSSSNGSKV 148
                                                                                                                                                                        Conservative
                                                                                                                                                                                            12.2%;
                                                                                                                                                                      22;
                                                                                                                                                                   Score 95; DB 15; Length 445; Pred. No. 0.25; Mismatches 59; Indels
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                                                                                                                        -----LALQSDARKSET
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US-09-880-748-1130
                              CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
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US-09-793-306-146
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                                                                                                                                                                                                                                                                                                                      Sequence 1130, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:
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SEQ ID NO 146
LENGTH: 597
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Patent No. US20020098200A1
                                                                                                                                                                                                                                                       APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind
FILE REFERENCE: PF523
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APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
TITLE OF INVENTION: of Tuberculosis
TILE REFERENCE: 014058-008740US
CURRENT FILING DATE: 2001-02-26
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR APPLICATION NUMBER: US 60/23,828
PRIOR FILING DATE: 2000-08-08
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 12.2%; Score 95; DB 9; Length 597; Local Similarity 27.4%; Pred. No. 0.36;
         APPLICATION NUMBER: 60/293,499
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; Sequence 594, Application US/09841132
; Patent NO. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOI
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INI
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION UNMER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
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US-09-880-748-1130
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Matches
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LENGTH: 1751
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NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1130
LENGTH: 251
TYPE: PRT
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Patent No. US2002006
GENERAL INFORMATION:
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APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469CB
CURRENT FILING DATE: 2001-04-23
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
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les 40; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 -- QSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQ-YGGNNAALVNQ 128
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20020061848A1
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27.7%;
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33.1%; Pred. No. 3.5;
ive 10; Mismatches 5
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                                                                     FOR TREATMENT INFECTION
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RESULT 7
US-10-369-493-20619
; Sequence 20619, Application US/10369493
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SOFTWARE: FASTSEQ for Windows Version 3.0/4.0
SEQ ID NO 594
LENGTH: 1751
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Best Local
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 3239
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PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
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CURRENT FILING DATE: 2001-06-15
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PRIOR APPLICATION NUMBER: 60/277,379
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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ORGANISM: C. Trachomatis D
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                                                                                                                                     125 L 125
                                                                                                                                                                          156 QRVTISCS--GSASNVGNNAVNWYQQLPGKPPKLLIYYDDLLPSGVSDRFSGSKSGTSAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 NADAWASSSPQSGSGATTVSNSGDSSSGSDSDTSETVPATAKGG-GLYTDKNLSITNITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40;
                                                                                                  214 L 214
                                                                                                                                                                                                                                                  106 ATTGALDMWGQGTLVTVSSGGGGGGGGGGGGG
                                                                                                                                                                                                           66 SETTITQSGYGNGADVGQGADN-YDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAA 124
                                                                                                                                                                                                                                                                                     18 ALAGVVPQWG------GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ---SDARK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 SGSALAGVVPQWGGGGN--HNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT-
                                                                                                                                                                                                                                                                                                                                       h 11.5%;
Similarity 28.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --QSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQ-YGGNNAALVNQ 128
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                         Score 89.5; DB 10;
Pred. No. 0.43;
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                           Length 251;
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COPE, LESLIE D.

APPLICANT: MACIVER, ISOBEL.

APPLICANT: FISKE, MICHAEL J.

APPLICANT: FREDENBURG, ROSS A.

FILE OF INVENTION. USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS

FILE REFERENCE: AMCY:024

CURRENT APPLICATION NUMBER: US/09/952,267

CURRENT APPLICATION NUMBER: US/09/952,267

CURRENT FILING DATE: 2001-09-12

PRIOR APPLICATION NUMBER: 09/336,447

PRIOR FILING DATE: 199-06-21

NUMBER OF SEQ ID NOS: 98

SOPTWARE: PATERILIN Ver. 2.1

SEQ ID NO 5

LENGTH: 892

TYPE: PDT
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; NAME/KEY: unsure
; LOCATION: (1)..(486)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-20619
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                                                   Query Match
Best Local S
Matches 38
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CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20619
LENGTH: 486
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Best Local:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 LPLFHVTGLGLMLTLQQAGGASVI 212
28 GGGNHN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 ALQSDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVG- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 SVVVAGTDYRDIVAGVLPSLGGVKKAYAIGDGSGPFAPFKDLASDTPFSAPEFGAADGFV 145
                                                      38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 AIVVSGS----ALAGVVPQWGGGGNHNGGGNSSGP------DSTLSIYQYGSANAAL
                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---- QYGGNNAALVNQTASDSSVM 136
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                                                     Conservative
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                                                                   11.2%; Score 87;
26.8%; Pred. No.
-GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGY----
                                                   15;
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Pred. No. 1.6;
24; Mismatches
                                                     Mismatches
                                                                                     DB 10;
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                                                      57;
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                                                                                    Length 892;
                                                      Indels
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                                                      32;
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                                                      Gaps
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RESULT 10
US-09-841-132-180
                                                                               ; ORGANISM: Chlamydia
US-09-841-132-180
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US-09-841-132-337
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                                                                                                                                                                                                                                                                                                                                                     Sequence 180, Application to Patent No. US20020061848A1 GENERAL INFORMATION:
       Matches
                                          Query Match
                                                                                                                                 SEQ ID NO 180
LENGTH: 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEQ ID NO 337 LENGTH: 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 337, Application US/09841132 Patent No. US20020061848A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                      APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                  NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                         FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bhatia, Ajay
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CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
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APPLICANT: Skeiky, Yas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 210121.469C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                    TYPE: PRT
     Local Similarity
les 43; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 GLYTDKNLSITNITGIIEIANNKATDVGGGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 LKAQASAG----NADAWASSSPQSGSGATTVSDSGDSSSGSDSDTSETVPVTAKGG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 LKVAAFAAIVVSGSALAGVVPQWGGGGN--HNGGGNSSGPDS----TLSIYQYGSANAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGIYGEDNITLSNLT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OATGEGSF---AAGVENKANAN 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGDSSTIGGG--YYNOATGEKSTVAGGRNNOATGNNSTVAGGSYNOATGNNSTVAGGSHN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYG---GNNAALV----N 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probst, Peter
                                                                                                                                                                                                                                                                                                                                                                                            Application US/09841132
     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yasir A.W.
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31.6%; Pred. No. 2.5;
vative 12; Mismatches
                     11.1%;
     12;
                     Score 86.5; I
Pred. No. 10;
     Mismatches
                                      DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58;
     58;
                                      Length 1752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 585;
     Indels
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 23;
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Gaps
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Sequence 2098, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:
APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-21
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, NAME/KEY: misc_feature
; OTHER INFORMATION: PPE
; NAME/KEY: misc_feature
; OTHER INFORMATION: gi|1781260
US-09-820-843A-21
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US-09-820-843A-21
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Publication No. US20030039933A1
GENERAL INFORMATION:
APPLICANT: COuncil of Scientific and Industrial
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: 063915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 21
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Best Local
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CURRENT EILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 354
TYPE: PRT
ORGANISM: M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 TSMFGGNSGVLNTGYGNSGFYNAAVNNTGIFVTGVMSSGFFNFGTGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258
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Pred. No. 1.9;
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US-09-880-748-2098
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Best Local S
Matches 24
Sequence 1494, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:
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SEQ ID NO 1153
LENGTH: 255
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2098
LENGTH: 253
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
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PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/277,379 FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                         13 VVSGSALAGVVPQWG-----GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDA 63
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US-09-880-748-1199
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PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
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Matches
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SEQ ID NO.1199
LENGTH: 253
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
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CURRENT FILING DATE: 2001-06-15
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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                                                                                                                     Local 5.
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Local Similarity 28.6%;
                                          107 VTARWGMDVWGQGTLVTVSSGGGGGGGGGGGGGGG------GSAQAVLTQPSSASGTP 156
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                                                                                     22 VVPQWG-----
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  -TTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHA-DQWNAKNSDITVGQYGGNNAAL 125
                                                                                                                                Conservative
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Pred. No. 1.8;
13; Mismatches
                                                                                   -GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSB
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Db 157 GQRVTISCSGSSSNIGSNVINWYQQLPRTAPKLLIHTNDQRPSGVPDRFSGSKSGTSGTL 216

Search completed: March 11, 2004, 19:18:38 Job time : 24.6 secs

Title: Perfect score: Sequence: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database : Total number of hits satisfying chosen parameters: Run on: OM protein - protein search, using sw model Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Searched: Scoring table: PIR 78:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* March 11, 2004, 18:24:14 ; Search time 10.3 Seconds (without alignments) 1410.186 Million cell updates/sec BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-543-407-22 776 283366 seqs, 96191526 residues 1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151 GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. 283366

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match Length	length DB	BID		Description
1	682	87.9	151	2 ЈС603	039	fimbrin protein ag
N	682	87.9		2 AI(AI0635	major curlin chain
w	521	67.1			S70788	curlin protein csg
4	499.5	64.4	152		D90806	curlin major subun
Ŋ	499.5	64.4		2 H89	H85665	hypothetical prote
თ	109	14.0			S42136	
7	109	14.0			E95965	
œ	102	13.1			T26667	hypothetical prote
9	98	12.6			E70663	
10	95	12.2			E70946	
11	94	12.1	407	2 T2	T21956	hypothetical prote
12	93.5	12.0			AD3143	
13	93.5	12.0			H98144	hypothetical prote
14	93.5	12.0	645	2 F70	F70825	probable PPE prote
15	93.5	12.0	1567	2 S1	S11672	ice nucleation pro
16			151	2 S70	S70787	curlin nucleator p
17	92.5	11.9	151	2 C9(C90806	minor curlin subun
18	92.5	11.9		2 G85	G85665	curlin minor chain
19		11.8			JC2143	ice nucleation act
20	91.5	11.8			JQ0188	ice nucleation pro
21	91			2 G7:	G71518	hypothetical prote
22	90.5	11.7			JC6040	fimbrin protein ag
23	90.5	11.7		2 AH(AH0635	nucleation compone
24	90.5	11.7		2 B7(B70987	probable PPE prote
25	89.5	11.5			S07053	ice nucleation pro
26	89))]	protein kinase sgg
27		11.2	251	2 D9	321	hypothetical expor
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11.0	11.0	11.0	11.0	11.0	11.0	11.1	11.1	11.1	11.1	11.1	11.2	11.2	11.2	11.2	11.2
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ALIGNMENTS

Oy 121 NNAALVNQTASDSSYMVRQVGFGNNATANQY 151	Qy 61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120	Qy 1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	Query Match 87.9%; Score 682; DB 2; Length 151; Best Local Similarity 90.7%; Pred. No. 1.2e-50; Matches 137; Conservative 2; Mismatches 12; Indels 0; Gaps 0;	C;Function: A;Description: major component of thin aggregative fimbriae A;Dete: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator A;Keywords: fimbria C;Keywords: fimbria F;1-20/Domain: signal sequence #status predicted <sig> F;21-151/Product: fimbrin protein agfA #status experimental <mat></mat></sig>	A;Accession: A44898 A;Status: preliminary A,Molecule type: protein A;Residues: 21-33 <co3> A;Note: sequence extracted from NCBI backbone (NCBIP:45936) C;Genetics: A;Gene: agfA</co3>	A;Experimental source: strain 27655-3b A;Note: the authors translated the codon ACG for residue 44 as Ile R;Collinson, S.K.; Emody, L.; Muller, K.H.; Trust, T.J.; Kay, W.W. J. Bacteriol. 173, 4773-4781, 1991 A;Title: Purification and characterization of thin, aggregative fimbriae from Salmonell. A;Reference number: A44898; MUID:91310586; PMID:1677357 A;Contents: 27655	A;Accession: JC6039 A;Molecule type: DNA A;Residues: 1-151 <col/> A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43599.1; PID:g1184714 A;Accession: PC6015 A;Molecule type: protein A;Residues: 21-52 <co2></co2>	RESULT 1 JC6039 JC6039 JC6039 JC6039 JC6039 JC6039 JC6039 JC6039 C; Decies: Salmonella enteritidis C; Decies: Salmonella enteritidis C; Decies: Salmonella enteritidis C; Decies: Salmonella enteritidis C; Decies: Salmonella enteritidis R; Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W. J. Bacteriol. 178, 662-667, 1996 A; Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae. A; Reference number: JC6039; MUID:96146512; PMID:8550497

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A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74126.1; A;Experimental source: strain K-12, substrain MG1655 R;Olsen, A.; Arngvist, A.; Hammar, M.; Sukupolvi, S.; Normark, S. Mol. Microbiol. 7, 523-536, 1993
                                                                                                                                                         Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: G64846
                                                                                                                                                                                                                                             A;Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Rile A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        curlin protein csgA precursor - Escherichia coli (strain K-12) N,Alternate names: csgA protein; major curlin protein C;Species: Escherichia coli C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change C;Accession: S70788; G64846; S31202; S34560; S34559 R;Hammar, M.; Arngvist, A.; Bian, Z.; Olsen, A.; Normark, S. Mol. Microbiol. 18, 661-670, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Expression of two csg operons is required for production A;Reference number: S70783; MUID:96414468; PMID:8817489 A;Accession: S70788
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A;Residues: 1-151 <HAM>
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Nature 413, 848-852, 2001

A;Authors: Parry, C: Quail, M: Rutherford, K: Simmonds, M: A;Title: Complete genome sequence of a multiple drug resistant A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AI0635
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A; Residues: 1-151 < PAR>
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R;Parkhill, J.; Dougan, G.; Jam
R;Parkhill, J.; Cronin,
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                                                                                                                Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                       ;Status: nucleic
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                                                                                                                                      acid sequence not shown; translation not
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90.7%;
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in, A.;
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Pred. No. 1.2e-50;
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    Salmonella enterica subsp.

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ey, M.;
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A; Molecule type: DNA
A; Residues: 1-152 < HAY>
A; Cross-references: GB:B;
A; Experimental source: st
C; Genetics:
A; Gene: ECs1420
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C;Date: 18-Uul-2001 #sequence_revision
C;Accession: D90806
R;Hayashi, T.; Makino, K.; Ohnishi, M.;
R;Hayashi, T.; Makino, K.; Ohnishi, M.;
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                                                                                                                                                                                                                                                                       A;Title: Complete genome sequence of enterohemorrhagic E A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: D90806
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D90806
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A; Accession: S34559
A; Molecule rvn
                                                                                                                                                                                                                                                                                                                                                                                                                   curlin major subunit CsgA [imported]
C;Species: Escherichia coli
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A; Molecule type: DNA
A; Residues: 1-133, 'RQRDSGWLW' <OLS3>
A; Cross-references: EMBL:L04979; NID:g290424;
A; Cross-references: strain K-12, substrain
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A;Map position:
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Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori,
                                                                       Conservative
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                                                                                     64.48;
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                                                                      Score 499.5; DE
Pred. No. 3e-35;
B; Mismatches
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Pred. No. 4.6e-37;
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QSDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYG 119

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A;Cross-references: EMBL:L03710
R;Martindale, D.W.; Taylor, F.M.
Nucleic Acids Res. 16, 2189-2201, 1988
A;Title: Multiple introns in a conjugation-specific gene A;Reference number: $03650; MUID:88189811; PMID:3357771
A;Accession: $03650
A;Molecule type: DNA
A;Residues: 236-250,'I',252-255,'N',257-773 <MAR>
                                                                                                                                                                                                        R;Taylor, F.M.; Martindale, D.W.
Nucleic Acide Ree. 21, 4610-4614, 1993
A;Title: Retroviral-type zinc fingers and glycine-rich repeats
A;Reference number: S42135; MUID:94051569; PMID:8233798
A;Accession: S42135
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A;Cross-references: GB:AE005174; NID:g12514574; PIDN:AAG55788.1;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: csgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein csgA [imported] - Escherichia coli (strain 0157:H7, substrain EDL93 C;Species: Escherichia coli (c;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: H85665 C;Accession: H85665 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-1748 <TAY>
A;Cross-references: EMBL;L03710; NID:g161751; PID:g161752
                                                                                                                                                                                                                                                                                                                                                                                R;Taylor, F.M.; Martindale, D.W. submitted to the EMBL Data Library, A;Reference number: S42136
                                                                                                                                                                                                                                                                                                                                                                                                                                        cnjB protein - Tetrahymena thermophi
C;Species: Tetrahymena thermophila
C;Date: 19-Mar-1997 #sequence revisi
C;Accession: S42136; S42135; 503650
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A;Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-
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Nature 409, 529-533, 2001
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;Molecule type: DNA
:Residues: 236-250,'I',252-255,'N',257-773 <MAR:
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F;1478-1491/Region: z
F;1501-1514/Region: z
F;1530-1543/Region: z
F;1530-1543/Region: z
F;1555-1569/Region: z
F;1592/Region: z
F;1602-1615/Region: z
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A;Genetic code: SGC5
A;Introni: 85/3; 136/1; 1
C;Keywords: zinc finger
F;1164-1450/Region: glyci
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A;Molecule type: DNA
A;Residues: 1-2174 <KUR>
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A;Gene: SMb21548
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A;Cross-references: GB:AL591985; PIDN:CAC49389.1; PID:g15140875; GS
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Amp
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.
A;Title: The composite genome of the legume symbiont Sinorhizobium |
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical glycine-rich protein [imported] - Sinorhizobium meliloti (strain 1021) C;Species: Sinorhizobium meliloti C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
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                                                                                           750 GLTLTTQGSHAAGIVAQS-VGGGGGTGGTASSYSAGI--
                                                                                                                                        57 -LALQSDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITV 115
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                                            GOYGGNNAA--LVNQTASDSSVMVRQVG 141
                                                                                                                                                                                          AIATAGAGAVGILAQSIGGGGGN----GGNATGGDAGFGSFQIGGGGGGGGYANTANVGFK 749
                                                                                                                                                                                                                     AIVVSGSALAGVVPQ--WGGGGNHNGGGNSSGPDSTLSIYQYGS------ANAA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Dreano, S.; Federspiel, N.A.; Fisher, R.F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.H.; Kiss, E.; Komp, C.; Lelaure
S.; Wells, D.H.; Wong, K.; Yeh, K
                                                                                                                                                                                                                                                                                      Indels
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                                                                                           GFTASVAV
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Rajandream, M.A.; Rogers, J.; Rutter, Nature 393, 537-544, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, A;Reference number: Z20252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein Y38E10A.q - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Decies: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T26667
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C;Species: Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues:
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Residues: 1-586 <WIL>
Cross-references: EMBL.AL110484; NID:e1542205; PIDN:CAB54408.1;
                                                                                                                                                                                                                                                                                                                                                          ;Cross-references: GB:Z83860; GB:AL123456; NID:g3261681; PIDN:CAB06165.1; PID:e290763;
;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary; nucleic acid sequence not shown; translation not
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;Introns: 105/2; 174/1; 248/1; 372/3; 436/3
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                                                                                                                                                                                                                                                                                                                Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Date: 17-Jul-1998 #sequence_revision; Accession: E70663
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Best Local
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  132 DSSVMVRQVGFGNNATAN 149
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                                                                                                                                                                                                                                                                                                                                                                                                      1-615 <COL>
                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QSDARKSETTITQSGYGNGAD----VGQGADNYDQLVTRVVT-----HEMAHADQWNAKN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRSVGFGAQQFGGSQFARPIPAGGGGGGGGGGGGGGGGGGG
                                                                                     YGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALV---NQTAS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGAGGGGAGGGKAGGAKNSASYGSSANEVKSVGFG----AQQY 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDITYGQYGGNNAALVNQTAS--DSSVMVRQVGFGNNATANQY 151
                                              FGNAGNINTGF-
                                                                                                                                      SGTGNIG----FGNSGNNNIGFFNSG-DGNIGFFNSGDGN--
                                                                                                                                                                               SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG 74
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                             12.6%;
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                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                         Score 98; DB;
Pred. No. 1;
16; Mismatches
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Pred. No. 0.44;
4; Mismatches
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                                              WNAGNLNTGFGSAGNGNVGIFDGGNSNSG
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Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, C.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F38B7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21956
                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, A;Reference number: Z19493
A;Accession: T21956
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A;Cross-references: EMBL:Z74033; PIDN:CAA98477.1;
A;Experimental source: clone F38B7
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                                                                                                                                                                                                                                A; Introns: 12/1; 57/3; 124/2; 163/1; 330/3
                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                        ;Gene: CESP:F38B7.3
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Best Local (
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Gene: PPE
                                                                                                                                                 Matches
                                                                                                                                                                                        Query Match
                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445 GTLN 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               392 GNAGDTNTGFGNAGFFNMGIGNAGNEDMGVGNGGSFNVGVGN--AGNQS-----VGFGNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 FGNSGNNNIGFFNSG-NNNVGFFNSGNNN
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Mycobacterium tuberculosis
                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26
                                                                                                                                                 34;
                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
    SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGA
                                                                   FGSGILAGSLLGYGLGSMWGGHHSYGGWGGGYGGGG------YGMAG---GYY 293
                                                                                                         FAAIVVSGSALA-GVVPQWGG------GGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.2%;
ilarity 27.4%;
Conservative 1
                                                                                                                                                 Conservative
12.1%; Score 94;
25.8%; Pred. No. :
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                                                                                                                                                 19;
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Pred. No. 1.7;
L4; Mismatches
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                                                                                                                                                    Mismatches
                                                                                                                                                                       No. 1.4;
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                                                                                                                                                                                                                                                                                                                                     GSPDB:GN00023; CESP:F38B7.3
                                                                                                                                                    43;
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                                                                                                                                                                                          Length 407
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hypothetical protein AGR_L_228 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002 C;Accession: H98144 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conserved hypothetical protein Atu4768 [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002 C;Accession: AD3143 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gor
                                                                                                                                                                                                                                                                                 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tur A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: H98144
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A;Molecule type: DNA
A;Residues: 1-145 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Authors: Yoo, H.; ster, E.W.
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Best Local :
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                                                                                                                                                                                                GB:AE007870; PIDN:AAK88682.1;
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21.8%;
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                                           64;
                                                                                                                                                                                                PID:g15158413; GSPDB:GN00170
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T.; Levy, R.; Li, M.; N
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GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGAD---NY--

88

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probable PPB protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: F70825
C;Accession: F70825
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple
A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                   A;Residues: 1-1567 <ZHA>
A;Cross-references: EMBL:X52970; NID:g48531; PIDN:CAA37140.1;
C;Superfamily: ice nucleation protein
                                                                                                                                                                                                                                                                        rce nucleation protein - Xanthomonas campestris
C;Species: Xanthomonas campestris
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-19C;Accession: S11672
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S11672
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                                                                                                                                                                    Mol. Gen. Genet. 223, 163-166, 1990
A; Title: Conserved repetition in the ice nucleation gene A; Reference number: S11672; MUID:91080859; PMID:2259339
A; Accession: 311672
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A;Experimental source: strain H3
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42;
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21;
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7Rv
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Pred. No. 2
                  Score 93.5;
Pred. No. 6
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    GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Doran J.L., Collinson S.K., Burian J., Sarlos G., Todd E.C.D.,
Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.;
"DNA-based diagnostic tests for Salmonella species targeting agfA,
the structural gene for thin, aggregative fimbriae.";
J. Clin. Microbiol. 31:2263-2273(1993).
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-i- FUNCTION: CURLIN IS THE STRUCTURAL
-COILED SURFACE STRUCTURES THAT ASSE
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SPECIES=S.enteritidis; STRAIN=27655-3B;
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-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AF

-COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH

TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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"A 718-kb DNA sequence of
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                                                          Salmonella enteritidis."
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T.,
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Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Ro
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Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."
                                                                                                                                                                                                                                                                                                                   STRAIN=0157:H7 / ATCC 43895;
MEDLINE=21218556; PubMed=11319125;
Uhlich G.A., Keen J.E., Elder R.O.;
"Mutations in the csgD promoter associated with variations in expression in certain strains of Escherichia coli 0157:H7.";
Appl. Environ. Microbiol. 67:2367-2370(2001).
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28-FEB-2003 (Rel. 41, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Major curlin subunit precursor.
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EMBL; AE000205; AAC74126.1; -.
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                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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NCBI_TaxID=83334;
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Escherichia coli O157:H7.
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STRAIN=0157:H7 / R:
STRAIN=21156231;
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01-NOV-1990
16-OCT-2001
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ONA RES. 8:11-22(2001).

-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AND THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE CURLICAN BIND TO THE BIND TO THE CURLICAN BIND TO THE BIND TO THE BIND TO THE BIND TO THE BIND TO
              MEDLINE-91080859; PubMed=2259339;
Zhao J., Orser C.S.;
"Conserved repetition in the ice nucleation
Xanthomonas campestris pv. translucens.";
                                                                                                                                                                      xanthomonas campestris (pv. translucens).
Bacteria; Proteobacteria; Gammaproteobacteria;
Xanthomonadaceae; Xanthomonas.
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Tobe T.,
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MBL outstation -
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RESULT 5
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Best Loc
Matches
STRAIN=K12 / MG1655;
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                SEQUENCE
                                                                                                                 MEDLINE=96414468; PubMed=8817489;
Hammar M., Arnqvist A., Bian Z., Olsen A., Normark S.;
"Expression of two csg operons is required for production of
fibronectin- and congo red-binding curli polymers in Escheri
                                                                                                                                                                                         SEQUENCE FROM
STRAIN=K12 / 1
                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 83334;
                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
Escherichia coli, and
Escherichia coli, O157:H7.
                                                                                                                                                                                                                                                                                                                                                                                              CSGB_EC
P39828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000258; Ice nucleatn.
Pfam; PF00818; Ice nucleation; 81.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE NUCLEATION;
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UENCE 1567 AA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no we
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTYSTAllization in supercooled water.

SUBCELIULAR LOCATION: Outer membrane (By similarity).

DOMAIN: COUNTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS

OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A

REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.

MISCELLANEOUS: A STRUCTURAL MODEL IS SUBGRIFTED IN WHICH THE IC

NUCLEATION PROTEIN DISPLAYS A SYMMETRY RUGGESTED IN WHICH THE ICS.

SIMILARITY: Belongs to the bacterial ice nucleation protein
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                                                              FROM
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W; C8B451D959ECAD63 CRC64;
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ACCORD

C90806; C90806. G85665; G85665. S70787; S70787.

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EMBL; X90754; CAA62281.1; -
EMBL; AE000205; AAC74125.1;
EMBL; D90741; BAA35831.1; -
EMBL; AE005315; AAG55787.1;
EMBL; AE005315; BAB34842.1;
                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINIS-211.16.231, PubMed-11.258796;
MEDINIS-211.16.231, PubMed-11.258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli 0157.H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
                                                                                                                                                           or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95157246; PubMed=7854117;
Arnqvist A., Olsen A., Normark S.;
"Sigma S-dependent growth-phase induction of the csgBA promoter
Escherichia coli can be achieved in vivo by sigma 70 in the abse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
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Mori H., Motomura K.,
Osmoei G., Seki Y., T
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STRAIN=0157:H7 / RIMD 0509952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
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MEDIINE-7661202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Oshima T., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.
Ikemoto K., Inada T., Itoh T., Kajihara M., Makino K., Masuda S., Miki T., Mizobuchi K.
Kimura S., Kitagawa M., Makino K., Masda S., Miki T., Mizobuchi K.
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=0157:H7 / EDL933 / ATCC 700
MEDLINE=21074935; PubMed=11206551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sampei G., Seki Y., Tagami H.,
Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the
corresponding to the 12,7-28.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gregor J.,
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                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                         the nucleoid-associated protein H-NS.";
Microbiol. 13:1021-1032(1994).
FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AFFORDED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF CURLIN MONOMERS.
                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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an email to license@isb-sib.ch)
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Matches 46
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Matches 32
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Fimbria;
SIGNAL
CHAIN
                                             Q47879;
01-NOV-1997
                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                        -!- DOMAIN: CONTAINS IMPERFECT REPEATS OF A CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RES PERIODICITY IS SUPERIMPOSED.
-!- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE IC NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE -!- SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                Michigami Y., Watabe S., Al "Cloning and sequencing of uredovora.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=KUIN-3;
MEDLINE=94264407; PubMed=7764866;
Metahan S., Abe K., Obata H.,
                                                                                                                                PIR; JC2143; JC2143.
HSSP; P06620; 1INA.
                                                                                                                                                          EMBL; D14992; BAA03636.1;
                                                                                                                                                                                or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pantoea ananas (Erwinia uredovora).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ce nucleation protein
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                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Ice nucleation proteins enacrystallization in supercooled water. SUBCELLULAR LOCATION: Outer membrane.
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 46;
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an email to license@isb-sib.ch).
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Signal; Complete
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: 15882
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           11.8%;
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MINOR CURLIN SUBUNIT
          Score 91.5; Dr
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5; Mismatches
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                       DB 1;
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16-OCT-2001
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                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                       InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 65.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 45.
                                                                                                                                                                                        EMBL; M26382; AAA24823.1;
PIR; JQ0188; JQ0188.
HSSP; P06620; IINA.
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                                                                                                   SEQUENCE
                                                                                                               Ice nucleation; Repeat; Outer membrane.
DOMAIN 162 1217 OCTAPEPTIDE
                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 85:239-242(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The consensus sequence of ice nucleation proteins herbicola, Pseudomonas fluorescens and Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=M1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Erwinia herbicola.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
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MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
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                                                 46;
                                                               Similarity
IATYGSTLSGTHQSQLIAGYGSTETAGDSSTLIAGYGSTGTAGADSTL-VAGYGSTQTA-
                        IVVSGSALAGVVPQW--GGGGNHNGGGNSS------GPDSTLSIYQYGSANAAL
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                                                                                                    1258 AA;
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(Rel. 14, Last sequence up
(Rel. 40, Last annotation
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084418;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=D/UW-3/Cx;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydia trachomatis.";
Science 282:754-759(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia trachomatis.
Bacteria; Chlamydiae;
                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                           PHCI-2DPAGE; 084418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of an obligate intracellular pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99000809;
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L6-OCT-2001 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)
                                                                                                                                                                                                          AB001314; ...
2DPAGE; O84418; -..
Pro; IPRO03368; Chlamydia PMP.
Pro; IPRO03368; Chlamydia PMP.
PF02415; Chlamydia PMP; 4;
PMG; TICRO1376; POMF repeat; 18.
PAMG; TICRO1376; POMF repeat; 18.
PAMG; TICRO1376; POMF repeat; 18.
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POTENTIAL.
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                                                                                     IIEIANNKATDVGGGA----YVKGTLTCENSHRLQFLKNSSDKQGGGIYGEDNITLSNL
                                                                                                                               NADAWASSSPOSGSGATTVSNSGDSSSGSDSDTSETVPATAKGG-GLYTDKNLSITNITG
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1. 40, Last annotation update)
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33.1%;
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RESULT 10
CSGB_SALTY
ID CSGB_SALTY
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Matches
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EMBL; AE016840; AA069400...,
Fimbria; Signal; Complete proteome.
Fimbria; Signal; Complete proteome.
POTENTIAL.
1 21 POTENTIAL.
NINOR CURLIN SUBUNIT.
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-I- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.
-COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AV
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONE
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Q8Z7M3;
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-22531367; PubMed-12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blatther F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi st
and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Basham D., Bavis R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Krogh A., Rutherford K., Simmonds M., Skelton J., Stevens K., White M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
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28-FEB-2003 (Rel. 41, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Minor curlin subunit precursor.
CSGB OR STY1180 OR T1777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=TY2 / ATCC 700931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21534947; PubMed=11677608;
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Enterobacteriaceae; Salmonella.
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SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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                                                                                                                                EGENNRAKVDQ--AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY
                                                                                                                                                                              E----MAHADQWNAKNSDIT-VGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                              GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ
                                                                                                                                                                                                                                                                          GSANAALALQSDARKSE-----TTITQSGYGNGADVGQ-GADNYDQL-----VTRVVTH
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28.8%;
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Typhi strains
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SEQUENCE
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Fimbria;
SIGNAL
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01-OCT-1996
01-OCT-1996
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Bacteriol, 178:662-667(1996).

-I- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DECREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE-21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman I
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-S.typhimurium; STRAIN-SR-11;
MEDLINE-98117058; PubMed-9457880;
MEDLINE-9817058; PubMed-9457880;
MEDLINE-9817058; PubMed-9457880;
MCOUTH fibers are highly conserved between Salmonella typhimurium an Escherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                                                                     EMBL; AJ002301; CAA05316.1; -.
EMBL; A2008749; AAL20073.1; -.
EMBL; U43280; AAC43598.1; -.
PIR; JC6040; JC6040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minor curlin subunit pre-
CSGB OR AGFB OR STM1143.
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Enterobacteriaceae; Salmor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fimbriae.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                 ARVRQEGSKLLSVISQ--EGGNNRAKVDQAGNYNFAYIEQTGNAN------DAS
                                                                   AAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSI YQYGSANAALALQSDARKSETT
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(Rel. 34, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                    Conservative
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; COFC5430E6DD361D CRC64;
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Matches 34
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Pfam; PF00818; Ice nucleation; 69.
PRINTS; PR00327; ICENUCLEATIN.
PR00317; ICE NUCLEATION; 49.
Ice nucleation; Repeat; Outer membrane.
DOMAIN 162 1281 OCTAPEFTID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: Ice nucleation proteins enable bacteria to crystallization in supercooled water.
-!- SUBCELLULAR LOCATION: Outer membrane (By similarity).
-!- DOMAIN: CONTAINS MANY IMPERFECT REPEATS OF THE CONSEN OCTAPEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleation activity.";
FEBS Lett. 258:297-300(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=553;
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Bacteria; Proteobacteria; Gammapro
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01-FEB-1991
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(Rel. 17, Last sequence up
(Rel. 40, Last annotation
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Pred. No. 7.1;
18; Mismatches
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SOFF

SEQUENCE

491 AA; 41979 MW;

ProDom; PD001223; PE region; 1.
Hypothetical protein; Complete
CONFLICT 312 312 G

Query Best I Matches

Local

Similarity

11.2%;

Score Pred.

Conservative

æ ~:

Mismatches 87;

45;

Indels

26;

Gaps

4

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8

Length 491;

AGVVPQWGGGGN-----HNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG

AGLIGHGGAGGNGGDGGHGGSGKAGGSGGSGGFGQFGGAGGLL-

Match

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265 75

YGNGGAAGSGGNGGD-AGTGVSSDGFAGLGGSGGRGGDAGLIGVGGGGGN YGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKUSD---ITVGQYGGN

121

264

GP63 LE: P23223;

LEIDO

STANDARD;

PRT;

590

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LEIDO

01-NOV-1991 10-OCT-2003

(Rel. 20, Created)
(Rel. 20, Last sequence update)
(Rel. 42, Last annotation update)
sin precursor (EC 3.4.24.36) (Cell
ace glycoprotein) (GP63 protein) (P

Leishmanolysin (Major surface

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                                                                                                                                                                                                                                                                   modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECISS=M.bovis; STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996
16-OCT-2001
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[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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[3]
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MEDLINE=22206494; PubMed
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10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical glycine-rich protein Rv2098c/MT2159/Mb2125c.
RV2098C OR MT2159 OR MTCY49.38C OR MB2125C.
Mycobacterium tuberculosis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YK98_MY
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Corynebacterineae; Mycobacteriaceae; Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                        SUBFAMILY.

SUBFAMILY.

CAUTION: Ref.1 sequence differs from that shown due to a CAUTION: Ref.1 sequence has been checked by frameshift in position 59. Ref.1 sequence has been checked by authors in Ref.1 and they report that no errors have been found.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS
                                                                                                                                                                       Z73966; CAA98228.1; ALT_FRAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYCTU
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I. Biochem. Parasitol. '48:173-184(1991).
FUNCTION: Has an integral role during the infection of macropha in the mammalian host.
CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl a Pl and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyr-|-Leu-Lys-Lys-|
COPACTOR: Binds 1 zinc ion per subunit (By similarity).
SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
SIMILARITY: Belongs to peptidase family M8.

9 8

infection of macrophages

glycoprotein

MEDLINE=92107220; SEQUENCE FROM N.A.

PubMed=1762629;

Leishmania donovani. Eukaryota; Euglenozo

Euglenozoa;

Kinetoplastida; Trypanosomatidae; Leishmania.

(Promastigote

surface

surface protease)

endopeptidase)

RESULT 13
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TubercuList; Rv2098c; InterPro; IPR000084; IPfam; PF00934; PE; 1.

PE_region

AE007065; AAK46440.1; BX248341; CAD96978.1; MT2159; -

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                                          This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                    "Three distinct RNAs for the surface protease gp63 expressed during development of Leishmania donovani promastigotes to an infectious form.";
J. Biol. Chem. 267:1888-1895(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=90205976; PubMed=2320059;

Miller R.A., Reed S.G., Parsons M.;

"Leishmania gp63 molecule implicated in cellular

Arg-61y-Asp sequence.";
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10-CCT-2003 (Rel. 42, Last annotation update)
10-CCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell surface prot
(Major surface glycoprotein) (GP63 protein) (Promastigote
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NCBI_TaxID=44271;
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In the mammalian host.
CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 are P1' and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.
COFACTOR: Binds 1 zinc ion per subunit (By similarity).
SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
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DT 10-OCT-2003 (Rel. 42, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DT Leishmanolysin precursor (EC 3.4.24.36) (Cell surface glycoprotein) (GP63 protein) (Protein)
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MEDLINE=91009116; PubMed=2145267;
Schneider P., Ferguson M.A.J., McConville M.J.,
Homans S.W., Bordier C.;
Homans S.W., Bordier C.;
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Pfam; PF01457; Peptidase M8; 1
PRINTS; PR00782; LSHMANOTVSI; 1
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PIR; A44951; A44951.
HSSP; P08148; 1LML.
                                                                                                                                                                                                        Button L.L., McMaster W.R.; "Molecular cloning of the major surface antigen of leishmania."; J. Exp. Med. 167:724-729(1988).
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF MEDLINE=88154764; PubMed=3346625;
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171:589-589(1990)
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SIGNAL
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PROSITE; PS00142; ZINC_PROTEASE; 1.

Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc;

Eymogen; Signal; Cell adhesion; GPT-anchor; 3D-structure; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@iab-sib.ch).
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InterPro; IPR001577; Peptidase_M8
Pfam; PF01457; Peptidase_M8; 1.
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MEDLINE=98416698; PubMed=9739094;
Schlagenhauf E., Etges R., Metcalf P.;
"The crystal structure of the Leishmania major surface proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95406217; PubMed=7675788; Schlagenhauf E., Etges R., Metcalf P.; "Crystallization and preliminary X-ray diffraction studies of "Crystallization and preliminary the metalloproteinase from Leishmania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e Leishmania major promastigote surface protease.",
Biol. Chem. 265:16955-16964(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 and P1 and basic residues at P2 and P3. A model nonapeptide is cleaved at -A1a-Tyr-|-Leu-Lys-Lys-.

COFACTOR: Binds 1 zinc ion per subunit.

SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. PTM: THE PHOSPHATIOYLINOSITOL MOIETY OF THE GPI-ANCHOR CONTAINS A FULLY SATURATED, UNBRANCHED 1-O-ALKT CHAIN (MAINIY C24:0) AND A MIXTURE OF FULLY SATURATED UNBRANCHED 2-O-ACYL CHAINS (C12:0, C14:0, C16:0, AND C18:0).

SIMILARITY: Belongs to peptidase family M8.
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      POTENTIAL.
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                                               asparagine
                                                         (POTENTIAL).
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SQ SEQUENCE 602 AA; 63953 MW; 982EF3245D87C43E CRC64;
Query Match 11.2%; Score 87; DB 1; Length 602;
Best Local Similarity 89.5%; Pred. No. 4.8;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 85 ADNYDQLVTRVVTHEMAHA 103
Db 251 ASRYDQLVTRVVTHEMAHA 269

Search completed: March 11, 2004, 18:34:57
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	vo	60	7	O	ຫ	4	w	N	1	Result No.
105	106	106.5	106.5	109	109	109.5	110	115	122	305.5	421.5	496.5	538	566.5	673	Score
13.5	13.7	13.7	13.7	14.0	14.0	14.1	14.2	14.8	15.7	39.4	54.3	64.0	69.3	73.0	86.7	Query
1422	179	3552	3501	2174	1748	502	130	139	29	76	150	152	149	150	152	Query Match Length DB
16	N	16	16	16	σ	16	16	16		N	N	. 16	Ŋ	N	N	BB
Q8EFU3	033801	Q8XSD6	90TY8Ö	Q92UU8	Q94821	Q8EIH4	Q89JI4	Q8EIH3	Q9S3J5	Q54069	Q7X237	Q8CW63	Q7X240	Q7X243	033802	ij
Q8efu3 shewanella	O33801 salmonella	Q8xsd6 ralstonia s	Q8y106 ralstonia s	Q92uu8 rhizobium m	Q94821 tetrahymena	Q8eih4 shewanella	Q89ji4 bradyrhizob	Q8eih3 shewanella	Q9s3j5 escherichia	Q54069 salmonella	Q7x237 enterobacte	Q8cw63 escherichia	Q7x240 citrobacter	Q7x243 citrobacter	O33802 salmonella	Description

ALIGNMENTS

Ş	뮹	Ş	В	8	M B Q L	SQ	Ŧ		RT	R :	R R	RA	RX	RΡ	RN	õ	ဂ္ဂ	8 6	9	B		ij	AC	IJ	RESULT
121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151	61 SDARKSETTITOSGYGNGADVGOGADNSTIELTONGFRNNATIDOMNAKNSDITVGQYGG 120	61 SDARKSETTITOSGYGNGADVGOGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120	1 MKLLKVAAFAAIVVSGSAVAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSGPDSTLSIYQYGSANAALALQ 60	Query Match 86.7%; Score 673; DB 2; Length 152; Best Local Similarity 89.4%; Pred. No. 3.7e-47; Matches 135; Conservative 3; Mismatches 13; Indels 0; Gaps 0;	E 152 AA;	NON TER 152 152	Immun. 6		Salmonella typhimurium SR-11 with mouse small intestinal epithelial	"Expression of thin aggregative fightiae promotes interaction of	Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z., Pfeifer J.D.,	MEDLINE=98053981; PubMed=9393832;	SEQUENCE FROM N.A.	[E]	NCBI TaxID=602;		Saimonella typnimurium. Bacteria: Proteobacteria: Gammaproteobacteria: Enterobacteriales:	AGPA.	Agfa protein (Fragment).	(Tremburel. 05, Last	(TrEMBLrel. 05, Created)		O33802 PRELIMINARY; PRT; 152 AA.	11 1

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RESULT 3
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Citrobacter freundii.
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                   "Zogaj X., Bokranz W., Nimtz M., Romling U.;
"Production of Cellulose and Curli Fimbriae by
Enterobacteriaceae Isolated from the Human Gast
Infect Immun. 72:4151-4158 (2003).
EMBL; AJ515701; CAD56675.1;
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EMBL; AJ515700; CAD56672.1; -.
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Bacteria; Proteobacteria;
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Jogaj X., Bokranz W., Nimtz M., Romling U.;
Jogaj X., Bokranz W., Nimtz M., Romling U.;
Jeroduction of Cellulose and Curli Fimbriae by Members of the Family
Jeroduction of Cellulose and Curli Fimbriae by Members of the Family
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                                                                                       Enterobacter sakazakii.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Enterobacter.
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MEDLINE=22388234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., S Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revaled by the complete genome of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                  NCBI_TaxID=28141;
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EMBL; AJ515702; CAD56678.1; -.
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Bacteria; Proteobacteria;
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"Non-curliation of Escherichia coli O78:K80 isolates associated IS1 inserti on in csgB and reduced persistence in poultry infect FEMS Microbiol. Lett. 175:247-253(1999).
EMBL; AJ131756; CAB45380.1; -.
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Alteromonadaceae; Shewanel
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Best Local S
Matches 39
                     Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Sott J., Beanan M., Brinkac L., Daugherty S., Medby R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vanathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Wueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanalla oneidensis."
                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel 23,
01-MAR-2003 (TrEMBLrel 23,
01-MAR-2003 (TrEMBLrel 23,
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Q89JI4;
01-JUN-2003
                                                                                                                                               MEDLINE=22297686; PubMed=12368813;
                                                                                                                                                                                                                                          Shewanella oneidensis
                                                                                                                                                                   STRAIN=MR-1;
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria;
Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                  Conserved hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003
01-JUN-2003
                                                                                                                                                                                                      NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                                     Q8EIH4;
                                                                                                                                                                                                                                                                                                                                  Q8EIH4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genomic sequence of nitrogen-fixing Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
EMBL; AP005954; BAC50564.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi N
Sasamoto M., Matsumoto M., Shimpo S., Tsuruoka H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphapro
Bradyrhizobiaceae; Bradyrhizobium.
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             Biotechnol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQW----NAKNSDITVGQYG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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AAN53941.1;
          20:1118-1123 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12699 MW;
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                                                                                                                                                                                                                                                                 protein.
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Last sequence up
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Pred. No.
                                                                                                                                                                                                                                                                                                                               PRT;
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Mismatches
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annotation update)
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., Wada T., Yan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
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RESULT 11

Q9482

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                                                                                                                                                                                                                                                           PROSITE;
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                              InterPro; IPR001878; Znf opfam; PF00098; zf-CCHC; 7 PRINTS; PR00939; CZHCZNFII SMART; SM00343; ZnF CZHC;
                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                "Retroviral-type zinc fingers and glycine-rich repeats encoded by cnjB, a Tetrahymena gene active during meios Nucleic Acids Res. 21:4610-4614(1993).
EMBL; X06462; CAB37323.1; -.
EMBL; L03710; AAC37171.1; -.
EMBC; D13710; AAC37171.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=88189811; PubMed=3357771;
Martindale D.W., Taylor F.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q94821; P92146; P92145;
01-FEB-1997 (TrEMBLrel.
01-FEB-1997 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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Hypothetical
SEQUENCE 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Faylor F.M., Martindale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thermophila."
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          1686
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GO:0003676; F:nucleic
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                                                                                                                                                                                 Similarity
      QTGGGWGSNDNQQQ
                                     GADVGQGA-DNYDQLVTRVVTHEMAHADQWNAKNSDITVGQ--YGGNNAA
                                                                                                                 QWGGGGNHNGG----GNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT----QSGYGN
                                                                                  QFGGGGNSNGGQSWGTSSGSDWN-----
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                                                                                                                                                              Conservative
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502 AA; 52441 MW;
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45; P92144; P92143; P
1. 02; Created)
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- QNENTGGGGWGSSNSNQTNNESSWGSNNQA
                                                                                                                                                          Pred. No. 3.9
1; Mismatches
                                                                                                                                                                             Score 109;
Pred. No. 3
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Pred. No. 0.79;
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P92142;
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Q8Y100
ID Q8Y10
AC Q8Y10
DT 01-MA
DT 01-MA
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CO RSC08
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CO Bacte
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R Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,

R Finan T.M., Weidner S., Wong K., Buhrmester J., Cowie A., Go

N Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Go

Golding B., Puehler A.;

"The complete sequence of the 1,683-kb pSymB megaplasmid fro

fixing endosymbiont Sinorhizobium mellioti.";

Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).

R EMBL; AL603645; CAC49389.1; -.

R GO; GO:0004601; P:peroxidase activity; IEA.

GO; GO:0004601; P:peroxidase activity; IEA.

GO; GO:0004601; P:peroxidase activity; IEA.
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Best Local Similarity
Matches 40; Conserv
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Q92UU8;
Q92UU8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Probable hemagglutinin-related protein.
RSC0887 OR RSO6116.
Ralstonia solanacearum (Pseudomonas solanacearum)
Bacteria; Proteobacteria; Betaproteobacteria; Bur
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InterPro; IPR002016; Peroxidase.
InterPro; IPR002016; Peroxidase.
InterPro; IPR002173; pfkB.

pfam; PF03797; Autotransporter; 1.
pR00517E; PS00435; PEROXIDASE 1; 1.
pR00517E; PS00583; PFKB KINASES 1; 2.
plasmid; Hypothetical protein; Complete proteome.
plasmid; Hypothetical protein; Complete proteome.
plasmid; Hypothetical protein; Complete proteome.
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RB0989 OR SWB21548.

Rhizobium meliloti (Sinorhizobium meliloti).

Plasmid pSymB (megaplasmid 2).

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                         Q8Y106
   STRAIN=GMI1000;
                                SEQUENCE FROM N.A.
                                                                                                                    Burkholderiaceae; Ralstonia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQYGGNNAA--LVNQTASDSSVMVRQVG
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                                                                                                                                                                                                                                                                                                                                                                                                         3501
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                                                                                                                                                       Burkholderiales;
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RESULT 14
QRXSD6
ID QRXSD
AC QRXSD
AC QRXSD
DT 01-MA
DT 01-OC
DE Proba
GN RSP05
OS Ralat
OC Bacte
OC Bacte
CC Burkt
RA [1]
RA [2]
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Best Local S
Matches 43
                       A Salamoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., A Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., A Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., A Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., A Siguier P., Thebault P., Whalen M., Wincker P., Levy M., A Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; L Nature 415:497-502(2002).

T. MEMBL, AL646079; CAD17691.1; -. R EMBL, AL646079; CAD17691.1; -. R GO; GO:0004519; F:endonuclease activity; IEA. GO; GO:0004519; F:endonuclease activity; IEA. R GO; GO:0003676; F:nucleic acid binding; IEA. R InterPro; IPR001804; Endonuclease. R InterPro; IPR001804; Endonuclease. R InterPro; IPR008619; Fil_haemagg. R InterPro; IPR00838; Haemagg; 20.
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QBXSD6; (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable hemagglutninn-related protein.
RSP0540 OR RS06117.
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Plasmid megaplasmid.
Bacteria, Proteobacteria; Betaproteobacteria; Bur
Burkholderiaceae; Ralstonia.
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Pfam; PF05860; Haemagg_act; 1.
PROSITE; PS01070; NUCLEASE_NON_SPEC;
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Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Arlat M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.
Chandler M., Choisne N., Claudel-Renard C., Scarin W., Schiex T.,
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
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EMBL; AL646061; CAD14589:1; -.
GO; GO:0004519; F:endonuclease
GO; GO:0003676; F:nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-GMI1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGSALAGVVPQWGGGGNHNGGG-NSSGPDSTLSIYQYGSANAA---
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29.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Betaproteobacteria; Burkholderiales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 106.5;
Pred. No. 14;
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RESULT 15
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Best Local S
Matches 43
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Plasmid;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cells.";
Infect. Immun. 65:5320-5325(1997).
EMBL; AJ000514; CAA04150.1; -.
SEQUENCE 179 AA; 19318 MW; A2BCCB648B3C0B0B CRC64;
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MEDLINE=98053981; PubMed=9393832;

Sukupolvi S.S., Lorentz R.G., Gordon J.I.,

Normark S.J., Rhen M.;

"Expression of thin, aggregative fimbriae p
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Salmonella.
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01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=602;
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                                                                                                                                                                                    133 SSVMVRQ 139
                                                                                                                                                                                                                                                  122 KGSGNKANITO----YGTQKTAVVVQKQSHM----AIQANIT--QYGTQKTAVVVQKQSH 171
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13.7%; Score 106.5;
Similarity 29.5%; Pred. No. 15;
43; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                      SGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALVNQTASD 132
                                                                                                                                                                                                                                                                                                                                                           MAIRVTO 178
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Complete proteome.
3552 AA; 352934 MW; C5432AABE2CCF59C CRC64;
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Result
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Maximum Match 10
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Perfect score:
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length: 2000000000
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                                                                                                                                                                                                                                                                     Match
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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
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The present invention describes a recombinant agfA gené (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene

homologous

native

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epicope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal

Disclosure; Page 138; 139pp; English.

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RESULT 2
AAB36347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for cellciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are usually strong against the inserted epitope, and hybrid fimbriae are easy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                  N-PSDB; AAC64623.
                                                                                                                        WPI; 2000-672631/65
                                                                                                                                                                   White AP, Doran JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
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Disclosure;

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English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC copy of that gene, and (4) eliciting an immune response in an animal.

CC comprising separating an amino acid polymer comprising a recombinant AgfA

CC protein containing a replacement segment or segments of foreign amino

CC acid sequence or sequences grown on a Salmonella, E. coli or

CC Enterobacteriaceae host cell, from the host cell and introducing the

CC polymer into the animal in conjunction with a carrier or diluent. (I) is

CC useful for the expression of recombinant AgfA protein which is useful for

CC eliciting an immune response in an animal. In a fimbrial presentation

CC 500,000 copies/cell), the hybrid fimbrin protein possesses both the

CC immunogenicity and adhesion properties relevant for an efficient live

CC vaccine, the carrier fimbrial subunit proteins are usually strong

CC immunogens, which may be important for directing an immune response

CC against the inserted epitope, and hybrid fimbriae are easy and

CC inexpensive to purify in large amount. The present sequence is given in

CC the exemplification of the present invention
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Matches
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                                                                                                                                                                                                           Salmonella enteritidis.
Escherichia coli.
                                    05-APR-1999;
                                                                        05-APR-2000; 2000WO-CA000356
                                                                                                                                                     WO200060102-A2
                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                  vaccine; immune response;
                                                                                                                                                                                                                                                                                      Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         AAB36355;
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36355 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                            AgfA::PT3#10 amino acid sequence SEQ ID NO:30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    back into the chromosome of the homologous species, replacing the native
(UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVTRVVTHEMAHA-----SVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                    99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 151
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Pred. No. 1.8e-62;
0; Mismatches 0
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ARESULT 4
AAR74625
ID AAR7
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Saln
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Best Local Similarity
Matches 143; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEFI7/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CSgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                       Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acid sequence or sequences grown on a Salmonella, B. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the
                                                       Salmonella; AgfA; vaccine
                                                                                                     AgfA sequence
                                                                                                                                           25-MAR-2003
26-JUN-1995
                                                                                                                                                                                                          AAR74625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       White AP,
                                                                                                                                                                                                                                              AAR74625 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNAT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                              protein; 151
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Pred. No. 4.2e-61;
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RESULT 5
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  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunization compositions, respectively, to elicit an immune response Salmonella in animals (e.g. food producing animals) and humans. (Updat on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
WPI; 2000-672631/65
                                                                                     05-APR-2000; 2000WO-CA000356
                                                                                                                               WO200060102-A2
                                                                                                                                                    Salmonella enteritidis.
                                                                                                                                                                          Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
                                                                                                                                                                                                          Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
                                                                                                                                                                                                                               26-FEB-2001
                                                                                                                                                                                                                                                     AAB36341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 151
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                     White AP,
                                                                 05-APR-1999;
                                                                                                                                                                                                                                                                          AAB36341 standard; protein; 151 AA
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                                                                                                           12-OCT-2000
                                           (UYVI-) UNIV VICTORIA
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                                                                                                                                                                                                                                                                                                                                                                                        SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT
                     Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                               (first entry)
                                                               99US-0127888P
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                      Collison SK,
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Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEV
                      Kay WW;
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(Updated
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RESULT 6
AAW23570
ID AAW2
XX AAW2
AC AAW2
AC AAW2
XY 25-M
DT 29-S
XY 29-S
XX Ente
XX Ente
XX Salm
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XX Salm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                            Misc-difference
                                                                                                         Salmonella
                                                                                                                                               Enteropathogenic bacteria;
                                                                                                                                                                                            Salmonella
                                                                                                                                                                                                                                      25-MAR-2003
29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escharichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                         AAW23570 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the argument of the present sequence is given.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                         enteritidis
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                                                                                                                                                                                                                                  (revised)
(first entry)
                                        Location/Qualifiers
                 /note= "Encoded by GCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.0%;
                                                                                                                                               enterobacteria; S.enteritidis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2:
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Pred. No. 4.1e-60;
2; Mismatches 11
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                                                                                                                                               antibody
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
             05-APR-2000; 2000WO-CA000356
                                                                                                               Salmonella enteritidis.
                                                                                                                                       vaccine; immune response;
                                                                                                                                                   Salmonella; agfA; chromosomal gene replacement;
                                                                                                                                                                                                                                                      AAB36346 standard;
                                      12-OCT-2000
                                                               WO200060102-A2
                                                                                                                                                                                                     26-FEB-2001
                                                                                                                                                                                                                              AAB36346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                  Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enteropathogenic bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYVI-) UNIV VICTORIA INNOVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-APR-1993;
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                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                    121 NNPALVNOTASDSSVMVROVGFGNNATANOY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138;
                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                     Н
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                           HEMAHANOTASDSSVMVROVGFGNNATANOY
                                                                                                                                                                                                                                                                                                                                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT
                                                                                                                                                                                                                                                                                                                                                                    SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 7; 85pp; English
                                                                                                                                                                          amino acid sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-00233788
                                                                                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.4%;
                                                                                                                                       immunogen
                                                                                                                                                                                                                                                      151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 689; DB
Pred. No. 5.2e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                      A
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                                                                                                                                                                                                                                                                                                                                            151
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                                                                                                                                                                                                                                                                                                                    151
                                                                                                                                                    fimbrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 151;
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                                                                                                                                                    epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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ARBSULT 8
AAB36353
ID AAB3
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AC AAB3
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DT 26-F
XX
DE AgfA
XX
KW Salm
KW Vacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC directing recombination of a recombinant gene into the chromosome of the Chomologous species; (3) directing recombination of a recombinant gene combination of a recombinant gene combination of a recombinant gene combination of the homologous species, replacing the native composition of that gene; and (4) eliciting an immune response in an animal, compositing separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino ccid sequence or sequences grown on a Salmonella, E. coli or containing a replacement segment or segments of foreign amino ccid golymer into the animal in conjunction with a carrier or diluent. (1) is ccid sequence animal in conjunction with a carrier or diluent. (1) is ccid useful for the expression of recombinant AgfA protein which is useful for celiciting an immune response in an animal. In a fimbrial presentation conjunction with a carrier or diluent (1) is ccid useful for the heterologous antigens are presented in high numbers (up to CC oppose) (cell), the hybrid fimbria protein possesses both the carrier fimbrial subunit proteins are usually strong communogens, which may be important for directing an immune response consists the inserted epitope, and hybrid fimbriae are easy and consists the inserted epitope, and hybrid fimbriae are given in the community of the present segments is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                   Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                           AgfA::PT3#8 amino acid sequence SEQ ID NO:26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 151 AA,
                                                                                                       26-FEB-2001
                                                                                                                                                                                       AAB36353 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 135; 139pp; English
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                                                                                                                                                                                                                                                                                                 121
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                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKLLKVAAFAAIVVSGSALAGVVFQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                 NNAALVNYDQLVTRVVTHEMAHA-----
                                                                                                                                                                                                                                                                                                                                       -----NYDQLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Doran JL,
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                                                                                                     (first entry)
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response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      describes a recombinant agfA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Collison
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replaced by a segment of a join enitors or a recommendations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 655;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3;
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                                                                                                                                                                                                                                                                                                                                       directing recombination of a recombinant gene into the chromosome of the chomologous species; (3) directing recombinant gene of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal. CC comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to $10,000 copies/cell), the hybrid fimbrin protein possesses both the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for a fimbrial an immune response
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                     Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 138; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                               the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                    immunogens, which may be important for directing an immune res
against the inserted epitope, and hybrid fimbriae are easy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200060102-A2
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                                                                                                                                                                                                                                                                                                                                                                                                   nexpensive to purify in large amount. The present sequence is given in
121
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                                                                               61
                                                                                                                         61
                                                                                                                                                                                                           _
                                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                     HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                        SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
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                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                     AA;
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                                                                                                                                                                                                                                                                                                                                                                                 얁'
                                                                                                                                                                                                                                                                       78.6%;
82.1%;
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                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                             present
                                                                                                                                                                                                                                                                     Score 609; DB 3;
Pred. No. 4.2e-52;
                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                               invention
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                                                                                                                                                                                                                                                     Indels
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AAB36351
ID AAB3
                                                                                                                                                                                      CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)

CC directing recombination of a recombinant gene into the chromosome of the CC homologous species; (3) directing recombination of a recombinant gene

CC back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal,

CC comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid golymer comprising a recombinant AgfA conditions of sequence grown on a Salmonella, E. coli or compose in a salmonella, E. coli or conjumer into the animal in conjunction with a carrier or diluent. (I) is cusful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to compose) cell), the hybrid fimbrin protein possesses both the carrier fimbrial subunit protein possesses both the carrier fimbrial subunit proteins are usually strong conjunction which are usually strong conjunction the inserted epitope, and hybrid fimbrine are easy and conversed the inserted epitope, and hybrid fimbriae are easy and conversed to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant agfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the
                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 137; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein useful for eliciting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AgfA::PT3#6 amino acid sequence SEQ ID
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                               MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSI YQYGSANAALALQ
MKLLKVAAFAAI VVSGSALAGVVPQWGGGGGNHNGGGNSSGPDSTLSI YQYGSANAALALQ
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73.6%;
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       directing recombination of a recombinant gene into the chromosome of the chomologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein seems both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response
                                                                                                                                                                                                                                                                                                                                The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEFIT/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which encodes foreign epitope or antigen, protein useful for eliciting immune respo
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Matches 124
The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Collison
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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RESULT 12
AAB36354
ID AAB36354
XX AAB36
AC AAB36
XX AGA
AC AAB36
XX Salmc
KW Vacci
XX Salmc
OS Esche
OS Synth
XX WO200
XX U0200
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Best Local S
Matches 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-2000; 2000WO-CA000356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AgfA::PT3#9 amino acid sequence SEQ ID NO:28
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                                                                                                                                                                                                                                                                                                                                                         Doran JL,
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Pred. No. 8.2e-52;
5; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                               SK,
                                                                                                                                                                                                                                                                                                                                                         Kay
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The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign D sequence which encodes a foreign epitope or antigen. Also describe

described

Disclosure; Page 138; 139pp; English.

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

AAC64630.

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RESULT 13
AAB36348
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CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene cc back into the chromosome of the homologous species, replacing the native cc copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or coll sequence or sequences grown on a Salmonella, E. coli or collymer into the animal in conjunction with a carrier or diluent. (I) is cuseful for the expression of recombinant AgfA protein which is useful for celiciting an immune response in an animal. In a fimbrial presentation cc system the heterologous antigens are presented in high numbers (up to collow the carrier fimbrial subunit protein possesses both the cimmunogenicity and adhesion properties relevant for an efficient live creatine, the carrier fimbrial subunit proteins are usually strong communogens, which may be important for directing an immune response consists the inserted epitope, and hybrid fimbriae are easy and consists the inserted epitope, and hybrid fimbriae are easy and consists the order of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
WPI; 2000-672631/65
                                         White AP,
                                                                                                                               05-APR-1999;
                                                                                                                                                                    05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                    12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                 Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                        Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
                                                                                    (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                             WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AgfA::PT3#3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB36348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB36348 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                               Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 AA;
                                      Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino
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                                                                                                                             99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid sequence SEQ ID
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81.5%;
                                         Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 600; DB Pred. No. 3.2e-3; Mismatches
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                                      SK,
                                         Kay WW;
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.2e-51;
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Sequence 151

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CC Sequent of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended (CC assembly system of strains of Salmonella, Bscherichia coli and CC Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) clirecting recombination of a recombination of a recombination of the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene into the chromosome of the chromosome of the homologous species; (a) directing an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or containing an immune response in an animal. In a fimbrial presentation for extern the host cell and introducing the sequence of the expression of recombinant AgfA protein which is useful for extern the host cell and introducing the security of the sequence of the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for extern the heterologous and animal. In a fimbrial presentation
                                                                                      system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in inexpensive to purify in large amount.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 136; 139pp; English.
                                                                  exemplification
                                                           of the present invention
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Matches
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                   121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                       1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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NNAALVNOTASDSSVMVROVGFGNNATANOY
                                                                 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
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81.5%;
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Pred. No. 9.5e-49;
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AC XXX DT

Escherichia coli CsgA amino acid sequence SEQ ID NO:7.

26-FEB-2001 (first entry)

Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen

Escherichia coli.

WO200060102-A2

12-OCT-2000

05-APR-2000; 2000WO-CA000356

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AgfA, CegA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinate gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for celiciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and context of the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 151 AA;
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                    E. coli CsgA subunit 15 kDa protein.
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                                                           04-DEC-2003
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                                                                                                                                                                                                                                        GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                                                                                                                                                                                                    TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
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                                                           (first entry)
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70.2%;
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Search completed: March Job time: 45.9 secs

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2004, 18:33:44

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Query Match
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Matches 105
                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a ma selected from sequences shown in ABR82642, ABR82648-49. The peptide antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmon or Shigella infection. The peptide that is immobilized on a solid su is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated peptide capable of binding a mammalian plasma prouseful in the manufacture of a medicament for the prevention treatment of a bacterial infection, such as Escherichia coli, or Shigella infections.
                                                                                                                                                                                                                                                                                                                                                                            Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 41-42; 42pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2002; 2002GB-00002275
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                                       HEMAHANQTASDSSVMVRQVGFGNNATANQY
GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
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                                                                                             TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
                                                                                                                                                                                           MKLLKVEAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
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Pred. No. 4.2e-44;
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Maximum Match 100%
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 59, Appl
Sequence 8, Appli
Sequence 8, Appli
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Sequence 2, Appli
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	34, App	71, App	4, Appl:	4, Appli	4, Appli	4, Appli	4, Appl:	4, Appl:	4, Appl:	5005, Ap	73, App	6, Appl	6, Appl	6, Appl	41, App.	42, App.	7973, A	

ALIGNMENTS

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RESULT 1
US-08-233-788A-59
                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200.
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 622-4900
TELEPAX: (206) 682-6031
TELEPAX: 723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 59, Application Patent No. 5635617
GENERAL INFORMATION:
Query Match
Best Local Similarity
Matches 138; Conserv
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.

ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
CCLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
NUMBER OF SEQUENCES: 61
                                                                                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center,
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STREET: 6300 Columl
CITY: Seattle
STATE: Washington
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RESULT 3
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US-08-233-788A-57
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Sequence 8, Application US/09196387 Patent No. 6277613 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                             Matches
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 3723836 SEEDANBERRY INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: lin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (200)
TELEFAX: 3723836 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 26-APR CLASSIFICATION: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: King, Joshua
REGISTRATION NUMBER: 35,570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                      61
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                                                                                                                                                                                                      22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
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                                                                                                                                                                                                                                                             99;
                                                                                                                                          GQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seattle
                                                                                                                GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 112
                                                                                                                                                                                  VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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Collinson, Karen S.
Clouthier, Sharon C:
Clouthier, Sharon C:
TVENTION: TO ATT MONELLA
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William W.
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US-09-841-835-8
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Best Local (
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APPLICANT: de Lan
APPLICANT: Smith,
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INFORMATION FOR SEQ ID NO:
                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                           TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS TITLE OF INVENTION: OF USE THEREOF NUMBER OF SEQUENCES: 12
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Klauber & Jackson
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       CITY: Hackensack
STATE: New Jersey
                                           STREET:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Similarity 28.4%;
42; Conservative 10
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Smith, Su
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Pred. No. 1.1;
16; Mismatches
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                                         4th Floor
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Length 673; Indels

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Best Local Similarity
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
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LENGTH: 673 amino acids
TYPE: amino acid
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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APPLICANT: Smith, Susan
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CLASSIFICATION:
IOR APPLICATION DATA:
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28.4%; Pred. No. 1.1;
ative 16; Mismatches
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Patent No. 6506587
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME: Jackson Esq., David A.
REGISTRATION UNDEER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
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CORRESPONDENCE ADDRESS:
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LENGTH: 949 amino acids
TYPE: amino acid
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APPLICANT: Smith, Susan
                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
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Local Similarity 28.4%;
les 42; Conservative 16
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SEQ ID NO:
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Pred. No. 1.8;
16; Mismatches
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; MOLECULE TYPE:
; HYPOTHETICAL:
US-09-196-387-2
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US-09-196-387-2
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Best Local Similarity
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                                                                                                                                                         TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/0
FILING DATE: June 10, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
TYPE: amino acid
TOPOLOGY: linear
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APPLICANT: Smith, Susan
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                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                            NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600
                                                                                                 TOPOLOGY:
                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/196,387 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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5. 6277613
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90.5;
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               DB 3;
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                Length 1327;
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US-09-841-835-2
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US-09-841-835-2
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                                                                                                                           Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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LENGTH: 1327 amino acids
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APPLICATION NUMBER:
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ADDRESSEE: Klauber & Jackson
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                                                                                                                                                                                                                                                                                                                                                        NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sin
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STATE: New Jerse
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158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG------DVSRVKRLVDA--- 204
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                       65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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                                                     VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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Smith, Susan
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28.4%;
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Pred. No. 2.8;
                                                                                                              Mismatches
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US-09-972-115A-8
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GENERAL INFORMATION:
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Best Local :
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SEQ ID NO 8
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APPLICANT: Walter, Funk D.
APPLICANT: Mieczyslaw, Piatyszek A.
TITLS OF INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/003C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Geron Corporation APPLICANT: Gregg, Morin B.
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ORGANISM: Homo sapiens
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                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.
COMPUTER: IBM COmpatible
COMPUTER: OFFERM. MICHORY
                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Word Perfect 6.1
URRENT APPLICATION DATA:
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                                                                                                                                   ZIP: 514-01
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42; Conserv
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                                                                                                                                                                                                                                                                                VENTION: NAKASHIMA et al.

VENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
VENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
VENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
VENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
VENTION: TO SAID POLYPEPTIDE
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                                                                                    3.50 inch,
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; Pred. No. 2.8;
16; Mismatches
                                                                                      1.44 MB storage
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US-09-198-452A-171
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                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 171
LENGTH: 1156
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 171, Application US/09198452A Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffais, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 35.4
29; Conservative
                                                                                                                                Matches
                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment-
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
TITLE OF INVENTION: and treatment of infection
                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/198,452A CURRENT FILING DATE: 1998-11-24
                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 9710-003-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 15-July-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: May 28, PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: F-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: peptide
LOCATION: from 1 to 738
IDENTIFICATION METHOD: 1
                                                                                                                                               Local Similarity
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916
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                                                                                                                              32;
                           95 NGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDSS 134
                                                                                             44 TLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTI------ELTQ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 ARKSETTITQSGYGNGADVGQG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                TVSPEDYAAVQAALA--AYVRKHESLIV-STYGLGAQEGQTSSKVTTLMRDLHAVEELVE
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                                                                                                                                Conservative
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VETYRLNRSDQILHRV--HSVLHSHLRDSDSS 947
                                                                                                                                             11.2%; Score 87; 32.0%; Pred. No.
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Pred. No. 1
                                                                                                                                Mismatches
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126 ANOTASDSSVMVRQVGFGNN 145

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US-09-336-447A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Moraxella catarrhalis
US-09-336-447A-15
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CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
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LENGTH: 339
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15, Application US/09336447A Patent No. 6310190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HANSEN, APPLICANT: AEBI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 889
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                                                                                                                                         69
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                                                               80 DVGQG-----ADNSTIELTQNGFRN----NATID---QWNAKNYDQLVTRVVTHEMAH 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQ----
                                                                                                                                                                                                                                                                                      39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 KVAAFAAIVVSGSALAGVVPQWGG------GGNHNGGGNSSGPDSTLSIYQYGSANAAL 57
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34; Conserv
FVGGGYKNLAEGDNATI---AGGFANLAEGDNATIAGGFENRAEGIDSVVSG-----GY 179
                                                                                                                                                                                                        GGGNHNGGGNSSGPDSTLSIYO---YGSANAALALQSDARKSETTITQSGY-----GNGA 79
                                                                                                                                     GAGRHNNVGGSAHHSGILGGWKNTVNGYTSAIVGGYGNETQGDYTFVGGGYKNLAKGNYT 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEBI, CHRISTOPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COPE, LESLIE D.
                                                                                                                                                                                                                                                                                      Conservative
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1998-02-18
1998-02-18
UMBER: US 60/094,190
1998-07-27
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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21.5%; Pred. No. 1.8;
tive 32; Mismatches
                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                           Score 83; DB 4;
Pred. No. 8.9;
6; Mismatches 5
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RESULT 15
US-08-541-780-2
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GENERAL INFORMATION:
APPLICANT: Quax, Wisset,
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US-07-731-157A-2
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Sequence 2, Application US/08541780 Patent No. 5935831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/07731157A Patent No. 5457032
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 720 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION.
NAME: RAE-VENTER PH.D.,
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/731,1
FILING DATE: 19910509
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90200962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Mutated beta-lactam acylase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONTWARE: PATENTIN POLOCAL SOFTWARE: PATENTIN PO
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                                                                                                                                                                                                                                                                   90 IELTQNGFRNNATIDQWNAK-----NYDQLVTRVVTHEMAHANQTASDSSVMVRQV 140
                                                                                                                                                                                                                                                                                                                                    58 HIYGVDAPSAFYGYGWAQARSQGDNILRLYGEAR----
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                                                                                                                                                                                                      VWLLTNGVPERA---QOWYAQQSPDFRANLDAFAAGI----NAYAQQNPDDISPDVRQV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRVLHRAASALVMATVIGLAPAVAFALAEPTSTPQAPIAAYKPRSNEILWDG----YGVP
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Pred. No. 9
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GENERAL INFORMATION:

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Search completed: March 11, 2004, 18:44:53 Job time: 13.4 secs
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Best Local Similarity 25.8%; Pred. No. 9.5;
Matches 46; Conservative 17; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/731,157
FILING DATE:
APPLICATION NUMBER: EP 90200962
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER PH.D., BARBARA
REFERENCE/DOCKET NUMBER: 32,750
REFERENCE/DOCKET NUMBER: GBRO-027/0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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LENGTH: 720 amino acids
TYPE: amino acid
TOPOLOGY: linear
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Van der Laan, Jan M.
APPLICANT: Lenting, Herman B.M.
TITLE OF INVENTION: Mutated beta-lactam acylase genes
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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STATE: CALIFORNIA
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                                                                                                                                               90 IELTQNGFRNNATIDQWNAK-----NYDQLVTRVVTHEMAHANQTASDSSVMVRQV 140
                                                                                                                                                                                                   58 HIYGVDAPSAFYGYGWAQARSQGDNILRLYGEAR--
                                                                                                                                                                                                                                               37 NSSGPDSTLSIYQYGSANA-----ALALQSDARKSETTITQSGYGNGADV-GQGADNST 89
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Beq
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1: /cgn2_6/prodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:*

6: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/prodata/1/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/prodata/1/pubpaa/US09A_PUBCOMB.pep:*

11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep:*

13: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep:*

14: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep:*

15: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep:*

16: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*

17: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*

18: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*

19: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*

16: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*

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              9 US-09-841-335-8

9 US-09-841-835-10

9 US-09-841-835-2

10 US-09-972-115A-8

14 US-10-199-937-4

14 US-10-156-761-9343

15 US-10-156-761-8763

16 US-10-156-761-11721

10 US-09-880-748-1165

10 US-09-880-748-1165

10 US-10-156-761-13168
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US-10-032-585-7876
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Compugen Ltd
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            Sequence 20638, A
Sequence 7876, Ap
Sequence 8, Appli
Sequence 10, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 9343, Ap
Sequence 171, Ap
Sequence 171, Ap
Sequence 11721, A
Sequence 1136, Ap
Sequence 1165, Ap
Sequence 1165, Ap
Sequence 1165, Ap
                                                                                                                                                                                                                                                                                                                              Description
Sequence
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ALIGNMENTS

RESULT 1 US-10-369-493-20638

GENERAL INFORMATION:

Sequence 20638, Application US/10369493 Publication No. US20030233675A1

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APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20638
LENGTH: 445
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                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                  Matches
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Rhodopseudomonas palustris
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(445)
OTHER INFORMATION: unsure at all Xaa locations
19
                                                                                                                                             42;
                                                                                                        7 AAFAA-----IVVSGSALAGVVPQWGGGG-----NHNGG-----GNSSGPDSTLSIYQY
                                                                                                                                                                     Similarity
                                                             AAFAADSNTVYLNQTGNDQQANITQSGNGNSVGAFNGNSGFLQENGTLSGA-NLLTVKQS
                                                                                                                                               Conservative
                                                                                                                                               14.3%; Score 111; DB 15; Length 445; 25.5%; Pred. No. 0.006; ive 25; Mismatches 68; Indels 3
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61; Indels 29; Length 673;

Gaps

DVSRVKRLVDA--- 204

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; TYPE: PRT; ORGANISM: Candida albicans US-10-032-585-7876
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US-10-032-585-7876
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TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Terry,
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                        TILE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS TILE OF INVENTION: OF USE THEREOF UMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8, Application US/09841835
> US20020076795A1
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28; Conserv
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Charles, F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith,
                                                                                                                                                                                                                                                                                                                  USA
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Smith, Susan
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                                                                             09/196,387
                                                                                                                                                          US/09/841,835
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                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 949 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 09/196,387
                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/841,83:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS TITLE OF INVENTION: OF USE THEREOF NUMBER OF SEQUENCES: 12
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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                                                                                                                 TELEPHONE: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Hackensack
STATE: New Jersey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 201-487-58
TELEFAX: 201-343-1684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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Smith, Susan
                                                                                                                                                  201-487-5800
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Pred. No. 1
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                                                                   Matches
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Patent No. US20020076795A1
                                                                                                     Query Match
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Best Local !
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APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
                                                                                                                                                                                                                                     TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
                                                                                                                                                      TOPOLOGY: 11
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy COMPUTER: IBM PC com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                     Local Similarity
                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                TELEPHONE: 201-487-58
TELEFAX: 201-343-1684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Hackensack
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 VAAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEÄA 157
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                                  6 VAAFAAI-VVSGSALAGVVPQWGGGGHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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28.4%; Pred. No. 1.9;
                                                                                     11.7%;
28.4%;
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                                                                 ; Score 90.5; Di
; Pred. No. 2.9;
16; Mismatches
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US-09-972-115A-8
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                                                                                                                                                                                                                                                   Sequence 4, Application US/1019937
Publication No. US20030190739A1
GENERAL INFORMATION:
APPLICANT: Christenson, Erik
APPLICANT: DeMaggio, Anthony J.
APPLICANT: Goldman, Phyllis S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 8
SEQ TH: 1327
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SOFTWARE: PatentIn Ver. SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                    FILE REFERENCE: 27866/36559
CURRENT APPLICATION NUMBER: US/10/199,937
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/606,035
PRIOR FILING DATE: 2000-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Geron Corporation
APPLICANT: Gregg, Morin B.
APPLICANT: Walter, Funk D.
APPLICANT: Mieczyslaw, Piatyszek A.
                                          PRIOR APPLICATION NUMBER: 60/141,582
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 178
                                                                                                                                                                                                           APPLICANT: DeMaggio, Anthony J.
APPLICANT: Goldman, Phyllis S.
APPLICANT: McElligott, David L.
APPLICANT: McElligott, David L.
TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: A Second Mammalian Telomerase FILE REPERENCE: 080/003C CURRENT APPLICATION NUMBER: US/09/972,115A CURRENT FILING DATE: 2001-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/128,577 PRIOR FILING DATE: 2000-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9343
TEXESTATE: 438
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US-10-289-762-171
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Sequence 171, Application US/10289762
Publication No. US20040006218A1
GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragritte of INVENTION: thereof and uses thereof, in particular for the diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Best Local :
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 249-262
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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Local Similarity 28.4%; Pred. No. 2.9;
1es 42; Conservative 16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                               KKVLQPELDKFEEQTGIKVKLEVVPWSDLLNRILTATTSGQGPDVLNIGNTWSASLQATG
                                                                                                                                                                                                                                                                                                                                      MRSIRAAAVGAVTMSLALAASAC----GGSSTGGGSNDSP-KTLT-YWASNQGASIAVD
                                                                                                                                                                                                                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALA--
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            11.4%; Score 88.5; DI 24.6%; Pred. No. 1.1; tive 23; Mismatches
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 RESULT 11
US-10-156-761-11721
; Sequence 11721, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
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GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: HATTORI, WASAHIRA

IITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2001-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109
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CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 171
LENGTH: 1156
                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8763, Application US/10156761 Publication No. US20030119018A1
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                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 482
                                                                                                                                                                                                                                                              Match 11.1%; Score 86; DB Local Similarity 30.2%; Pred. No. 2.3; es 38; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
358
                                       126 ANOTAS 131
                                                                                      307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 916 MG-----VETYRLNRSDOILHRV--HSVLHSHLRDSDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     859 TVSPEDYAAVQAALA--AYVRKHESLIV-STYGLGAQEGQTSSKVTTLMRDLHAVEELVE
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                                                                                                                                                                                                                    8 AFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 11.2%; Score 87; DB Similarity 32.0%; Pred. No. 5.5;
SARTGS
                                                                                    -TEWLVGASSGGDDGGGGGTCTAAQLLGNNGFESGAT--TWTAS-----SDVITNSSGE 357
                                                                                                                              TTITQSGYGNGADVGQGADNSTIE--LTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAH 125
                                                                                                                                                                          AFFATSTFGS---GRVAFWGDSSPIDDGTGQSGNTLYDGWNDTGATNAALALNA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
363
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                                                                                                                                                                                                                                                                                                          DB 14; Length 482;
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                                                                                                                                                                                                                                                                   58;
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106 ATTGALDMWGRGTLVTVSSGGGGGGGGGGGGGG---

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                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-880-748-1136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Streptomyces avermitilis US-10-156-761-11721
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIKA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                               SOFTWARE: PatentIn Ver.
SEQ ID NO 1136
LENGTH: 254
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SEQ ID NO 11721
                                                                Matches
                                                                                    Query Match 10.8%;
Best Local Similarity 24.5%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: PF523
                                                                                                                                                                                              LENGTH: 29
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/293,499
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/277,379 FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 SGSAPSGGRADPGRAHGGSPTPSVSSGGGGGGGGGGGTSTGGSATL-----GGPÄALSV 176
18 ALAGVVPQWG------GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSE- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 -- GFRNNAT ---- IDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 QSDARKS-----ETTITQSGYGNGAD------VGQ-GADNSTIELTQN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 SGSALAG------VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STPVREASDKRWCEKVTVSFHNTGGGAARSGTVTFGTHIIGALGIDWATIESTEDLPVPI 236
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HORIKAWA, HIROSHI
                                                                  Conservative
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; Pred. No. 1.2;
18; Mismatches
                                                           ; Score 84; DB 10; Length 254; pred. No. 1.6; 1); Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
                                                                61; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISTEAMA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILLING DATE: 2002-05-29
CURRENT FILLING DATE: 2002-05-29
CURRENT FILLING DATE: 2002-05-29
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                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
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US-09-880-748-1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/21,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
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NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1165
LENGTH: 254
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APPLICANT: Ruben et al.
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            Sequence 13168, Application US/10156761 Publication No. US20030119018A1
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PRIOR APPLICATION NUMBER: 60/293,499
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PRIOR APPLICATION NUMBER: JP 2001-204085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 10.8%; Score 84; DB Local Similarity 24.5%; Pred. No. 1.6; Pes 37; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 QTITISCTGSDSNIGAGYDVHWYQHLPGTAPKLLIYVNTNRPSGVPDRFSGSKSGTLASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 VVT----HEMAHANQTASDSSVMVRQVGFGN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 ATTGALDMWGRGTLVTVSSGGGGSGGGGGGGGGGG-----GSAQAVLTQPSSVSGTPG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 VITGLQAEDEADYYCQSYDLSLTGRNYVFGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 VITGLOAEDEADYYCOSYDLSLTGRNYVFGS 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 TTITQSGYGNGADVGQGAD-----NSTIELTQNGFRNNATIDQWNAKNYDQLVTR 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 ALAGVVPQWG------GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSE-
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Search completed: March 11, Job time: 25.6 secs
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US-09-952-267-15
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                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.7%; Score 83; DB 10; Length 889; Best Local Similarity 27.9%; Pred. No. 10; Matches 39; Conservative 16; Mismatches 51; Indels
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Publication No. US20030032772A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 10.8%; Score 83.5; D
Best Local Similarity 24.6%; Pred. No. 2.8;
Matches 43; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HANSEN, E
APPLICANT: AEBI, CE
APPLICANT: COPE, LE
APPLICANT: MACIVER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/952,267
CURRENT FILLING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 09/336,447
PRIOR FILING DATE: 1999-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.1
                                                                                               180
                                                                                                                                        126 ANQTASDSSVMVRQVGFGNN 145
                                                                                                                                                                                         129
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                                                                                                                                                                                                                                80 DVGQG-----ADNSTIELTQNGFRN----NATID---QWNAKNYDQLVTRVVTHEMAH 125
                                                                                                                                                                                                                                                                                 69
                                                                                                                                                                                                                                                                                                                             28 GGGNHNGGGNSSGPDSTLSIYQ---YGSANAALALQSDARKSETTITQSGY-----GNGA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 IELTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDSSVMVRQVGFGN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 WTPITDSRIAAHGYNVINAAFPV---IRSDGTALWEDGMDTGVKVATPAEMCQAKASGQT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 NSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGAD-----NST 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              σ
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                                                                                            ANOATGESSTV---AGGSNN 196
                                                                                                                                                                                       FVGGGYKNLAEGDNATI---AGGFANLAEGDNATIAGGFENRAEGIDSVVSG-----GY 179
                                                                                                                                                                                                                                                                                 GAGRHNNVGGSAHHSGILGGWKNTVNGYTSAIVGGYGNETQGDYTFVGGGYKNLAKGNYT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRLLAVALTAAVLTPLSIATAPTASAADTCAVKSRPSGKVLQGYWENWDGSSNGVHPPFG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEBI, CHRISTOPH
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                   2004, 19:18:39
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                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Title:
Perfect score:
Sequence:
                                                                                                                                   Run on:
                                                                                                                                                                            OM protein - protein search, using sw model
                                                                                    March 11, 2004, 18:24:14; Search time 10.3 Seconds (without alignments) 1410.186 Million cell updates/sec
1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151
                        US-09-543-407-24
775
                                                                                                                                                                                                                                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Searched: BLOSUM62 Gapop 10.0 , Gapext 0.5 283366 seqs, 96191526 residues

Scoring table:

Total number of hits satisfying chosen parameters:

283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	B	, –	
1	690	89.0	151	2	JC6039	fimbrin protein ag
2	690	9	151	N	1063	rlin cha
ω	533		151	N	S70788	curlin protein csg
4.	11	٥,	152	N	9080ea	major su
u	511.5	66.0	152	N	H85665	
o	101	•	409	N	T20847	
7	99	12.8	1748	N	S42136	cnjB protein - Tet
80	8		151	N	JC6040	fimbrin protein ag
9	٠	12.7	151	N	AH0635	nucleation compone
10	٥.		151	N	S70787	curlin nucleator p
11	٥,	12.5	151	Ŋ	C90806	minor curlin subun
12	٥.		151	N	G85665	curlin minor chain
13	Ψ		552	N	D70604	probable PPE prote
14	'n	11.9	440	N	AD1539	auga
15	92.5	11.9	1028	N	A56038	μ.
16	92.5	11.9	1213	N	S16356	ovo protein - frui
17	90	•	145	N	AD3143	conserved hypothet
18	90	11.6	145	N	H98144	hypothetical prote
19	90		347	N	B39112	
20	89.5		256	N	T03371	glycine-rich prote
21	89		262	N	S00275	tail fiber protein
22	89	٠	573	N	C86266	9.21 pr
23	89		2174	N	E95965	hypothetical glyci
24	88.5		321	ν	A47369	
25	87	•	590	۳	A45621	Bin (
26	87	11.2	599	N	B42049	_
27	87	11.2	599	N	A44951	leishmanolysin (EC
28	87			د		
		٠	602	۲	PL0221	Teraumanorysin (EC

4 4 5 4	43	42	41	40	39	38	37	36	S S	ω 4	S S	32	31	30
82.5 82	83	83.5	83.5	84	84	84.5	85	85	85	85.5	96	86	. 87	87
10.6	10.7	10.8	10.8	10.8	10.8	10.9	11.0	11.0	11.0	11.0	11.1	11.1	11.2	11.2
343 382	639	1635	423	764	439	340	967	575	401	438	582	447	1537	1537
NN	N	N	N	2	N	ν	N	N	N	N	N	N	N	N
T05221 F90892	C42049	AI0452	T19581	H71607	AC1182	A83401	S66852	S35327	C88571	T35789	F70675	G84687	C81558	F86509
hypothetical prote probable outer mem	leishmanolysin (EC	hemolysin [importe	hypothetical prote	hypothetical prote	probable sugar ABC	hypothetical prote	hypothetical prote	protein kinase sgg	protein C05B5.3 (i	probable secreted	probable PPE prote	probable disease r	conserved hypothet	CT147 hypothetical

ALIGNMENTS

Qy 1:	Qy dd	Db Qy	Query Match Best Local Matches 13	A; Gene: agfA C; Function: A; Description: majo: A; Description: majo: A; Note: fimbriae bi: C; Keywords: fimbria F;1-20/Domain: sign: F;21-151/Product: f.	A; Contents: 27655 A; Accession: A44898 A; Status: prelimina A; Molecule type: pr A; Residues: 21-33 < A; Note: sequence ex	A; Molecule A; Residues: A; Experimen A; Note: the R; Collinson J. Bacterio A; Title: Pu A; Reference	RESULT 1 JC6039 fimbrin protein agfA C;Species: Salmonell C;Date: 31-Dec-1996 C;Accession: JC6039 R;Collinson, S.K.; C J: Bacteriol. 178, 6 A;Title: Salmonella A;Reference number: A;Raccession: JC6039 A;Molecule type: DNA A;Rocession: 1-151 C A;Raccession: PC6015 A;Accession: PC6015	
121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151 ;	61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120	1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGHHNGGGHSSGFDSTLSIYQYGSANAALALQ 60	atch 89.0%; Score 690; DB 2; Length 151; Sal Similarity 91.4%; Pred. No. 4.7e-51; 138; Conservative 2; Mismatches 11; Indels 0; Gaps	C; Genetics: A;Gene: agfA A;Gene: agfA C;Function: A;Description: major component of thin aggregative fimbriae A;Description: major component of thin aggregative fimbriae A;Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator C;Keywords: fimbria C;Keywords: fimbria F;1-20/Domain: signal sequence #status predicted <sig> F;21-151/Product: fimbrin protein agfA #status experimental <mat></mat></sig>	A;Contents: 27655 A;Accession: A44898 A;Atatus: preliminary A;Molecule type: protein A;Residues: 21-33 <co3> A;Note: sequence extracted from NCBI backbone (NCBIP:45936)</co3>	Type: protein 21-52 <co2> 21-52 <co2> tal source: strain 27655-3b authors translated the codon ACG for residue 44 as Ile authors translated the codon ACG for residue 44 as Ile , S.K.; Emody, L.; Muller, K.H.; Trust, T.J.; Kay, W.W. 1. 173, 4773-4781, 1991 1. 173, 4773-4781, 1991 2. 173, 4773-4781, 1991 2. 173, 4773-4781, 1991 3. 173, 4773-</co2></co2>	RESULT 1 JC6039 fimbrin protein agfA precursor - Salmonella enteritidis C;Species: Salmonella enteritidis C;Species: Salmonella enteritidis C;Accession: JC6039; DC6015; A444898 R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W. J. Bacteriol. 178, 662-667, 1996 A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae A;Reference number: JC6039; MUID:96146512; PMID:8550497 A;Accession: JC6039 A;Accession: JC6039 A;Accession: COL> A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43599.1; PID:g1184714 A;Accession: PC6015	
			0;	.		from Salmonella	ià e .	

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A;Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;PARKHILL,
th, T.; Connerton, P.; LLU.....
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A;Authors: Parry, C.; Quail, M.; Rutherford arug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete genome sequence of a multiple genome sequen
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R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.
Mol. Microbiol. 18, 661-670, 1995
A;Title: Expression of two csg operons is required for production A;Reference number: S70783; MUID:96414468; PMID:8817489
A;Accession: S70788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: csgA protein; major C;Species: Escherichia coli
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A; Residues: 1-151 <HAM>
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A; Residues: 1-151 < PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      major curlin
                                 Residues: 1-151 <BLAT>;Residues: 1-151 <BLAT>;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74126.1; Experimental source: strain K-12, substrain MG1655 (Olsen, A.; Arnqvist, A.; Hammar, M.; Sukupolvi, S.; Normark, S.; Olsen, A.; Arnqvist, A.; Hammar, M.; Sukupolvi, S.; Normark, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62282.1; PID:g1147564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                           Molecule type: DNA
                                                                                                                                                                                                                             Status: nucleic acid sequence not
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Matches
                                                                                                                                                                                                                                                                      Accession: G64846
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91.4%;
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Pred. No. 4.7e-51
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ies, R.M.; Dowd,
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e, N.; Farrar,
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A; Status; preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-152 < HAY>
A; Cross-references: GB: BA000007; PIDN: BAB34843.1; PID: g13360880;
A; Cross-references: GB: BA000007; PIDN: BAB34843.1; PID: g13360880;
A; Cross-references: GB: BA000007; PIDN: BAB34843.1; PID: g13360880;
                                                                                                                                                                                                                                                                                                                           R;Hayashi, T.; Makino, gasawara, N.; Yasunaga, DNA Res. 8, 11-22, 2001
                                                                                                                                                                                                                                                                           A;Title: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: D90806
                                                                                                                                                                                                                                                                                                                                                                             C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: D90806
                                                                                                                                                   A; Gene:
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C;Species: Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;21-151/Product:
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A; Accession: $34559
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A; Residues: 21-4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: The RpoS sigma factor relieves H-NS-mediated transcriptional repression A;Reference number: S31202; MUID:93211294; PMID:8459772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           i)Description: major component of wild-type curli; interaction between CsgA and Note: curli are thin, coiled fibers expressed on the surface of Escherichia co and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers i1-20/Domain: signal sequence #status predicted <SIG>
                                                                                             Query Match
Best Local
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                        MKLIKVAAFAAIVVSGSAIAGVVPQW-GGGGNHNGGGNSSGPDSTISIYQYGSANAAIAI
MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAL
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                                                                                                                                                                                                                                                                                                                                                Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii
Kasunaga, T.; Kuhara, S.; Shiba, T.; Hattori,
                                                                            Conservative
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                                                                    Score 511.5; Db 2;
Pred. No. 4.6e-36;
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Pred. No. 7.1e-38;
8; Mismatches 27
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W3110
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Shinagawa,
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QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVV

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hypothetical protein F13E9.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t C;Accession: T20847
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C;Accession: H85665

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; F.

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; F.

R;Perna, N.T.; Classes, Davis, N.W.; Lim, A.; Dimalanta, E.; Potamon

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: H85665
                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, A;Reference number: Z19332 A;Accession: T20847
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A; Residues: 1-409 <WIL>
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R; McMurray, A.
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A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein csgA [imported] - Escherichia coli (strain 0157:H7, substrain EDL93
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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A;Introns: 32/1; 275/3; 337/3
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Best Local S
Matches 104
                                                                                                                                                                                                                                     ;Cross-references: EMBL:Z69383; PIDN:CAA93412.1; GSPDB:GN00022; CESP:F13E9;Experimental source: clone F13E9
                                                                                                                                             Superfamily:
                                                                        Matches
                                                                                       Query Match
Best Local
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                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAL
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SGQQASGSMNSFGGQGGYGQNQNGFGGQSGFSGQSGWGSNSLSSANSNGNNNQG--SSSG
                                  SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGNGAAVDQTASNSTVNVTQVGFGNNATAHQY 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   loricrin
                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  #sequence_revision 15-Oct-1999 #text_change 02-Aug-2002
                                                           13.0%; 5-
23.3%; Pred
3.3%; 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.0%;
                                                                    Score 101; DB
Pred. No. 0.4;
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 511.5; DB 2
Pred. No. 4.6e-36;
                                                                                                                                                                                                                                                                                                             from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                  February
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                        DB 2;
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                                                                      66;
                                                                                                          Length 409
                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J.D.; Rose, D.J.; Mayher Potamousis, K.; Apodaca
                                                                        30;
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                                                                      Gaps
193
                                    74
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RESULT
JC6040
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                                                                                                                                                                                                                                                                                                                                                                 F;1626-1748/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S42136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cnjB protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: cnjB
                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192
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A; Molecule type: DNA
A; Residues: 1-1748 <TAY>
A; Residues: 1-1748 <TAY>
A; Cross-references: EMBL:LO3710; NID:g161751; PID:g161752
A; Cross-references: EMBL:LO3710; NID:g161751; PID:g161752
R; Taylor, F.M.; Martindale, D.W.
Nucleic Acids Res. 21, 4610-4614, 1993
Nucleic Acids Res. 21, 4610-4614, 1993
A; Title: Retroviral-type zinc fingers and glycine-rich repeats
A; Reference number: S42135; MUID:94051569; PMID:8233798
A; Accession: S42135; MUID:94051569; PMID:8233798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Tetrahymena thermophila C;Date: 19-Mar-1997 #sequence revision C;Accession: S42136; S42135; S03550 R;Taylor, F.M.; Martindale, D.W. submitted to the EMBL Data Library, Oct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Genetic code: SGC5
A;Introns: 85/3; 136/1; 157/3; 201/2; 290/2; 327/3; 499/1; 573/2; 607/3; 708/3; 777/3;
C;Keywords: zinc finger
F;1164-1450/Region: glycine-rich
F;1451-1464/Region: zinc finger CCHC motif
F;1478-1491/Region: zinc finger CCHC motif
F;1501-1514/Region: zinc finger CCHC motif
F;1530-1543/Region: zinc finger CCHC motif
F;1557-1568/Region: zinc finger CCHC motif
F;1579-1592/Region: zinc finger CCHC motif
F;1579-1592/Region: zinc finger CCHC motif
F;1579-1592/Region: zinc finger CCHC motif
F;1602-1615/Region: zinc finger CCHC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-1
A;Residues: EMBL:L03710
A;Cross-references: EMBL:L03710
R;Martindale, D.W.; Taylor, F.M.
Nucleic Acids Res. 16, 2189-2201, 1988
A;Title: Multiple introns in a conjugation-specific gene from Tetrahymena thermophila.
A;Reference number: 803650; MUID:88189811; PMID:3357771
A;Accession: 803650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 236-250,'I',252-255,'N',257-773
A;Cross-references: EMBL:X06462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: S42136
1723 ----WGSNNQAS 1730
                                                                                                                                                                                                                                         1640 OFGGGGNSNGGOSWGTSSGSDWN
                                                                                                                                                                                                                                                                                                  25 QWGGGGNHNGG---GNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT----QSGYGN
                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                    QTGGGWGSNDN-----QQQQNENTGGGGWGSSN--
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                                                     ROVGEGNNATAN 149
                                                                                                                                                                             GADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDSSVMV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NYDQLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNKSLTTNQINEQ---ASNWASANSVQAQYIQYETNRSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tetrahymena thermophila
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zinc finger
glycine-rich
                                                                                                                                                                                                                                                                                                                                                                                          12.8%;
                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                        Score 99; DB 2
Pred. No. 3.1;
16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                              31;
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                                                                                                                                                                                                                                            COSNVOESTITSSGGWGSSGSGN
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1748;
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                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                       -SNOTNNESS---
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C;Species: Sal
C;Date: 31-Dec
C;Accession: C
   curlin nucleator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleation component of curlin monomers [imported] - Salmonella C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change C;Accession: AH0635
                                                                                                                                                                                                                                                                                              A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                            A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Tille: Complete genome sequence of a multiple drug resistant Salmonella enterica serovA;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 413,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Parkhill, J.; Dougan,
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A;Title: Salmonella enteritidis agfBAC operon encoding thin, A;Reference number: JC6039; MUID:96146512; PMID:8550497
A;Accession: JC6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Collinson, S.K.; Clouthier, S.C.; Doran, J. Bacteriol. 178, 662-667, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: agfB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type:
                                                                                                                                                                                                                                                                                                                                              ;Molecule type: DNA
;Residues: 1-151 <PAR>
                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S.; Moule, S.; O'Gaora,
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;1-21/Domain: signal sequence #status
;22-151/Product: fimbrin protein agfB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Cross-references: GB:U43280; NID:g1184712; Experimental source: strain 276755-3b
                                                                                                                                                                                                                                                                                                                              Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
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                                                                                                                                                                                                                                                                                              STY1180
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                                                                                                                                                                                                                           34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               848-852, 2001
                                                                                                                                                                                                                                            Similarity
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                                                                                                                  NGFRNNATIDQWNAKNYD-QLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                EGENNRAKVDQ--AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
                                                                                                                                                    GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ 73
                                                                                                                                                                                      GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST-----IELTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGGNNRAKVDQ--AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST-----IELTQ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGFRNNATI DQWNAKNYD-QLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          minor component of thin aggregative fimbriae se bind to fibronectin, plasminogen, tissue plasminogen
   protein
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                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                            GB:AL513382;
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 csgB
                                                                                                                                                                                                                                        12.7%;
 precursor
                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                        Score 98.5; D
Pred. No. 0.21
17; Mismatches
                                                                                                                                                                                                                                                                                                                         PIDN: CAD08267.1; PID:g16502314; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K.D.; Thomson, N.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              predicted <SIG>
#status predict
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thomson, N.R.; Pickard, D.; Wain, J.; Cher, Davies, R.M.; Dowd, L.; White, N.;
 Escherichia
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                                                                                                                                                                                                                                      .21;
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                                                                                                                                                                                                                        48;
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 coli
                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 151;
                                                                                                                                                                                                                        Indels
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(strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aggregative fimbriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:g1184713
                                                                                                                                                                                                                      19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enterica subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
K-12)
                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Farrar
                                                                                  A;Gene:
                                                                                                                                                  A; Molecule type: DNA A; Residues: 1-151 <HAY>
                                                                                                                                                                                                  A; Reference number: A; Accession: C90806
                                                                                                                                                                                                                                                     gasawara, N.; Yasunaga,
DNA Res. 8, 11-22, 2001
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                                                                                                                A; Experimental
                                                                                                                                                                                                                                                                                     R;Hayashi,
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                                                                                                                                                                                 A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: csgB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
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Matches
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                Matches
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              30;
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                                Similarity
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              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                      A99629;
                              12.5%;
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minor curlin subunit precursor CsgB [imported] - C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-200 C;Accession: C90806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Description: minor component of wild-type curli; interaction between CsgA and CsgB A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli the and H-kninogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-21/Domain: signal sequence #status predicted <SIG> F;2-151/Product: minor curlin chain #status predicted <MAT>
                                                                                                                                                                                                   A; Title: Complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Experimental source: strain Ki2, substrain W3110
A;Note: the mucleotide sequence was submitted to the EMBL Data Library, August R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Rile R;Blattner, D.J.; Mau, B.; Shao, Y.
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A;Title: Expression of two csg operons is required for A;Reference number: S70783; MUID:96414468; PMID:8817489
A;Accession: S70787
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A; Title: The complete genome sequence of Escherichia coli A; Reference number: A64720; MUID:97426617; PMID:9278503
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Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:g13360879; GSPDB:GN00154
Experimental source: strain 0157:H7, substrain RIMD 0509952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 GSANAALALQSDARKSE-----TTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGSSNRAK-IDQTGDYNLAYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAPGIAAAAGYDLANSEYNFAVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid sequence not shown; translation not
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ce: strain K-12, substrain MG1655
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                                                                                                                                                                                                                                                                 K.; Ohnishi,
, T.; Kuhara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.5%; Score 96.5; DB 2; 25.6%; Pred. No. 0.31;
                                                                                                                                                                             quence of enterohemorrhagic Escherichia MUID:21156231; PMID:11258796
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                                                                                                                                                                                                                                                           Kurokawa, K
Shiba, T.;
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                                                                                                                                                                                                                                                                                                                                                        18-Jul-2001
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24;

Mismatches

46; 2

17;

Gaps

4

Score 96.5; DB Pred. No. 0.31;

BB

Length 151;

SALAGVVPQWGGGGNHNGGGNSGPDSTLSIYQYGSANAALALQSDA 63 	Qy 15 SGSALAGV- Db 353 SGSGNIGVE
12.1%; Score 93.5; DB 2; Length 552; larity 27.9%; Pred. No. 2.4; Conservative 11; Mismatches 58; Indels 37; Gaps 7;	Query Match Best Local Similarity Matches 41; Conser
GB:292774; GB:AL123456; NID:g3261729; PIDN:CAB07133.1; PID:g1877289 ce: strain H37Rv	A; Cross-references: GB: 292774; A; Experimental source: strain C; Genetics: A; dene: PPE C; Superfamily: Phaseolus glyci
ry; nucleic acid sequence not shown; translation not shown A	A;Accession: 0,0004 A;Status: preliminary; A;Molecule type: DNA A;Molecule type: COT
~ @ ×	qares, Fiphering
sch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Sles, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.	; Brosch, ; Davies, M.A.; Rog
e PPE protein - Mycobacterium tuberculosis (strain H37RV) es: Mycobacterium tuberculosis 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 sion: D70604	D70604 probable PPE protein C;Species: Mycobacter C;Date: 17-Jul-1998 # C:Accession: D70604
	RESULT 13
WNAKNYDQLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATANQY 151	Qy 106 WNAKNYD : Db 74 EGSSNRA
GSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQ 105	Qy 51 GSANAAL : Db 14 GAPGIAA
12.5%; Score 96.5; DB 2; Length 151; Similarity 25.6%; Pred. No. 0.31; 10; Conservative 24; Mismatches 46; Indels 17; Gaps 4;	Query Match Best Local Similari Matches 30; Cons
Molecule type: DNA Molecule type: DNA Residues: 1-151 <sto> Cross-references: GB.AE005174; NID:g12514573; PIDN:AAG55787.1; GSPDB:GN00145; UWGP:Z16 Experimental source: strain O157:H7, substrain EDL933 Genetics:</sto>	A; Molecule type: DNA A; Residues: 1-151 <st A; Cross references: G A; Experimental source C; Genetics: A; Gene: CsgB</st
puence of enterohemorrhagic Bscherichia coli O157:H7. A85480; MUID:21074935; PMID:11206551	A;Title: Genome sequence of A;Reference number: A85480; A;Recession: G8565;
ikett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew t, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, t, 2001	R;Perna, N.T.; Plunkett 1 iller, L.; Grotbeck, E.J Nature 409, 529-533, 2001
precursor, CsgA homolog [imported] - Escherichia coli (strain 0157:H7) hia coli #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001	G85655 G85656 Gurlin minor chain precursor, curlin minor chain precursor, C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence C;Date: 16-Feb-2001 #sequence
T TÄTTMANNGGNÄTTIMTNINTMÖGTGMANNGGNÄATTWINGGTÄAT	SIII.T 12
VTRVVTHEMAHANQTASDSSVMVRQVGFGNNATANQY : : : : :	Qy 106 WNAKNYDQL
GSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQ 105	Qy 51 GSANAAL : Db 14 GAPGIAA

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3 LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD

62.

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DNA-binding protein ovo - fruit fly (Drosophila melanogaster)
C;Specias: Drosophila melanogaster
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change
C;Accession: A56038
R;Garfinkel, M.D.; Wang, J.; Liang, Y.; Mahowald, A.P.
Mol. Cell. Biol. 14, 6809-6818, 1994
A;Title: Multiple products from the shavenbaby-ovo gene region of A;Reference number: A56038; MUID:95021209; PMID:7935398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entia D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Ack, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1539
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A;Residues: 1-1028 <GAR>
A;Cross-references: GB:U11383; NID:g520526; PIDN:AAB60216.1; PID:g520527
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A;Cross-references: GB:AL592022; PIDN:CAC96084.1; PID:g16413303; GSPDB:GN00178
A;Experimental source: strain Clip11262
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                                                                                                                                                                        A;Cross-references: FlyBase:FBgn0003028
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Query Match
Best Local S
Matches 40
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                                               11.9%; Score 92.5; 26.7%; Pred. No. 5
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Voss, H.; Wehland
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11, 2004, 18:14:48;

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GenCore version (c) 1993 - 2004

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Scoring table: Sequence: Title: Perfect score:

BLOSUM62 Gapop 10.0 ,

Gapext 0

US-09-543-407-24 775

Searched

141681 segs,

52070155 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CTIS.";
Nature 413:848-852(2001).
SEQUENCE FROM N.A.
SPECIES-S. Lyphi; STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayh
Burland V., Kodoyianni V., Schwartz D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=S.typhimurium; STRAIN=LTZ / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney B.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES-S.typhimurium; STRAIN-SR-11;
MEDLINE-98117058; PubMed-9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
Romling U., Bian C., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium an Escherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
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01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2093 (Rel. 42, Last annotation update)
Major curlin subunit precursor (Fimbrin SEF17).
CSGA OR AGFA OR STW1144 OR STW1181 OR T1776.
Salmonella typhimurium,
Salmonella typhi, and
Salmonella enteritidis.
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SPECIES=S.typhi; STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of LT2.";
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Enterobacteriaceae; Salmonella.
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MBN DROME
YHC3 YEAST
KF1A HUMAN
YZ17 AQUAE
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ICEV PSESX
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            hew G.F.,
Blattner
              Rose D.J.,
F.R.;
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CSGB_SALT

TNKI_HUMAN MSA2_PLAF2

CSGA_ECOLI CSGA_ECOS7

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VG38_BPT2

GP63_LEICH
GP63_LEIMA
GP63_LEIME
OMPB_RICJA
YKO3_CAESL
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PER_DROWI

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CEAK ECOLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
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SPECIES-S.enteritidis; STRAIN-27655-3B;

MEDLINE-91310586; PubMed-1677357;

Collinson S.K., Emoedy L., Mueller K.-M., T;

"Dirification and characterization of thin,
                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.; "DNA-based diagnostic tests for Salmonella species targeting agfA, the structural gene for thin, aggregative fimbriae."; J. Clin. Microbiol. 31:2263-2273(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 21-33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96146512; PubMed=8 Collinson S.K., Clouthier
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94013373; PubMed=8104955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=S.enteritidis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 21-151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., "Salmonella enteritidis agfBAC operon encoding thin, agg:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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                                                                         61
                                                                                                            61
                                                                                                                                                                                                                          138;
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JC6039; JC6039.
                                                                                                                                                                                                                                         Similarity
                     HEMAHANQTASDSSVMVRQVGFGNNATANQY
                                                                                          SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT
                                                                                                                                                                  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                                                                                                                                                                                                                      Signal; Complete
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6146512; PubMed=8550497;
                                                                                                                                                                                                                                                                                               151
                                                                                                                                                                                                                        Conservative
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SVMVRQVGFGNNATANQY ->
REF. 6).
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                                                                                                                                                                                                                                     690; DB 1;
No. 1.4e-51;
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aggregative fimbriae
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SEQUENCE FROM N.A.
STRAIN=K12 / MC4100;
STRAIN=96414468; PubMed=8817489;
MEDLINE=96414468; PubMed=8817489;
MEDLINE=9641468; 
MEDLINE=9641489;
J. Bacteriol. 173:4773-4781 (1991).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.
-COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
FIBRONECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FAVO....STRAIN=KIZ / MG1655;
STRAIN=KIZ / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Riley M., Collado-Vides J., Riley M., Collado-Vides J., Riley M., Collado-Vides J., Riley M., Collado-Vides J., Riley M., Riley M., Collado-Vides J., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Rile
                                                                                                                                                                Salmonella enteritidis."
                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93023873; PubMed=1357528;
Arnqvist A., Olsen A., Pfeifer J.,
"The Crl protein activates cryptic
fibronectin binding in Escherichia
Mol. Microbiol. 6:2443-2452(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A 718-kb DNA sequence of the Escherichia corresponding to the 12.7-28.0 min region DNA Res. 3:137-155(1996).
                                                                                                                                                                                               MEDLINE=91310586; PubMed=1677357; Collinson S.K., Emoedy L., Trust T Purification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 21-40.
STRAIN=K12 / YMEL;
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P28307;
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"The RpoS sigma factor relieves
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STRAIN=K12 / W3110;
MEDLINE=93211294; PubMed=8459772;
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nce 277:1453-1474(1997).
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(Rel. 34, Last sequence up)
(Rel. 41, Last annotation
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SIMILARITY:

BELONGS TO THE CSGA/CSGB FAMILY.

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RESULT 3
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AC 093U<sup>2</sup>4;
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Fimbria;
SIGNAL
                 STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7."
                                                                                                                                                                                                                                                                                                STRAIN=0157:H7 / ATCC 43895;

MEDLINE=21218556; PubMed=11319125;

Uhlich G.A., Keen J.E. Elder R.O.;

Uhutations in the csgD promoter associated with variations expression in certain strains of Escharichia coli 0157:H7.m

Appl. Environ. Microbiol. 67:2367-2370(2001).
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28-PEB-2003 (Rel. 41, Last sequence up
28-PEB-2003 (Rel. 41, Last annotation
Major curlin subunit precursor.
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Escherichia coli O157:H7.
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STRAIN=0157:H7 / E
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NCBI_TaxID=83334;
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3L; D90741; BAA35832.1; -.
3L; D90742; BAA35840.1; -.
2; S70788; S70788.
3Cene; EG11489; C89A.
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yok Hayashi T., Makino K., Ohnishi M., Kurokawa K., Tanaka M., Tob Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasu Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasu Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RComplete genome sequence of enterohemorrhagic Escherichia cc O157:H7 and genomic comparison with a laboratory strain K-12. DNA Res. 8:11-22(2001).

-I- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AN TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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SEQUENCE FROM N
STRAIN=0157:H7
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Fimbria;
MEDLINE=21534947; PubMed=11677608; Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wa: Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Minor curlin subunit precursor.
CSGB OR STY1180 OR T1777.
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                                                                                                                                                                                                                                                                                   Salmonella typhi.
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                                                                                                                                                                                                                                         Salmonella
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MAJOR CURLIN SUBUNIT.
77777004DDE91243 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 511.5;
Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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K-12.";
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Tobe T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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RESULT 5
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Best Local S
Matches 34
SPECIES=S.typhimurium; STRAIN=SR-11; MEDLINE=98117058; PubMed=9457880; Romling U, Bian Z., Hammar M., Sierralta W.D., Normark S. "Curli fibers are highly conserved between Salmonella typh Escherichia coli with respect to operon structure and regu Bacteriol. 180:722-731(1998).
                                                                                            SEQUENCE FROM N.A.
                                                                                                                     Enterobacteriaceae; Salmonella.
NCBI TaxID=602, 592;
                                                                                                                                                                Salmonella typhimurium, and Salmonella enteritidis.
                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEF17
CSGB OR AGFB OR STM1143.
                                                                                                                                                                                                                                                                    CSGB SALTY
P55226;
                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fimbria; Signal; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22531367; PubMed-12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.,
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
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Nature 413:848-852(2001).
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Quail M.A., Rutherf
Whitehead S., Barre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feltwell T., Hamlin N., Haque A., Hien T.T., Ho. Krogh A., Larsen T.S., Leather S., Moule S., O'(Quail M.A., Ritherford K., Simmonds M., Skelton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriol 185:2330-2337 (2003).

- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLICOLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY TEMPERATURES BELOW 37 DEGREES CELSTUS. CURLI CAN BIND TELERONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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                                                                                                                                                                                                                                                                                                                                                           74
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AE016840; AA069400.1; -.
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                                                                                                                                                                                                                                                                                                                                                                             NGFRNNATIDQWNAKNYD-QLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                    GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST-----IELTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                   STANDARD;
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16254 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 98.5; I
Pred. No. 0.09
L7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MINOR CURLIN SUBUNIT: 161C54326E573495 CF
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                                                                                                                                                                                                         minor subunit)
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                                                                                                                                                Enterobacteriales;
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                regulation.
                                typhimurium
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RESULT 6
CSGB_ECOI
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Best Local
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CSGB_ECOLI
P39828;
           Bacteria; Proteobacteria; Gammar
Enterobacteriaceae; Escherichia,
NCBI_TaxID=562, 83334;
                                                                                    01-FEB-1995 (Rel. 31, Created)
01-OCT-1996 (Rel. 34, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A.
SPECIES=S.typhimurj
SPECIES=S.1334948;
NCBI_TaxID=562,
[1]
                                                           Escherichia coli, and Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fimbria; Signal; Complete proteome.
SIGNAL 1 21 POTENTIAL.
CHAIN 22 151 MINOR CURLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ002301; CAA05316.1; -.
EMBL; AE008749; AAL20073.1; -.
EMBL; U43280; AAC43598.1; -.
PIR; JC6040; JC6040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=S.enteritidis; STRAIN=27655-3B; MEDLINE=96146512; PubMed=8550497; Collinson S.K., Clouthier S.C., Doran J.L., Ban "Salmonella enteritidis agfBAC operon encoding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21334948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.
Countrey L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney B.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Watareth D. Willow D. W., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      timbriae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ryan E., Sun H., Florea L. Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriol. 178:662-667(1996).
FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.
COLLED SURRACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONE
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                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                               EGGNNRAKVDQ--AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY
                                                                                                                                                                                                                                                                                               NGFRNNATIDOWNAKNYD-QLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                        GSANAALALQSDARKSB-----TTITQSGYGNGADVGQ-GADNST-----IELTQ
                                                                                                                                                                                                                                                                                                                             GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SG10609; csgB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               16182 MW;
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                                          Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 98.5;
Pred. No. 0.
                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              INOR CURLIN SUBUNIT.
COFC5430E6DD361D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                        update)
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                                           Enterobacteriales;
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aggregative
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SEQUENCE FROM .... STRAIN-KL2 / MC4100; STRAIN-KL2 / MC4100; MEDLINE-96414468; PubMed-8817489; MEDLINE-964414468; PubMed-8817489; Hammar M., Arngvist A., Bian Z., Olsen A., Normark S.; "Expression of two csg operons is required for production "Expression of two csg operons is required in Esche"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21156231; PubMed=11250796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Kurokawa T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli 0157.H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.", Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                        Arnqvist A., Olsen A., Normark S.;
"Sigma S-dependent growth phase induction
"Secherichia coli can be achieved in vivo be
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MEDLINE=21074935; PubMed=11206551;
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Science 277:1453-1474(1997).
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                                                                  the nucleoid-associated protein H-NS.";
Microbiol. 13:1021-1032(1994).
FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLICULED SURFACE STRUCTURES THAT ASSEMBLE PREFERNTIALLY AT GROY TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
CURLIN MONOMERS.
SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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by sigma 70 in the absence
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STRAIN-Oregon-R;
MEDLINE=91293102; PubMed=1712294;
MEDLINE=91293102; PubMed=1712294;
MEDLINE=91293102; PubMed=1712294;
Mevel-Ninio M.T.M., Terracol R., Kafatos
"The ovo gene of Drosophila encodes a zin
for female germ line development.";
EMBO J. 10:2259-2266(1991)
                                                                                                                                                                                                                                                                  Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.; "Multiple products from the shavenbaby-ovo gene region melanogaster: relationship to genetic complexity."; Mol. Cell. Biol. 14:6809-6818(1994).
                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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EcoGene; EG12621; CsgB.
Fimbria; Signal; Complete proteome.
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EMBL; AE000205; AAC74125.1; -.
EMBL; D80741; BAA35831.1; -.
EMBL; AE005315; AAG55787.1; -.
EMBL; AP002554; BAB34842.1; -.
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MEDLINE=95021209; PubMed=7935398;
Mind J. Liang Y.,
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                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                   FUNCTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF ILINE CELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION.
SUBCELLILAR LOCATION: Nuclear (potential).

DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND ACCUMULATES IN NURSE CELLS DURING COGENESIS. STORED IN THE IS RAPIDLY LOST IN THE EMBRYOS EXCEPT FOR ITS CONTINGRESING IN THE GERM LINE PRECURSOR POLE CELLS.

SIMILARITY: Contains 4 C2H2-type zinc fingers.
             SWISS-PROT entry is copyright. It is produced
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(Rel. 42, Last annotation
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MINOR CURLIN SUBUNIT
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PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;
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                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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-!- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosy
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Chi N.-W., Lodish H.F.;
"Tankyrase is a Golgi-associated mitogen-activated presubstrate that interacts with IRAP in GLUT4 vesicles.
J. Biol. Chem. 275:38437-38444 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith S., de Lange T.,

"Cell cycle dependent localization of the
to nuclear pore complexes and centrosomes.

J. Cell Sci. 112:3649-3656(1999).
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MEDLINE=21602874; PubMed=11739745;
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TNKS OR TNKS1 OR TINI OR TINF1 OR PARPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99454782; PubMed=10523501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 282:1484-1487(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith S., Giriat I., Schmitt A., de Lange
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99040105; PubMed=9822378;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human telomeres.";
1. Cell. Biol. 22:332-342(2002).
- FUNCTION: May regulate vesicle
                                                                                                                                                                                                                                         PTM: Upon insulin-stimulation, phosphorylated on serine residues by MAPK kinases.

PTM: ADD-ribosylated (-auto).

SIMILARITY: Belongs to the PARP family.

SIMILARITY: Contains 15 ANK repeats.

SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nicotinamide + {ADP-D-ribosyl} (N+1)-acceptor.

SUBUNIT: Oligomerizes and associates with TNKS2. Interacts with the cytoplasmic domain of the TNESP/Otase in SLC2A4/GLU74-vesicles. Binds to the N-terminus of telomeric TRF1 via the ANK repeats. SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi an with juxtanuclear SLC2A4/GLU74-vesicles. A minor proportion is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               also found at nuclear pore complexes and around the pericentriolar matrix of mitotic centromeres. During interphase, a small fraction of TNKS is found in the nucleus, associated with TRF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: May regulate vesicle trafficking and modulate subcellular distribution of SLC2A4/GLUT4-vesicles. Has I
                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=095271-2; Sequence=VSP_004538, VSP_004539;
Note=No experimental confirmation available;
SSUE SPECIFICITY: Ubiquitous; highest levels in testis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=095271-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2)
                      noved. Usage by and for (See http://www.isb-sib.
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at human telomeres.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith
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REPEAT 215 240 ANK 1.
REPEAT 248 280 ANK 2.
REPEAT 368 401 ANK 3.
REPEAT 401 433 ANK 5.
REPEAT 434 466 ANK 6.
REPEAT 521 556 ANK 7.
REPEAT 557 589 ANK 8.
REPEAT 590 622 ANK 9.
REPEAT 716 748 ANK 11.
REPEAT 716 748 ANK 11.
REPEAT 716 748 ANK 12.
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SMART; SM00248; ANK; 17.

SMART; SM00454; SAM; 11.

PROSITE; PS50008; ANK REPEAT; 15.

PROSITE; PS50297; ANK REP REGION; 1.

PROSITE; PS50105; SAM DOMĀIN; 1.

PROSITE; PS50105; SAM DOMĀIN; 1.

PROSITE; PS50105; SAM DOMĀIN; 1.

PROSITE; PS50105; SAM DOMĀIN; 1.

PROSITE; PS50105; SAM DOMĀIN; 1.

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PROSITE; PS50105; SAM DOMĀIN; 1.

PROSITE; PS50105; SAM DOMĀIN; 1.
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EMBL; AF082558; AAC79843.1;
EMBL; AF082559; AAC79844.1;
HSSP; Q00420; IAWC.
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                                                                                                                                                                                       GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG-----
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POLY-PRO.
POLY-SER.
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/FTId=VSP_004539.
H->A: LOSS OF ACTIVITY; WHEN ASSOCIATED
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Q03646;
01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum (isolate Nig32 / Nigeria).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=70150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
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01-OCT-1996 (Rel. 34, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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-!- SUBCELLULAR LOCATION: Attached to the membrane
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Yam; PF00985; MSA 2; 1.
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                                         VVTHEMAHANQTASDSSVMVRQVGFGNNATAN 149
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347 AA;
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34, Last annotation updat
antigen 2 precursor (MSA-
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RESULT 10 VG38_BPT2 ID VG38_BPT2 AC P07875;

STANDARD;

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Best Local
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01-NOV-1991
01-NOV-1991
10-OCT-2003
                                 Webb J.R., Button L.L., McMaster K.W. "Heterogeneity of the genes encoding of Leishmania donovani.";
                                                            MEDLINE=92107220; PubMed=1762629; Webb J.R., Button L.L., McMaster R.W.
                                                                                                                                                                                                                                                                                             LEIDO
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Raede I., Drexler K., Eschbach M.L., Henning U.;
"DNA sequence of genes 38 encoding a receptor-recognizing bacteriophages T2, K3 and of K3 host range mutants.";
J. Mol. Biol. 194:31-39(1987).
-i- FUNCTION: Vg38 is at the tip of the long tail fibers the phage recognition site for the cellular receptor.
-i- MISCELLANEOUS: THIS PHAGE USE OUTER MEMBRANE PROTEINS
                                                                                              STRAIN=LV9
                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                Eukaryota; Euglenozoa;
NCBI_TaxID=5661;
                                                                                                                                                Leishmania donovani
Eukaryota; Euglenoz
                                                                                                                                                                                      endopeptidase)
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01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF05268; GP38; 1.
Fiber protein; Phage re
SEQUENCE 262 AA; 258
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T4-like viruses
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Viruses; dsDNA viruses,
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nterPro; IPR007932; Tail_fibre_GP38.
Biochem. Parasitol. 48:173-184(1991). FUNCTION: Has an integral role during in the mammalian host.
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1988 (Rel. 08,
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1990 recognizing r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-profit institutions as long as its content is and this statement is not removed. Usage by and fo requires a license agreement (See http://www.isb-sib.an email to license@isb-sib.ch).
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protein (Protein Gp38).
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Pred. No. 1.2;
9; Mismatches 38; Indels
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01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell)
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Eukaryota; Euglenozoa;
NCBI_TaxID=44271;
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PROPEP
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InterPro; IPR001577; Peptidase.
Pfam; PF01457; Peptidase_M8; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M60048; AAA29244.1; -. P08148; 1LML.
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L outstation -
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MEDLINE=90205976; SEQUENCE FROM

PubMed=2320059;

Kinetoplastida;

Trypanosomatidae; Leishmania

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                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       Zymogen;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed during development of promastigotes to an infectious J. Biol. Chem. 267:1888-1895(19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M80672; AAA29238.1; -. EMBL; M28527; AAA29235.1; -.
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Arg-Gly-Asp
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PRINTS; PR00782; LSHMANOLYSIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EROPS; M08.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: Preference for P1' and basic residues at P2 and P3 cleaved at Ala-Tyr-|-Leu-Lys-Lys-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to peptidase family M8.
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                                                             Similarity
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267:1888-1895(1992).
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LOCATION: Attached to the membrane
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molecule implicated in cellular adhesion lacks an
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                                                                                                 63848 MW;
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                                              Score 87; DB Pred. No. 4.4; 0; Mismatches
266
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P3'. A model r
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nembrane by a GPI-anchor.
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Schlagenhauf E., Etges R., Metcalf P.;
"Crystallization and preliminary X-ray diffraction studies
leishmanolysin, the major surface metalloproteinase from Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schneider P., Ferguson M.A.J., McConville M.J., Mehlert A Homans S.W., Bordier C.;
"Structure of the glycosyl-phosphatidylinositol membrane the Leishmania major promastigote surface protease.";
J. Biol. Chem. 265:16955-16964(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Button L.L., McMaster W.R.;
"Molecular cloning of the major surface antigen of leishmania.";
J. Exp. Med. 167:724-729(1988).
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Eukaryota; Euglenozoa;
EURI_TaxID=5664;
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01-AUG-1988 (Re
                                         EMBL; Y00647; CAA68673.1;
                                                                                                   modified and this statement is not removentities requires a license agreement (S
                                                                                                                                          the European Bioinformatics Institute. There are no rest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Structure
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(Major surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteins 22:58-66(1995).
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                                                                                                                                                                                                                                              C14:0, C16:0, AND C18:0).
SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Has an integral role in the mammalian host.
PL0221; PL0221
1LML; 17-SEP-9
                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
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el. 14, Last sequence update)

el. 42, Last annotation update)

precursor (EC 3.4.24.36) (Cell

glycoprotein) (GP63 protein) (F
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InterPro; IPR001577; Peptidase M8.

Pfam; PF01457; Peptidase M8; 1.

PRINTS; PR00782; LSHMANOIYSIN.

PROSITE; PS00142; ZINC PROTBASE; 1.

Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc;

Hydronan: Signal; Cell adhesion; GPI-anchor; 3D-structure; Lipoprotein.
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STRAIN=MNYC/BZ/62/M379;
MEDLINE=93149206; PubMed=8426614;
Medlina-Acosta E., Karess R.E., Russell D.G.;
"Structurally distinct genes for the surface mexicana are developmentally regulated.";
                                                                                                                                                   Leishmania mexicana.
Eukaryota; Euglenozoa;
NCBI_TaxID=5665;
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(Rel. 32, Last sequence update)
(Rel. 42, Last annotation update)
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ace glycoprotein) (GP63 protein) (
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63953 MW;
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89.5%;
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Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc;
Zymogen; Signal; Cell adhesion; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; M08.001; -.
GlycoSuiteDB; P43150; -.
InterPro; IPR006025; Pept
InterPro; IPR001577; PeptI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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PRINTS; PR00782; LSHMANOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X64394; CAA45733.1;
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FUNCTION: Has an integral role during in the mammalian host.

CATALYTIC ACTIVITY: Preference for hyour and basic residues at P2 and P3'.

Cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.

COFACTOR: Binds 1 zinc ion per subunity.
                                                                                                                                                                                                  Local Similarity
les 17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amastigote forms.
SIMILARITY: Belongs to peptidase family
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(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                  Conservative
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                                                              STANDARD;
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CHAIN
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                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: THE 120 MDJ SURPACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN MISCH MAY PLAY A ROLE AS A RICKETSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Outer membrane protein B precursor (168 kDa surface-layer protein) (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB) (Yong B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptid
                                                                                                                                                                                                                                                                                                        TIGRFAM8;
                                                                                                                                                                                                                                                                                                              InterPro; IPR006315; Autotransport.
InterPro; IPR005546; Autotransporter.
95am; PP03797; Autotransporter.
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Rickettsiaceae; Rickettsieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            layer with hexagonal symmetry.
SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (By similarity).
SUBCELLULAR LOCATION: Cell wall. This bacterium is covered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity).
FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
                                                          548
                                                                                                                509
 601
                            122
                                                                                    6
                                                                                                                                                                          45;
                                                                                                                                                                                       Similarity
                                                    ---TLTLGGANISANGGTINFQANGGTIKLTST--QNNIVVDCDLAIATDQ
                                                                                    SETTITOSG----YGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVTH
                                                                                                                                             VAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSI YQYGSANAALALQSDARK
                                                                                                                                                                                                                                                                                         S-layer; Cell wall.
SSLTNAQTLTISGT---
                              EMAHANQTASDSSVMVRQVGF--GNNATANQY 151
                                                                                                                   VLAAGAITLDGSATI -----TGDIGNGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                       non-profit institutions as long
                                                                                                                                                                                                                                                                                                    TIGR01414; autotrans_barl;
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 -IGIIGANNTTLGOF
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Pred. No.
                                                                                                                                                                                                                                                         120 kDa SURFACE-EXPOSED PROTEIN
32 kDa BETA PEPTIDE.
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L outstation -
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	80	7	6	s	4.	ω	2	Ļ	Result No.
99	99.5	100	100	101	103	104	109	122	122	385	431.5	508.5	553	591.5	681	Score
12.8	12.8	12.9	12.9	13.0	13.3	13.4	14.1	15.7	15.7	49.7	55.7	65.6	71.4	76.3	87.9	Query Match Length
1748	171	362	151	409	362	7716	139	502	29	76	150	152	149	150	152	Length
ۍ	16	16	N	v	16	16	16	16	N	2	N	16	N	N	N	BB
Q94821	Q89JI3	Q8EV84	Q7X238	Q19414	Q89D03	Q7UWZ8	Q8EIH3	Q8EIH4	Q9S3J5	Q54069	Q7X237	Q8CW63	Q7X240	Q7X243	033802	ij
Q94821 tetrahymena	Q89ji3 bradyrhizob	Q8ev84 mycoplasma	Q7x238 enterobacte	Q19414 caenorhabdi	Q89d03 bradyrhizob	Q7uwz8 rhodopirell	Q8eih3 shewanella		Q983j5 escherichia	Q54069 salmonella	Q7x237 enterobacte	Q8cw63 escherichia	Q7x240 citrobacter	Q7x243 citrobacter	O33802 salmonella	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
90.5	90.5	91	91.5	91.5	92.5	92.5	92.5		92.5	92.5	93	93	93.5	93.5	93.5	93.5	93.5	94	94.5	95.5	95.5	95.5	95.5	96	96	96.5	ā	98
11.7	11.7	11.7	11.8	11.8	11.9	11.9	11.9	11.9	11.9	11.9	12.0	12.0	12.1	12.1	12.1	12.1	12.1			12.3					12.4	12.5		12.6
1209	152	191	1615	1422	1354	1351	1222	1222	440	348	3552	3501	623	552	552	453	453	179	453	1286	624	160	151	157	154	160	151	713
16	N	w	N	16	ທ	ហ	v	Ŋ	16	13	16	16	16	16	16					N	w	16	ν	16	16	16	16	v
Q89CK5	Q7X241	Q8TFA6	Q9KKA8	Q8EFU3	Q8MPN4	Q8SX56	Q8T8L9	Q9W4F0	Q92DG1	093397	Q8XSD6	Q8Y106	Q8VIY0	Q7TW76	P96840	Q9NGF7	Q9NGF6	033801	Q9N6M8	Q841Y5	Q8NIV1	Q8CW64	Q7X244	Q88HG0	Q89JI5	Q83RU7	Q7UCZ1	Q9N8N5
Q89ck5 bradyrhizob	Q7x241 citrobacter	Q8tfa6 saccharomyc	Q9kka8 rickettsia		Q8mpn4 drosophila	Q8sx56 drosophila			Q92dg1 listeria in	-	Q8xsd6 ralstonia s	Q8y106 ralstonia s		Q7tw76 mycobacteri			Q9ngf6 drosophila		Q9n6m8 drosophila		Q8niv1 neurospora	4	Q7x244 citrobacter	. Q88hg0 pseudomonas	Q89ji5 bradyrhizob	Q83ru7 shigella fl	Q7uczl shigella fl	Q9n8n5 trypanosoma

ALIGNMENTS

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121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151	61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120	61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120	1 MKILKVAAFAAIVVSGSAVAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	Local Similarity 90.1%; Pred. No. 2e-46; hes 136; Conservative 3; Mismatches 12;	Query Match 87.9%; Score 681; DB 2; Length 152;	SEQUENCE 152 AA; 15401 MW; 9DA7DADC2364B006 CRC64;	NON_TER 152 152	65:5320-5325		n mouse small intes	"Expression of thin, aggregative fimbriae promotes interaction of	SURUPOIVI S.S., MOTERICZ K.G., GOTGON J.I., BIRN 4., FLETTER J.D.,	1=9393832;	SEQUENCE FROM N.A.		NCBI TaxID=602;		Bacteria: Proteobacteria: Gammaproteobacteria: Enterobacteriales:	Salmonalla typhimurium	AGFA.	EC-2001 ((TrEMBLrel. 05,	-1998 (TrEMBLrel.	033802;	O33802 PRELIMINARY; PRT; 152 AA.	IT 1
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Q7X243
ID 247
AC Q7
DT 011
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GN CS
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OC BA
OC BA
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RT FR
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Matches 119
                                                                                                                                                   Zogaj X., Bokranz W., Nimtz M., Romling U.; Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4158 (2003).

EMBL; AJ515701; CAD56675.1; -. SEQUENCE 149 AA; 15260 MW; 946DD52017F648FD CRC64;
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01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7X240
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Curlin-csgA
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Q7X243;
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                                                                                                                                                                                                                                                                                                                                                                   Enterobacteriaceae; Citrobacter.
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Bacteria; Proteobacteria;
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MKLLKVAAFAAIVVSGSALAGVVFOWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ
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74.8%;
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78.8%;
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Last sequence update)
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                                                                    Score 553; DB
Pred. No. 2.5e
5; Mismatches
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Pred. No. 2.3e
L2; Mismatches
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2.5e-36;
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                                                                                                         Length
                                                                    Indels
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RESULT 5
Q7X237
ID 207X2
AC Q7X2
AC Q7X2
AC Q7X2
AC Q7X2
CDT 01-C
DT 01-C
DT 01-C
CUTI
GN CSGA
OS Ente
OC Bact
OC Batt
III
RN [1]
RN [1]
RN [1]
RP SEQI
RA Zoga
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QRESTLT

QRES
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Best Local
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Q7X237;
01-OCT-2003
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MEDLINE=22388234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., S Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure results by the complete genome of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                     NCBI_TaxID=28141;
[1]
                                                                                                                Enterobacteriaceae;
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Infect. Immun. 72:4151-4158(2003).
EMBL; AJ515702; CAD56678.1; -.
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                      Escherichia coli.
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Pred. No. 2.1e-23;
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01-MAR-2003
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Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., Meyer T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., DeBoy R.T., Dodson R.J., Durkin A.S., White O., Wolf A.M., Wanathevan J., Weidman J., Imparaim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
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MEDLINE=99314153; PubMed=10386375;

La Ragione R.M., Collighan R.J., Woodward M.J.;

"Non-curliation of Escherichia coli O78:K80 isolates associated with
"Non-triation in csgB and reduced persistence in poultry infection.'
FEMS Microbiol. Lett. 175:247-253(1999).

EMBL; AJ131756; CAB45380.1; -.

MON TER 29 29
                                                                                                                                                                                                            Hypothetical protein; Complete SEQUENCE 502 AA; 52441 MW;
                                                                                                                                                                                                                                                                       "Genome sequence of the dissimilatory Shewanella oneidensis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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NCBI_TaxID=70863;
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 351
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27.0%;
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Pred. No. 0.12;
2; Mismatches 57;
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                                                                    Hypothetical protein; SEQUENCE 7716 AA;
                                                                                                                                                                                      "Complete genome sequence of strain 1.";
                                                                                                                                                                                                                                                 Gloeckner F.O., Kube M., Bauer M., Teeli
Ludwig W., Gade D., Beck A., Borzym K.,
Schlesner H., Amann R., Reinhardt R.,
                                                                                                                                                                                                                                                                                                                                         MEDLINE=22735913; PubMed=12835416;
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Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C. Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanam M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., "Genome sequence of the dissimilatory metal ion-reducing bacterium
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Nat Riotechnol, 20:1118-1123(2002).
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                                                                                                                        Natl. Acad. Sci. U.S.A. 100:8298-8303(2003)
BX294135; CAD72214.1; -.
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Eukaryota; Metazoa; Nematoda; Rhabditidae; Peloderinae; Caer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genomic sequence of nitrogen-fixing Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002). BRG52907.1; -...
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Bacteria; Proteobacteria; Alphaproteobacteria;
Bradyrhizobiaceae; Bradyrhizobium.
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MEDLINE=22844998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Sasamoto S., Watanabe A., Shimpo S., Tsuruoka H., Wada T., Yamada
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Tabata S.;
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362 AA; 39058 MW;
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Caenorhabditis.
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Pred. No. 2.
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D447EE0D4E8433EC CRC64;
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                    Rhabditida;
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RESULT 13
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Matches 35
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Matches 37
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EMBL; AJ515702; CAD56677.1;
                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                       Enterobacteriaceae; Enterobacter.
NCBI_TaxID=28141;
                                                                                                                                                                                                                                                                Enterobacter sakazakii.
Bacteria; Proteobacteria;
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                                                                                                                                                                                                         STRAIN-Fec:
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        investigating biology.";
Science 282:2012-2018(1998).
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T20847; T20847.
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37; Conserv
                                                                                                    Similarity
                                                                   AAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETT
                                                                                                                                                                                                                                                                                                                                                                                                                  NNKSLTTNQINEQ---ASNWASANSVQAQYIQYETNRSA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                        NYDQLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YGN--GADVGQGADNSTIE---LTQNGFRNN--------ATIDQWNAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGQQASGSMNSFGGQGGYGQNQNGFGGQSGFSGQSGWGSNSLSSANSNGNNNQG---SSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG
ITODGYGNSAKIIOKGSGNRANITOYGTOKTAVVVO----KOSOMAIRVI
                     ITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVV 119
                                             AQIRQEGSKLLS
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                                                                                         Conservative
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31.8%;
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                                                                                       Score 100; DB
Pred. No. 1.6;
12; Mismatches
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Last annotation update)
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Pred. No. 4.3;
6; Mismatches 66
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RESULT

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RESULT 15
Q89JI3
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Q89JI3;
01-JUN-2003
01-JUN-2003
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Q8EV84;
01-MAR-2003
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EMBL, AP004172; BAC44476.1; -.

Interpro; IPR000437; Prok lipoprot S.

PROSITE; PES00013; PROKAR_LIPOPROTEIN; 1.

Lipoprotein; Complete proteome.

SEQUENCE 362 AA; 38547 MW; 8DA27F70D19D354F CRC64;
                                                                                                                         STRAIN=USDA 110;
MEDLINE=22484998; PubMed=12597275;
MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Iriguchi Maranaha A., Idesawa K., Iriguchi Maranaha A., Idesawa K., Iriguchi Maranaha
                                                                                                                                                                                                              Bradyrhizobium japonicum.
Bacteria; Proteobacteria;
Bradyrhizobiaceae; Bradyr
                                                                                                                                                                                                                                                  CsgA protein.
CSGA OR BLL5300.
                                                                                                                  Sasamoto S., Watanabe A., Kohara M., Matsumoto M.,
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01-OCT-2003
                                                           EMBL;
                                                                   "Complete genomic sequence of nitrogen-fixing Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                NCBI_TaxID=375
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                                                                                                         Tabata S.;
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                                                           AP005954; BAC50565.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKIKKIKLLKALALTGAFGIVATVPVIVSSCSSTSDNNGGNGNNNNNGNQDGNGQQQTEI
                                                                                                                                                                                                                                                                                                                                                                                   FTESTFKGD-TYETWSAKVGDKKGT-----YAQASKQLDIKSINDLETQLGDSNN 169
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(TrEMBLrel.
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Bradyrhizobium.
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M., Shimpo s
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shimpo S., Tsuruoka H.,
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Matches	40; Conservative 21; Mismatches 63; Indels 31; Gaps 4;	
Qy	1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	
Db	40 MRKLFFASVAVLALSSAAQAA	
Qγ	61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVT 116	
Db	79 NGLTNDSSSTTQIGILNGASIMQGTSSPSLNNVSTVNQAGVQNSATTGQVAFGNNGSAIT 138	
Q.	DSS.	
ф	139 QNSFGPPALQNNSASVGQLSFGINTSTVSQ 168	
Search completed: Ma Job time : 32.5 secs	Search completed: March 11, 2004, 18:40:45 Job time : 32.5 secs	

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Result
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AgfA sequ
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26-FEB-2001 AAB36353;

(first entry)

AgfA::PT3#8 amino

acid sequence

SEQ

ij NO:26 AAB36353 standard;

protein;

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
96	96	96	96.5	96.5	97.5	97.5	98.5	100	100	100	100	100	102	105	107	111	111	111	112
12.3	12.3	12.3	12.3	12.3	12.5	12.5	12.6	12.8	12.8	12.8	12.8	12.8	13.0	13.4			14.2		
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ALIGNMENTS

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmontella, Escherichia coli and Enterobacteriacese for the production of finbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinantion of a recombinant gene homologous species; (3) directing recombinantion of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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N-PSDB; AAC64629.
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Escherichia coli.
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RESULT 2
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Best Local
Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                            N-PSDB; AAC64626.
                                                                                                                                                          WPI; 2000-672631/65.
                                                                                                                                                                                                             White AP, Doran JL,
                                                                                                                                                                                                                                                                                                                                 05-APR-1999;
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                                                                                                                                                                                                                                                                     (UYVI-) UNIV VICTORIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AgfA::PT3#5 amino acid sequence SEQ ID NO:20
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                                                                                                                                                                                                          Collison SK, Kay WW
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Disclosure;

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137; 139pp;

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
26-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella; AgfA; vaccine
                                       (UYVI-) UNIV VICTORIA INNOVATION (KING/) KING J.
                                                                                                                                                       26-APR-1993;
                                                                                                                                                                                                                                   26-APR-1994;
                                                                                                                                                                                                                                                                                                          10-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                  WO9425598-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR74625 standard; protein; 151 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AgfA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
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Pred. No. 2.5e-60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune respons Salmonella in animals (e.g. food producing animals) and humans. (Upo on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described
                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                              Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB36341 standard;
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                                                                                                                                     WPI; 2000-672631/65.
N-PSDB; AAC64617.
                                                                                                                                                                                                                                                             05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                    WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                    Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
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                                                       Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                   05-APR-1999;
                                                                                                                                                                                                                                                                                         12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                         vaccine; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-358275/44.
                                                                                                                                                                                                          (UYVI-) UNIV VICTORIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNAALVNOTASDSSVMVROVGFGNNATANOY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                                                                                                                                                                                                       response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; 151
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Pred. No. 1.1e-58;
                                                                                                                                                                             SK,
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(Updated
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           copy of that gene, and (4) eliciting an immune response in an animal, or copy of that gene, and (4) eliciting an immune response in an animal, and (2) eliciting an immune response in an animal, or comprising separating a replacement segment or segments of foreign amino acid polymer comprising a recombinant AgfA or protein containing a replacement segment or segments of foreign amino acid polymer containing a replacement segment or segments of foreign amino acid polymer into or sequences grown on a Salmonella, E. coli or compared the animal in conjunction with a carrier or diluent. (1) is conjumer into the animal in conjunction with a carrier or diluent. (1) is conjumer into the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted spitope, and hybrid fimbriae are easy and incorporative to purify in large amount. The present sequence is given in
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Best Local Similarity
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Collinson SK,
                                                                                                                                                                                                                                                                                                  Salmonella
                                                                                                                                                                                                                                                                                                                                                                             Salmonella
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29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW23570;
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                                                                                                                                                03-JUN-1997
                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                      Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
                                     (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP
                                                                          26-APR-1993;
                                                                                                               26-APR-1994;
                                                                                                                                                                                       US5635617-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                                                                                                                                  enteritidis
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(first entry)
Kay WW,
                                                                          93US-00054452.
                                                                                                               94US-00233788.
                                                                                                                                                                                                                                            Location/Qualifiers 123
                                                                                                                                                                                                                          /note= "Encoded by GCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; 151 AA
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   Doran JL
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Pred. No. 1.1e-58;
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RESULT 6
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Best Local Similarity
Matches 136; Conserv
               Recombinant
                                         N-PSDB; AAC64625.
                                                      WPI; 2000-672631/65
                                                                                White AP,
                                                                                                                                05-APR-1999;
                                                                                                                                                         05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                      12-OCT-2000
                                                                                                                                                                                                                                                     Escherichia
                                                                                                                                                                                                                                                                  Salmonella enteritidis
                                                                                                                                                                                                                                                                                                      Salmonella; agfA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                              WO200060102-A2
                                                                                                                                                                                                                                                                                                                                 AgfA::PT3#4
                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                             AAB36349 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
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N-PSDB; AAT74142.
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 binant agfA gene
encodes foreign
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                                                                              Doran JL,
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                                                                                                                                                                                                                                                     COLL
                                                                                                                                                                                                                                                                                                                                 amino
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                                                                                                         VICTORIA.
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                                                                                                                                                                                                                                                                                          response;
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having a segment replaced by a epitope or antigen, expresses r
                                                                               Collison
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                                                                                                                                                                                                                                                                                        immunogen.
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Pred. No. 3.3e-58;
2; Mismatches 13
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                                                                              Kay ww
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  recombinant
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          DNA sequence
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which

05-APR-2000; 2000WO-CA000356

12-OCT-2000

WO200060102-A2 Synthetic

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RESULT 7
AAB3633
XX AAB363
AC AAB3
XX AAB3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cc back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, cc comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino card sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is cuseful for the expression of recombinant AgfA protein which is useful for celliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the cimmunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong cimmunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and considered to purify in large amount. The present sequence is given in the exemplification of the present invention
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Matches
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                                                                                                                                                                                                                                                                                                           Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella; agfA; chromosomal gene replacement; fimbrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria mubunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene
                                                                                                                                                                                                                                                                       Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                           vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AgfA::PT3#9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 WNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 LVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid sequence SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                           ımmunogen
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Pred. No. 4.7e-57;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                           epitope;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 128; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 151 AA;
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vaccine; immune response; immunogen
                    Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                         AgfA::PT3#1 amino acid sequence SEQ ID NO:12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
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                                                                                                26-FEB-2001
                                                                                                                                                                         AAB36346 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 138; 139pp; English
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                                                                                                                                                                                                                                                                                                  RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                        SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHA-----F
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAAL---
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                                                                                              (first entry)
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gene has been replaced by a segment of a foreign DNA
encodes a foreign epitope or antigen. Also described a
n aggregative fimbriae (SEF17/TAF) nucleation depended
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73.6%;
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Pred. No. 1.8e
0; Mismatches
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence in the present sequence is given in the present sequence in the present sequence is given in the present sequence in the present sequence is given in the present sequence in the present sequence is given in the present sequence in the present sequence is given in the present sequence in the present sequence is given in the present sequence in the present sequence is given in the present sequence in the present sequence is given in the present sequence in the present sequence is given in the present sequence in the present sequence is given in the present sequence in the present sequence is given in the present sequence in the present sequence is given in the present sequence in the present sequence is given in the present sequence in the present 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exemplification of the present invention
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121
                                                           121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                     LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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   NNAALVNYDQLVTRVVTHEMAHANNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                             78.5%;
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                                                                                                                          /GNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                               6,
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 614; DB 3;
Pred. No. 3.5e-51;
                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kay WW
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 151;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT

AAB36347

AAB36347 standard;

protein; 151

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                                                                                                                                                         AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively, (2)
Cd directing recombination of a recombinating gene into the chromosome of the
Cmonlogous species, (3) directing recombination of a recombination of a recombination of a recombination of the chromosome of the
Cd copy of that gene; and (4) eliciting an immune response in an animal,
Cd comprising separating an amino acid polymer comprising a recombinant AgfA
Cd protein containing a replacement segment or segments of foreign amino
Cd acid sequence or sequences grown on a Salmonella, E. coli or
Cd Enterobacteriaceae host cell, from the host cell and introducing the
Cd polymer into the animal in conjunction with a carrier or diluent. (1) is
Cd useful for the expression of recombinant AgfA protein which is useful for
Cd useful for the expression of recombinant AgfA protein which is useful for
Cd system the heterologous antigens, are presented in high numbers (up to
Cd 500,000 copies/cell), the hybrid fimbrin protein possesses both the
Cd immunogenicity and adhesion properties relevant for an efficient live
Cd vaccine, the carrier fimbrial subunit proteins are usually strong
Cd immunogens, which may be important for directing an immune response
Cd against the inserted epitope, and hybrid fimbriae are easy and
Cd inexpensive to purify in large amount. The present sequence is given in
Cd the exemplification of the present invention
                                                                             Matches
                                                                                               Query Match
Best Local
                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA seguence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SER17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 136; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-672631/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enteritidis
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AgfA::PT3#2 amino acid sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AP, Doran JL,
                                                                                               Similarity
                           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                       151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   foreign epitope or learning immu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0127888P.
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                                                                                             78.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collison
                                                                       Score 612; DB
Pred. No. 5.5e
5; Mismatches
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                                                                         e 612; DB 3; I
. No. 5.5e-51;
ismatches 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   response in animal.
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                                                                                                             Length 151
                                                                           Indels
                                                                         0,
                                                                         Gaps
 60
                                     60
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The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA compared which encodes a foreign epitope or antigen. Also described are: (C1) use of thin aggregative fimbriae (SEF1/T/RA) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant QfA, CgA and AgfA-homologue fimbria subunits, respectively; (2) cc directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E coli or acid sequence or sequences grown on a Salmonella, E coli or containing an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the carrier fimbrial subunit for an emune response in an efficient live vaccine, which may be important for directing an emunual strong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 138; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-672631/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant agfA gene having a segment replaced by a foreign DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYVI-) UNIV VICTORIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      æ
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RESULT 11
AAB36351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CegA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or
                                                                                                                                                                                                                                                                       Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
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                                                                                                                                                                                                                                        Disclosure; Page 137; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella enteritidis.
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                                                                                                                                                                                                                                                                                                                                                                                      White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-2000; 2000WO-CA000356.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine; immune response;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                      2000-672631/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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82.1%;
                                                                                                                                                                                                                                                                                                                                                                                      Collison
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                                                                                                                                                                                                                                                                                                                                                                                      SK,
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                                                                                                                                                                                                                                                                                                                                                                                      Kay
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.1e-50;
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Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                             Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                     the exemplification of the present invention
121
                                        121
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                        NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                               LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                  SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
                                                                                                                                                                                                               MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                            76.9%;
                                                                                                                                                                                                                                                        4.
                                                                                                                                                                                                                                                                            Score 601; DB 3;
Pred. No. 6.3e-50;
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                                        151
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RESULT 12
AAB36355
ID AAB36
WPI; 2000-672631/65.
N-PSDB; AAC64631.
                                                                                                                                                                         Synthetic.
                                                                                                                                                                                      Salmonella enteritidis
                                                                                                                                                                                                     vaccine;
                                                                                                                                                                                                            Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                   05-APR-1999;
                                                                                                                                05-APR-2000; 2000WO-CA000356
                                                                                                                                                           WO200060102-A2
                                                                                                                                                                                                                          AgfA::PT3#10 amino acid sequence SEQ ID NO:30.
                                                                                                                                                                                                                                        26-FEB-2001
                                                                                                                                                                                                                                                                   AAB36355
                                                                                                     (UYVI-) UNIV VICTORIA
                                                                                                                                             12-OCT-2000
                                                                                                                                                                                Escherichia
                                                                                                                                                                                                    1mmune response;
                                                                                                                                                                                                                                                                   standard;
                                                                                       Doran JL,
                                                                                                                                                                                 COL1.
                                                                                                                                                                                                                                        (first entry)
                                                                                                                   99US-0127888P
                                                                                                                                                                                                                                                                  protein;
                                                                                        Collison
                                                                                                                                                                                                     ımmunogen
                                                                                       SK,
                                                                                       Kay ww
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Recombinant agfA gene having a segment replaced by a foreign which encodes foreign epitope or antigen, expresses recombing protein useful for eliciting immune response in animal.

antigen, expresses recombinant une response in animal.

DNA sequence

Disclosure; Page 139; 139pp; English.

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described

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RESULT 13
AAB36348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC back into the chromosome of the homologous species, replacing the native C copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a carrier or diluent. (1) is CC useful for the expression of recombinant AgfA protein which is useful for CC system the heterologous antigens are presented in high numbers (up to CC 500,000 copies/cell), the hybrid fimbrin protein possesses both the CC immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong CC against the inserted epitope, and hybrid fimbrine are easy and constraint in converte, in larva smanner that are easy and constraint of converted to cover the converted politope, and hybrid fimbrine are easy and constraints of covering the cover the covering an immune response constraints the inserted epitope, and hybrid fimbrine are easy and constraints the inserted epitope.
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White AP, Doran JL,
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                                                                                                                                                                                     05-APR-2000; 2000WO-CA000356
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunogens, which may be important for directing an immune ragainst the inserted epitope, and hybrid fimbriae are easy a inexpensive to purify in large amount. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
                                                                                                                                                                                                                                                                                                                 WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AgfA::PT3#3
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                                                                (UYVI-) UNIV VICTORIA

    use of thin aggregative fimbriae (SEF17/TAF) nucleation
assembly system of strains of Salmonella, Escherichia coli a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune response;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDARKSETTITQSGYGNGADVGQGADNSTIBLTQNGFRNNATYDQLVTRVVTHEMAHAGG
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81.5%;
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Pred. No. 7.8e-50;
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RESULT 14
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                                                                                                                                                                        Escherichia
                                                                                                                                                                                                                                                                        Salmonella; agfA; chromosomal gene replacement; fimbrin;
                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2001
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                                                                                                                                                                                                                                            vaccine;
                                                                                                                                                                                                                                                                                                                                            Escherichia coli CsgA amino acid sequence SEQ ID NO:7
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2000WO-CA000356

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RESULT 15
ABR82651
ID ABR82
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AC ABR82
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DT 04-DE
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DE E. CC
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Best Local S
Matches 104
                    E. coli CegA subunit 15 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
                                                           04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                  ABR82651;
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                                                                                                                                                                                                                                                                                                             LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                  NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                     GNGAAVDOTASNSSVNVTQVGFGNNATAHQY 151
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                                                                                                                                   standard; protein;
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ilarity 68.9%;
Conservative 1
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                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
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Pred. No. 2e-42;
8; Mismatches
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Search completed: March Job time: 46.9 secs

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Best Local S
Matches 103
                                                                                                                                                                                                                                                                                       The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABR82642, ABR82648-49. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma is also useful as a reagent for determining the ability of a plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infections.
                                                                                                                                                                                                                                               Sequence 151
                                                                                                                                                                                                                                                                              protein to bind
15 kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 41-42; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bjoerck L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JAN-2002; 2002GB-00002275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003064446-A2
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121
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                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                                                                                                                    Similarity
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                        NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                        LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
                                                             TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
                                                                                                                        MKLLKVEAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSEINIYQYGGGNSALALQ
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                                                                                                                                                                                     Conservative
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                                                                                                                                                                                    Score 518; DB 7;
Pred. No. 6.2e-42;
8; Mismatches 30
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151
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein -
                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.
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782
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 Issued_Patents_AA:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                Length
BB
        US-08-233-788A-59
US-08-233-788A-57
US-09-235-788A-57
US-09-072-596-199
US-09-072-596-199
US-09-072-967-204
US-09-072-967-204
US-09-336-447A-5
US-09-328-352-6167
US-09-328-352-6167
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US-09-196-387-8
US-09-196-387-10
US-09-196-387-10
US-09-196-387-10
US-09-196-387-2
US-09-196-387-2
US-09-196-387-13
US-09-196-387-13
US-09-36-47A-13
US-09-36-47A-13
US-09-356-47A-13
US-09-356-47A-13
US-09-356-3739
US-09-336-115C-6
US-09-336-115C-6
US-09-336-3739
US-09-439-520A-18
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                                                                                                                                                         Sequence 59, Appl
Sequence 57, Appl
Sequence 204, App
Sequence 199, App
Sequence 311, App
Sequence 31, Appli
Sequence 3, Appli
Sequence 4764, Ap
Sequence 6167, Ap
Sequence 26438, A
Sequence 8, Appli
Sequence 8, Appli
Sequence 10, Appli
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                                            Sequence
Sequence
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         10, Appl
10, Appl
2, Appli
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13, Appli
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30227, A
10179, Appli
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	76	76	76	76	76	76	76.5	76.5	76.5	76.5	76.5	77	77	77	77	77	77	77
	9.7	9.7	9.7	9.7	9.7	9.7	9.8	9.8	9.8	9.8	9.8	9.8	9.8	9.8	9.8	9.8	9.8	9.8
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ALIGNMENTS	US-08-304-626-2	US-08-158-232-2	US-08-063-170-2	US-07-675-772-2	US-07-876-280-2	US-07-792-259-17	US-08-169-927-2	US-09-336-447A-9	US-09-168-406A-2	US-08-331-515A-2	US-08-458-023B-6	US-09-543-681A-5434	US-08-617-697-10	US-08-617-697-9	US-08-719-641-10	US-08-728-470-10	US-08-719-641-9	US-08-728-470-9
	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 17, Appl	Sequence 2, Appli	Sequence 9, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 5434, Ap	Sequence 10, Appl	Sequence 9, Appli	Sequence 10, Appl	Sequence 10, Appl	Sequence 9, Appli	Sequence 9, Appli

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COUNTRY U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentII Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DCCKET NUMBER: 920043.403C2
TELECOMOUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELECX: 372836 SEEDANBERRY
INFORMATION FOR SED ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acids
TYPE: amino acids
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US-08-233-788A-59
Query Match
Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Collineon, Karen S.
APPLICANT: Collineon, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
NUMBER OF SEQUENCES: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 59, Application US/08233788A Patent No. 5635617
                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
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STREET: 6300 Columb
CITY: Seattle
STATE: Washington
    87.9%; ilarity 90.1%; Conservative
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00 Columbia Center,
    Score 687; DB 1; Length 15: Pred. No. 7e-60; Indels 13; Indels
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                                              Length 151
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US-09-056-556-204
                                                                      RESULT
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; MOLECULE TYPE: protein
US-08-233-788A-57
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US-08-233-788A-57
               Sequence 204, Application US/09056556 Patent No. 6350456
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Best Local (
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APPLICANT: Doran,
APPLICANT: Kay, Wil
APPLICANT: Collinge
APPLICANT: Clouthie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 57, Application US/08233788A
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                             GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                                                              VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGADV
                                                                                                                                                                                             VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
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Collinson, Karen S.
Clouthier, Sharon C.
: Clouthier, Sharon C.
: INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TANVENTION: OF SALMONELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                120 amino acids
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                                                                                                                                                                                                                                                                    64.8%;
llarity 87.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             622-4900
                                                                                                                                                                                                                                                                    Score 507; DB 1; Length 120; Pred. No. 2.1e-42; Mismatches 12; Indels
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Matches
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                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVID J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 204:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
                                            CORRESPONDENCE ADDRESS:
                                                                 NUMBER OF SEQUENCES:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
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                            ADDRESSEE:
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                                                                            Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Romald C.
NVENTION: COMPOUNDS AND M
         6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  943 amino acids
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Dillon, Davin C.
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Dillon, Davin C.
VENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
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                            SEED and BERRY LLP
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Mismatches
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                                                                                                                          SOFTWARE: Pa
SEQ ID NO 131
LENGTH: 943
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Matches
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                                                                          -09-477-135A-131
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6572865
                                                                                                                                                                            PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1996-0
                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 089
PRIOR FILING DATE: 1997-12-15
                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/477,135A CURRENT FILING DATE: 2000-01-03
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
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SEQUENCE CHARACTERISTICS:
LENGTH: 943 Aminimum Type
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER:
                                                                               TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/072,596 FILING DATE: 05-MAY-1998 CLASSIFICATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                  Local Similarity
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STRANDEDNESS:
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12.8%; Score 100; DB 26.0%; Pred. No. 0.2; Live 12; Mismatches
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                                   DB 4; Length 943;
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TOPOLOGY:
US-09-072-967-204
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                                                                                                                                                    Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVID J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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504 GFGNAGDFNQGFANT------GNNNIGFANTGNNNIGIGLSGDNQQGFNIASGWNS 553
                                                                  464 GSGNIGVFNVGSGSLGNYNIGSGN-----LGIYNIGFGNVGDY------NV 503
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                                  74 GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN------ 121
                                                                                                    16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA 73
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                                                                                                                                                                                                                                                                             943 amino acids
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                                                                                                                                      Conservative
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Hendrickson, Ronald C.
VENTION: COMPOUNDS AND
VENTION: AND DIAGNOSIS
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Dillon, Davin C.
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                                                                                                                                                      Score 100; DB 4; Length 943; Pred. No. 0.2;
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                                                                                                                                      Mismatches
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US-08-864-038A-3
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: Kunio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (212)986-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 15-July
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: May 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Word Perfect 6.1
RRENT APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION TO THE STREET APPLICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
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                                                                                                                       ---LAAALAAAGAGGGLGGGGGGGALAAALAAAGAGGGGFGGLGGL
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                                                                                                                                                                                                                                                             LLKSSASASASASASAG
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from 1 to 738
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ION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR

ION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID

ION: CONTAINING SAID FOLYPEPTIDE PRODUCED THERBEY, METHÓD OF PRODUCING

ION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                               12.6%;
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                                                                                                                                                                                                                                                                                                                                                                              Score 98.5; DB Pred. No. 0.2; 11; Mismatches
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4764
LENGTH: 975
                                                                                                                                                                                                                                       Query Match
Best Local :
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GENERAL INFORMATION:
                                                                                                                                                                                                                      Matches
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Best Local S
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CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
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                                                                                                                                                                                                                                                                                                                    ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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ITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 892
                                                                                                                                                                                                                  Local Similarity es 37; Conserv
                                                        338 NSFTLIGNSS---SSSVNTAPTTTSNTVNDNDTID--NGNSGGTGSGSGNGSGDGLLNGA 392
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                                                                                                                                                                           15 SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAG 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 -----GNGADVGQGADNSTI--ELTQNGFRNNATIDQWNAKNSDITVGQYG---GNNAAL 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 GGGNHN------GGGNSS---GPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGY
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ASDSSVMVRQVGFGN 144
                                                                                                                                   NGTGDSG-VSALGGSGNGSGDGAGNGIASGNGEHNYGIGNGNGDDVDITAPITGVLNISG 337
                                                                                           ----YGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQT 129
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FISKE, MICHAEL J
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                                                                                                                                                                                                                    Conservative
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27.4%;
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27.7%; Pred. No.
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                                                                                                                                                                                                                                     Score 91.5; DI
Pred. No. 1.4;
                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                        DB 4;
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                                                                                                                                                                                                                                                                           US-09-252-991A-26438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: Rubenfie APPLICANT: MARC J. Rubenfie TITLE OF INVENTION: NUCLEIC TITLE OF INVENTION: AERUGIN FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                              SEQ ID NO 26438
LENGTH: 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26438, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 6167
LENGTH: 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6167, App
Patent No. 6562958
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                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                 Local
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                                                                                                                   366 ILSHEVSVAAVGQANAAGDGSGQVHVAQGPAGANASDSNGVTIVQQQPAVDLAAGANGTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 TVGQYGGNNAALVNQTASDSSV--MVRQVGF 142
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                                         426 AVQSQSGANIGSGANGISVVQSQNGANIGAGASDISVVQSQNSPNIGSGVNGVTVVQSQN
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                                                                            64 RVVTHEMAHAGYG------NGADVGQGADNSTIELTQN-----GFRNNATIDQWN
                                                                                                                                                        13 VVSGSALAGVVPQWGGGGNHNG------GGNSSGPDSTLSIYQYGSANAALYDQLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 NAALYDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 MKKLAIASALLSALAVSGAANA-YQAEVGGSYNYLDPDNGSSVSKFGVDGTYYFNPVQTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLLKVAA--FAAIVVSGSALAGVVPQWGGGGNH----NGGGNSS-GPDSTLSIYQYGSA 53
                                                                                                                                                                                                                 Similarity
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  AKN----SDITVGQYGGNNAALVNQTASDSSVMVRQVG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MARC J. Rubenfield et al.

AVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1998-02-18
                                                                                                                                                                                                                 11.0%; Score 86; DB 4; Length 1415; 23.9%; Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.3%; Score 88; DB 4; Length 273, 28.5%; Pred. No. 0.6;
                                                                                                                                                                                               21; Mismatches
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                                                                                                                                                                              RESULT 13
US-09-841-835-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                34;
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GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEI
TITLE OF INVENTION: OF USE T
NUMBER OF SEQUENCES: 12
                                                                                                                   Sequence 8, Application US/09841835
Patent No. 6506587
GENERAL INFORMATION:
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APPLICATION NUMBER: 09/095,221
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
APPLICANT: de Lange, .....
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS
TITLE OF INVENTION: OF USE THEREOF

TITLE OF OF ORDITANCES: 12
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                             158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    486 GANIGSGASGITVVQ--SQNGANIGSGASGISVVQSQSG
                                                                                                                                                                                                                                                                                                                   62 -VTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                   99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA
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29.6%; Pred. No.
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RESULT 14
US-09-196-387-10
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                              APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CTTY: Hackensack
                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 673 amino acids
                  APPLICATION NUMBER: FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                      ADDRESSEE:
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40, 6277613
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                                                                                                                                                                                       New Jersey
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411 Hackensack Avenue,
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                           US/09/196,387
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Pred. No. 7.
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APPLICANT: de Lan
APPLICANT: Smith,
                                   TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERRENCE/DOCKET NUMBER: 600-:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS LENGTH: 949 amino acids
                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 09/0:
FILING DATE: June 10, 19:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: OF USE THEREOF
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                                                                    TELEFAX:
                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
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                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                          COMPUTER:
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REFERENCE/DOCKET NUMBER: 600
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB
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seq length: 2000000000
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1: /cgn2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

5: /cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

6: /cgn2 6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

7: /cgn2 6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

8: /cgn2 6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2 6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

10: /cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

11: /cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

12: /cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

13: /cgn2 6/ptodata/1/pubpaa/US09 NEW PUB.pep:*

14: /cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

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Gapop 10.0 , Gapext 0.5
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 9 US-09-93-306-146
9 US-09-996-634-131
0 US-09-997-182-131
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4 US-10-193-002-199
5 US-10-369-493-20619
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1 US-10-233-553-23
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Sequence 20638, A
Sequence 146, App
Sequence 131, App
Sequence 131, App
Sequence 199, App
Sequence 199, App
Sequence 204, App
Sequence 20619, A
Sequence 27, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 11, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
                                                                                                                                                                                                                                                                                                       Description
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ALIGNMENTS

US-10-369-493-20638

Sequence 20638, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:

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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
ITITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
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Best Local Similarity
Matches 46; Conserv
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LOCATION: (1). (445)
OTHER INFORMATION: unsure at all Xaa locations
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19 AAFAADSNTVYLNQTGNDQQANITQSGNGNSVGAFNGNSGFLQENGTLSGA-NLLTVKQS
                                                                                                                                                                   7 AAFAA-----IVVSGSALAGVVPQWGGGG-----NHNGG-----GNSSGPDSTLSIYQY
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27.5%; Pred. No. 0.0019;
rive 20; Mismatches 60; Indels 41;
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PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR PELICATION NUMBER: 08/990,823
PRIOR PILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
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SEQ ID NO 146
LENGTH: 597
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Patent No. US20020098200A1
                                                                                                                                                                                                FILE REFERENCE: 61260
CURRENT APPLICATION NUMBER: US/09/996,634
CURRENT FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                             APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences
TITLE OF INVENTION: immunostimulatory Peptides
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TITLE OF INVENTION: of Tuberculosis
FILE REFERENCE: 014058-008740US
CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR FILING DATE: 2000-08-08
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RESULT 5
US-09-997-181-131
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US-09-997-182-131
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PRIOR FILLING DATE: 2000-01-03
PRIOR PPLICATION NUMBER: 08/990,823
PRIOR FILLING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR APPLICATION NUMBER: 60/000,254
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 131
LENGTH: 943
                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
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Publication No
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 131
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NUMBER OF SEQ ID NOS: 169
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CURRENT FILING DATE: 2001-11-28
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TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
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TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
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Pred. No. 0.22;
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Application US/09997181 o. US20030049269A1

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RESULT 6
US-10-193-002-199
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Publication No. US20030135026A1
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PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
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CURRENT FILING DATE: 2001-11-28
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PRIOR FILING DATE: 1996-06-14
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TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
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                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                              Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 --- NAAL VNQTASDSSVM---- VRQVGFGNNATAN 149
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                                                                                                                                                                         COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                             STATE: Washington
APPLICATION NUMBER: US/10/193,002 FILING DATE: 10-Jul-2002
                                                                                                                                                                                                                                   CITY: Seattle
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Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
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Dillon, Davin C.
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RESULT 7
US-10-084-843-204
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 199:
                                   COMPUTER READABLE FOOM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILLING DATE: 25-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Ronald C.
AND DIAGNOSIS OI
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FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 199:
                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                554 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            464 GSGNIGVFNVGSGSLGNYNIGSGN-----LGIYNIGFGNVGDY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN------ 121
APPLICATION NUMBER: US/09/072,967 FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                 STATE: Washington
                                                                                                                                                                                                                                                                                                         CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 943 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                            ADDRESSEE: SEED and BERRY LLP STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (20
TELEFAX: (206)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Maki, David J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/10084843
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Dillon, Davin C.
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Pred. No. 0.22;
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                                                                                                                                                                                                                                                                                                                              701
                                                                                                                                                                                                                                                                                                                              Fifth Avenue
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SEQ ID NO 20619
LENGTH: 486
                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(486)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 204:
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les 40; Conserv
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REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                         145 -----VIIHTAAVGGRPRGALISQG--NLLI-----
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                                                                                                                         86
                                                                                                                                                            11 AIVVSGS----ALAGVVPQWGGGGNHNGGGNSSGP-----DSTLSIYQYGSANAAL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN----
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                                                                                                                                                                                                      l Similarity
37; Conserv
                                                                                                                       SVVVAGTDYRDIVAGVLPSLGGVKKAYAIGDGSGPFAPFKDLASDTPFSAPEFGAADGF-
                                                                               YDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVG- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---NAALVNQTASDSSVM----VRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 943 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
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                                                                                                                                                                                                      Conservative
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  QYGGNNAALVNQTASDSSVM 136
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STRATION NUMBER: 31,392
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25.7%;
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                                                                                                                                                                                                                       Score 98.5; DB 15;
Pred. No. 0.14;
                                                                                                                                                                                                      Mismatches
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                                         -- AQSSLVDAWRLTEADVNLGM 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 943;
                                                                                                                                                                                                                                          Length 486;
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                    35;
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US-09-820-843A-21
; Sequence 21, Application US/09820843A
; Publication No. US20030039963A1
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                                                                                 US-09-820-843A-21
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Query Match
Best Local Simi
Matches 34;
                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0
SEQ ID NO 21
LENGTH: 354
TYPE: PRT
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Publication No. US20030032772A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local
                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/820,843A CURRENT FILING DATE: 2001-03-30 NUMBER OF SEQ ID NOS: 118
                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: Q63915
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Council of Scientific and Industrial ResTITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 09/336,447
PRIOR FILING DATE: 1999-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/952,267
CURRENT FILING DATE: 2001-09-12
                                                                                            NAME/KEY: misc_feature
OTHER INFORMATION: PPE
NAME/KEY: misc_feature
OTHER INFORMATION: gi|1781260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: AMCY:024
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                                                                                                                                                                             ORGANISM: M. tuberculosis FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDEXBURG, ROSS A.
FITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 892
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                    Similarity
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    Conservative
                  11.8%;
27.6%;
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    12;
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Score 92; DB 10
Pred. No. 0.42;
12; Mismatches
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                                      DB 10; Length 354;
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    43;
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    Indels
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    34;
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RESULT 12
US-10-233-553-11
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; ORGANISM: Homo sapiens US-10-233-553-11
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; ORGANISM: Homo
US-10-233-553-23
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Publication No. US20030125285A1
GENERAL INFORMATION:
APPLICANT: NIPPON SHINYAKU CO.,LTD.
APPLICANT: HIRABAYASHI, Kazuko
APPLICANT: YANO, Junichi
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Matches
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                                                                   PRIOR APPLICATION NUMBER: JP 2001-267385
PRIOR FILING DATE: 2001-09-04
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 23
LENGTH: 591
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APPLICANT: HIRABAYASHI, Kazuko
APPLICANT: YANO, Junichi
TITLE OF INVENTION: Method of examining the efficacy of therapy with nucleic acid
FILE REFERENCE: B-345
CURRENT APPLICATION NUMBER: US/10/233,553
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: JP 2001-267385
PRIOR FILING DATE: 2001-09-04
                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/233,553
CURRENT FILING DATE: 2002-12-19
                                                                                                                                                                                           TITLE OF INVENTION: Method of examining the efficacy of therapy with nucleic FILE REFERENCE: B-345
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                                                      LENGTH: 894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 GADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 GGGG-----NHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGN
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US-10-185-990-11
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US-10-185-990-10
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                                                                                                                                                                                                                                           Sequence 11, Application US/10185990 Publication No. US20030073109A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 1621
TYPE: PRT
ORGANISM: BACILLUS SUBTILIS
                                                                                                                        SEQ ID NO 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
 Matches
               Query Match
Best Local Similarity
                                                                                                                                  APPLICANT: Pan, Jae-Gu
TITLE OF INVENTION: JAE GU PAN ET AL
FILE REFERENCE: 02589,000100
CURRENT APPLICATION NUMBER: US/10/185,990
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
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Best Local (
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CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Pan, Jae-Gu
TITLE OF INVENTION: JAE GU PAN
FILE REFERENCE: 02589.000100
                                                                          ORGANISM: Bacillus subtilis
                                                                                          TYPE: PRT
                                                                                                       LENGTH: 1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                54 NAALYDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDI 113
 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 GSALAG-----VVPQWGG----GGNHN------
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                                                                                                                                                                                                                                                                                                                                                       TAG-YGS-----TQTAQEGSNLT--AGYGSTGTA 308
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 Conservative
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               11.3%;
27.1%;
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27.1%; Pred. No. 6.3;
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27.1%; Pred. No. 1
 21;
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Score 88.5; DE Pred. No. 6.3; 21; Mismatches
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 41;
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                            Length 1626;
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 51;
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slatter, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 105/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 18460
LENGTH: 1649
TYPE: PRT
ORGANISM: Lactococcus lactis
US-10-369-493-18460
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Search completed: March 11, 2004, 19:18:39 Job time : 24.6 secs
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US-10-369-493-18460
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Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18460, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
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                                                                                                                                                          115 VGQYGGNNAALVNQTASDSSVMV, 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 GSTLSGDNHSRLIAGYGSNETAGNHSDLIAGYGSTGTAGYGSTQTSGEDSSLTA-GYGST 241
                                                                                                              766 GGNYG---QAGVETIAGDSTVNV 785
                                                                                                                                                                                                                 712 EGGGYT---ATTKWGNTTAQVNQGQVNWFLSGGSWGDLYNTG---SATVNVYNGYINAIT 765
                                                                                                                                                                                                                                                                                                                       655 WGGGGTVWTYRQAFLQNGNSYLIHNNDIARWTYGGQSNGSQVGNS---YNILNGAIVDTL 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 GSALAG-----VVPOWGG---GGNHN--------GGGNSSGPDSTLSIYQYGSA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 NAALYDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                        62 VTRVVTHEMAHAGYGN-GADVGQGADN-----STIELTQNGFRNNATIDQWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                              26 WGGGGN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                11.2%; Score 87.5; DB 15; 30.8%; Pred. No. 8.1; tive 10; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                              ---HNG-----GGNSSGPDSTLSIYQYGSANAALYDQL 61
                                                                                                                                                                                                                                                                                                                                                                                                                        46; Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1649;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on: March 11, 2004, 18:24:14; Search time 10.3 Seconds (without alignments)
1410.186 Million cell updates/sec

Title: Perfect score: Sequence: US-09-543-407-26 782

1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 283366

283366 seqs, 96191526 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	ტ	Ŋ	4.	w	N	_	NO.	Result
94	95	95.5	96.5	97	97.5	97.5	100	102.5	102.5	102.5	104.5	105	105.5	106	107	107	107.5	112	112	112	113	114.5	114.5	501.5	501.5	523	692	692	score	•
12.0	12.1	12.2	12.3	12.4	12.5		12.8	٠	13.1	13.1	13.4	13.4	13.5	13.6	13.7	13.7	13.7	14.3	14.3	14.3	14.5		14.6	64.1	64.1	66.9	88.5	88.5	Match	
599	652	1651	447	615	1213	1028	3300	1655	1567	552	1258	590	645	1034	151	151	1322	151	151	151	2174	145	145	152	152	151	151	151	Length	
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	2	N	N	N	2	28	}
B42049	E97857	JC1340	G84687	E70663	S16356	A56038	D70575	E97835	S11672	D70604	JQ0188	E70946	F70825	JC2143	AH0635	JC6040	S07053	G85665	C90806	S70787	E95965	H98144	AD3143	H85665	D90806	S70788	AI0635	JC6039	ID	
leishmanolysin (EC	cell surface antig	mbra	probable disease r		ein	ы		hypothetical prote	o	probable PPE prote	ice nucleation pro	probable PPE prote	probable PPE prote	ice nucleation act	nucleation compone	fimbrin protein ag	ice nucleation pro	curlin minor chain	minor curlin subun			hypothetical prote	conserved hypothet	hypothetical prote	curlin major subun	curlin protein csg		fimbrin protein ag	Description	

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trfA protein	T14004	N	1390	11.5	90	4.
hypothetical	T26667	N	586	11.5	90	ï
probable PPE	E70969	N	3716	11.6	90.5	Ñ
ice nucleation pro	SNPSO	_	1200	11.6	90.5	ï
probable	A70762	N	678	11.6	91	0
probable	F70675	N	582	11.7	91.5	Ö
cnjB protein	S42136	Ň	1748	11.8	92	œ
probable	B70520	N	1436	11.8	92	7
probab	B70663	N	354	11.8	92	Ď
probable	B70987	N	1053	11.8	92.5	Ü
probab	B70524	N	963	11.8	92.5	4.
leishmanolysin	C42049	N	639	11.8	92.5	ũ
protein	S35327	N	575	11.8	92.5	N
hypothetical	E70768	N	434	11.9	93	μ
leishmanolysin	A44951	N	599	12.0	94	ö

ALIGNMENTS

Q	Д	95 87	Query Ma Best Loo Matches	A;Desc A;Note C;Keyw F;1-20 F;21-1	A; Molecule t: A; Residues: A; Note: sequ C; Genetics: A; Gene: agfA	A; Reference A; Contents: A; Accession A; Status: p	R;Coll J. Bac A;Titl	A; Molecule A; Residues: A; Experiment	A;ACCE A;Mole A;Resi A;Cros	J. Bac A;Titl A;Refe	C;Date C;Acce	JC6039 fimbri	
121 NNAALVNQTASDSSYMVRQVGFGNNATANQY 151	61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120 	1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60 	Query Match 88.5%; Score 692; DB 2; Length 151; Best Local Similarity 90.7%; Pred. No. 3.6e-51; Matches 137; Conservative 2; Mismatches 12; Indels 0; Gaps 0;	A;Description: major component of thin aggregative fimbriae A;Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator C;Reywords: fimbria F;1-20/Domain: signal sequence #status predicted <sig>F;21-151/Product: fimbrin protein agfA #status experimental <mat></mat></sig>	A;Molecule type: protein A;Residues: 21-33 <co3> A;Note: sequence extracted from NCBI backbone (NCBIP:45936) C;Genetics: A;Gene: agfA</co3>	A;Keterence number: A44898; MULD:91310586; FMID:167/357 A;Contents: 27655 A;Accession: A44898 A;Status: preliminary	T. Bacteriol. 173, 4773-4781, 1991 J. Bacteriol. 173, 4773-4781, 1991 J. Bacteriol. 173, 4773-4781, 1991 J. Fille: Purification and characterization of thin, aggregative fimbriae from Salmonell	A; MoLecule type: protein A;Rolecule type: protein A;Residues: 21-52 <co2> A;Residues: 21-52 <co2> A;Experimental source: strain 27655-3b A:Dote: the authors translated the codon ACG for residue 44 as Ile</co2></co2>	A;ACCEBBION: U-0039 A;Molecule type: DNA A;ReBidueB: 1-151 <col/> A;Cross-references: GB:U43280; NID:gl184712; PIDN:AAC43599.1; PID:gl184714 A.ACCESSION: PC6015	J. Bacteriol. 178, 662-667, 1996 A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae. A;Reference number: JC6039; MUID:96146512; PMID:8550497	C;Dete: 31-Dec-196 #sequence revision 31-Dec-1996 #text_change 08-Oct-1999 C;Dete: 31-Dec-196 #sequence revision 31-Dec-1996 #text_change 08-Oct-1999 C;Detession: JC6039; PC6015; R44898	KESULI 1 UC6039 fimbrin protein agfA precursor - Salmonella enteritidis	•

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A;Title: The complete genome sequence of Escherichia coli K-12 A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: G64846
                                                                                                                                                                                                                                                                                                                                                      A;Reference number: S70783; MUID:96414468; PMID:8817489
A;Accession: S70788
                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01-Mar-2002
C;Accession: S70788; G64846; S31202; S34560; S34559
R:Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.
                                                                                                                                                                                       A;Note: the nucleotide sequence was submitted to the EMBL Data Library, R;Blattner, F.R.; Plukett III, G.; Bloch, C.A.; Perna, N.T.; Burland, A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X90754; NID:gl147558; PIDN:CAA62282.1; PID:gl147564
A;Experimental source: strain K12, substrain W3110
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A;Title: Expression of two csg ope
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S70788
                                                                                             A; Molecule type: DNA
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A; Residues: 1-151 < HAM>
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      th, T.; Connerton, P.; Cronin, A.;
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; R
A;Title: Complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         """ curin chain precursor [imported] - Salmonella enterica subsp. enteri C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: A10635
                                                                            A; Residues: 1-151 <BLAT>
                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type:
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                                       ;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74126.1; Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 137
                                                                                                                   Status: nucleic
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     sen, A.; Arnqvist, A.; Hammar, M.; Sukupolvi, S.; Normark,
Microbiol. 7, 523-536, 1993
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                                                                                                               acid sequence
                                                                                                                                                                                                                                                                                                                                        acid sequence not shown;
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csgA protein; major curlin protein
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Cronin, A.;
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e of a multiple drug res
:21534947; PMID:11677608
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Pred.
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Davis,
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No. 3.6e-51;
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                                                                                                                 translation not shown
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lrug resistant
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V.; Riley,
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QLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG

MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAL

60 59

119

MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALYD

30;

1:

Gaps

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Similarity

Conservative

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DNA Res. 8, 11-22, 2001
A,Title: Complete genome sequence of enterohemorrhagic Escherichia
A:Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                A; Experimental source:
                                                                                                                                    A; Cross-references:
                                                                                                                                                  A; Residues: 1-152 <HAY>
                                                                                                                                                                      A; Molecule type:
                                                                                                                                                                                                                                                                                    gasawara,
                                                                                                                                                                                                                                                                                                    R;Hayashi,
                                                                                                                                                                                                                                                                                                                        C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: D90806
                                                                                                                                                                                                                                                                                                                                                              curlin major subunit CsgA [imported] -
C;Species: Escherichia coli
                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: major component of wild-type curli; interaction between CsgA and CsgB A;Noce: curli are thin, coiled fibers expressed on the surface of Escherichia coli the and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-133,'RQRDSGWLW' <OLS3>
A;Cross-references: EMBL:L04979; NID:g290424;
A;Experimental source: strain K-12, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 21-42;44-50 <OLS2> R;Olsen, A.N.; Arnqvist, A.M. submitted to the EMBL Data Lib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;21-151/Product: curlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-133, 'RQRDSGWLW'
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A; Accession: S34559
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A; Residues: 1-6,'V',8-151 <OLS1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: csgA
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                                                                                                                                                                                                                                                                                  Makino, K.; Ohnishi,
asunaga, T.; Kuhara,
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                                                                                                              GB:BA000007; PIDN:BAB34843.1; ce: strain 0157:H7, substrain 1
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64.1%; Score 501.5; DB 2
67.1%; Pred. No. 3.4e-35;
cive 19; Mismatches 30
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8; Mismatches
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Pred. No. 5.3e-37;
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Shiba, T.;
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W3110
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A;Cross-references: GB:AE005174; NID:g12514574; PIDN:AAG55788.1; A;Experimental source: strain O157:H7, substrain EDL933 C;Genetics: A;Gene: CsGA
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AD3143
                                                                                                                                                                                                       ster, E.W.
A;Title: The Genome of the N
A;Reference number: AB2577;
A;Accession: AD3143
                                                                                                                                                                                                                                                                                             C;Date: 11-Jan-2002 #sequence_revision 11-Jar C;Accession: AD3143 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, erage, G.; Gillet, W.; Grant, C.; Guenthner, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein Atu4768 [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein csgA [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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Best Local S
Matches 102
                                                                                                                       Cross-references: GB:AE008689; PIDN:AAL45562.1; Experimental source: strain C58 (Dupont)
                                                                                                                                                         Residues: 1-145 <KUR>
                                                                                                                                                                        Molecule type: DNA
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                                                                       linear chromosome
 Conservative
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                  14.6%;
25.2%;
                                                                                                                                                                                                                           Natural Genetic Engineer Agrobacterium tumefaciens C58; MUID:21608550; PMID:11743193
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 26;
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Score 114.5; DB 
Pred. No. 0.0088; 
86; Mismatches !
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Pred. No. 3.4e-35;
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Potamousis,
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RESULT
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A.; Liu, F.; Wollam, C.; Allinger, M.;
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein AGR_L_228 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002 C;Accession: H98144
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A; Residues: 1-145 < KUR>
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                                                                                                             ALYDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITV 115
                                                                                                                                                   MIRKSFIASALVALVGLSAAAPAMANDVRIEQYGWSNSAGGAQEGYGNRIRTYQNGGYN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQFGSNHTTILTQDGNGNIAAGVQVGRGCSANVSQ 131
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Pred. No. 0.0088;
6; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miller, N.; Blanchard, M.; Qurollo, Doughty, D.; Scott, C.; Lappas, C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGNHNGGGNSSGPDSTLSIYQYGSANA
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                                                                                                                                                                                                                                                            Length
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; Markelz, B.
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RESULT E95965

C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001 hypothetical glycine-rich protein [imported] - C; Species: Sinorhizobium meliloti Sinorhizobium meliloti (strain 1021) mag

P.; Vorholter,

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A,Title: The complete sequence of the 1,683-kb pSymB megaplasmid

A,Reference number: A95842; MUID:21396508; PMID:11481431

A,Accession: E95965

N2-fixing

F.J.;

Hernai end

A; Status: preliminary

PID:g15140875; GSPDB:GN00167

Abola, P.; Ampe, F.; Barloy-Hubler S.; Federspiel, N.A.; Fisher, R.F.

A;Molecule type: DNA
A;Residues: 1-2174 <KUR>
A;Residues: 1-2174 <KUR>
A;Residues: 1-2174 <KUR>
A;Cross-references: GB:AL591985; PIDN:CAC49389.1; PID:g1:
A;Cross-references: GB:AL591985; PIDN:CAC49389.1; PID:g1:
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.W.; Puhler, A.; Abole
R;Galibert, F.; Finan, T.M.; Lowis, R.W.; Dreano, S.;
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.;
L.; Hyman, R.W.; Jones, T.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.;
A;Title: The composite genome of the legume symbiont Sinc , D.H.; Kiss, B.; Komp, C.; Lelaure, S.; Wells, D.H.; Wong, K.; Yeh, K Sinorhizobium meliloti.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: F64846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X90754; NID:gl147558; PIDN:CAA62281.1; PID:gl147563
A;Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Augu
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; R
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         curlin nucleator protein csgB precursor - Escherichia coli (strain K-12) % Alternate names: csgB protein; curlin nucleation component; minor curl: C;Species: Escherichia coli C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01-Mar-20-20 C;Accession: S70787; F64846 F8;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S. Mol. Microbiol. 18, 661-670, 1995 Mol. Microbiol. 18, 661-670, 1995 A;Title: Expression of two csg operons is required for production of fib: A;Reference number: S70783; MUID:96414468; PMID:8817489
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S70787
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A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-151 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: nucleic
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A;Contents: annotation
C;Genetics:
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Best Local S
Matches 40
                                                                                                                                                                    Matches
                                                                                                                                                                                     Query Match
Best Local Similarity
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Similarity 27.0%;
                                        -NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                  GIAAAAGYDLANSEYNFAVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
                                                                                                                        GSANAALYDQLVT--RVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFR----
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Pred. No. 0.23;
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V.; Riley,
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C;Date: 30
                   ice nucleation protein inaA - C;Species: Erwinia ananas
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30-Sep-1991
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iller, L.; Grotbeck, E.J.; Davis, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          curiln minor chain precursor, CsgA homolog [importor, Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence revision 16-Feb-2001
C;Paccession: G8565
                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-151 <S
                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Genome sequence of enterohemorrhagic Escherichia coli Ó157:H7
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasr iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:g13360879; A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: C90806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Hayashi, T.; Makino, I
gasawara, N.; Yasunaga,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       minor curlin subunit precursor CsgB [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli (C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
                                                                                                                                                                                                                                                                                                                                                                       A; Accession: G85665
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                                                                                                                                                                                                                                                                                                                                                         Status: preliminary
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:Experimental source: strain O157:H7, substrain EDL933
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Best Local (
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Best Local
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                                 - NNATIDOWNAKUSDITVGOYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
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SNRAKIDQTGDYNL-AYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY
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Yasunaga, T.; Kuhara,
                                                                                                                                                         Conservative
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Pred. No. 0.01
17; Mismatches
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Pred. No. 0.015;
7; Mismatches 49
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Shiba, T.;
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; Hattori,
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imalanta, E.;
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Shinagawa,
                                                                                                                                                       14;
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#sequence_revision

30-Sep-1991

#text_change

26-Aug-1999

Erwinia

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fimbrin protein agfB precursor - Salmonella enteritidis (;Species: Salmonella enteritidis C;Species: Salmonella enteritidis C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_char C;Accession: JC6040 R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A. J. Bacteriol. 178, 662-667, 1996 A;Reference number: JC6039; MUID:96146512; PMID:8550497 A;Accession: JC6040
nucleation component of curlin monomers [imported] - Salmonella C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change C;Accession: AH0635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:U43280; NID:gl184712; PIDN:AAC43598.1; PID:gl184713
A;Experimental source: strain 276755-3b
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: agfB
C;Function:
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A; Residues: 1-151 <COL>
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C;Superfamily: ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: An ice nucleation active gene of Erwinia ananas. Sequence similarity to A;Reference number: S07053; MUID:90092494; PMID:2599095 A;Accession: S07053
                                                                                                AH0635
                                                                                                                RESULT
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FEBS Lett. 258, 297-300,
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Keywords: fimbria
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                                                                                                                                                                                                          RNNATIDOWNAKUSDIT-VGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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O, 1989
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Pred. No. 0.039;
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Pred. No. 0.38;
9; Mismatches
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                                                                            enterica subsp.
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Search Job tim

completed: March

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2004,

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C;Accession: UC2143

R;Michigami, Y.; Watabe, S.; Abe, K.; Obata, H.; Arai, S. Biosci. Biotechnol. Biochem. 58, 762-764, 1994

A;Title: Cloning and sequencing of an ice nucleation active A;Reference number: JC2143; MUID:94264407; PMID:7764866

A;Accession: JC2143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                th, T.; Connerton, P.; Cronin, A.; Davie, K.; Davies, K.; Noule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AH0635
A;Accession: AH0635
                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-1034 <MIC>
C; Comment: This protein consists of
C; Superfamily: ice nucleation protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JC2143
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A;Molecule type: DNA
A;Residues: 1-151 <PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ice nucleation active protein - Erwinia uredovora (strain KUIN-3)
C;Species: Erwinia uredovora
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999
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                                                                                                                                                                                 27 GGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGADVGQGAD
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Similarity 29.9%;
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T--AGYGSTOTAGE
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                                                                        ----LTA-GYGSTQTAQE--
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Pred. No. 0.039;
7; Mismatches
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Salmonella enterica
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: March 11, 2004, 18:14:48; Search time 6.3 Seconds (without alignments) 1248.031 Million cell updates/sec

Title: US-09-543-407-26

Perfect score: 782
Sequence: 1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database :

SwissProt_42:*

SUMMARIES

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SEQUENCE FROM N.A. SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931; MEDLINE=22531367; PubMed=12644504; Deng W., Liou SR., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;	SEQUENCE FROM N.A. SPECIES=S.typhi; STRAIN=CT18; MEDLINE=21534947; PubMed=11677608; Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18."; Nature 413:848-852(2001).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609; MCClelland,M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2."; Nature 413:852-856(2001).	Salmonella typhi, and Salmonella enteritidis. Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Bacteria; Proteobacteria: Gammaproteobacteria; Enterobacteriacea; Salmonella. NCBI_TaxID=602, 601, 592; [1] SEQUENCE FROM N.A. SPECIES=S.typhimurium; STRAIN=SR-11; SECIES=S.typhimurium; STRAIN=SR-11; MEDI_INE=9817058; PubMed=9457880; MEDI_INE=9817058; PubMed=9457880; ROmling U., Bian Z., Hammar M., Sierralta W.D., Normark S.; ROmling U., Bian Z., Hammar M., Sierralta W.D., Normark S.; Turil fibers are highly conserved between Salmonella typhimurium and Escherichia coli with respect to operon structure and regulation."; J. Bacteriol. 180:722-731(1998).	

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Query Match
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Matches 137
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-- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT
-- COILED SURFACE STRUCTURES THAT ASSEMBLE PRE
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURI
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MEDLINE=91310586; PubMed=1677357;
Collinson S.K., Emoedy L., Mueller K.-M., Trust T.J., Kay W.W.;
"Purification and characterization of thin, aggregative fimbriae
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1L; AE008749; AAL20074.1; -.

1L; AL627269; CAD08268.1; -.

3L; AE016840; AA063399.1; -.

1L; U42380; AAC43399.1; -.

126039; U76039; U76039.

Gene; SG10608; CsgA.
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"The RpoS sigma factor i
repression of csgA, the
Escherichia coli.";
Mol. Microbiol. 7:523-53
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Oshima T., Alba H., Baba T., Fujita K., Hayashi I Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai Kimura S., Kitagawa M., Makino K., Masuda S., Mi Mori H., Mocomura K., Nakamura Y., Nashimoto H., Sampei G., Seki Y., Tagami H., Takemoto K., Wada Yano M., Horiuchi T.;
                                                                                                                         STRAIN=K12 / YMEL;
MEDLINE=93023873; PubMed=1157528;
Arnqvist A., Olsen A., Pfeifer J.,
"The Crl protein activates cryptic
fibronectin binding in Escherichia
Mol. Microbiol. 6:2443-2452(1992).
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P28307;
01-DEC-1992
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                                                                  MEDLINE=91310586; PubMed=1677357; Collinson S.K., Emoedy L., Trust T. "Purification and characterization
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Mau B., S
                                             Salmonella enteritidis."
J. Bacteriol. 173:4773-4
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna
Riley M., Collado-Vides J., Glasner J.D., Rode C.K
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.
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                      FUNCTION: CURLIN IS THE STRUCTURAL SUBUNCOILED SURFACE STRUCTURES THAT ASSEMBLE
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                                              173:4773-4781(1991).
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            BELOW
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st A., Bian Z., Olsen A.,
o csg operons is required
congo red-binding curli pc
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                      SUBUNIT OF THE CURLI.
                                                                               Kay W.W.;
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M., Kashimoto K.,
da S., Miki T., Mizobuchi K.,
imoto H., Nishio Y., Saito N.
K., Wada C., Yamamoto Y.,
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STRAIN=0157:H7 / ATCC 43895;

STRAIN=0157:H7 / ATCC 43895;

MEDLINE=21218556; PubMed=11319125;

Uhlich G.A., Keen J.E., Elder R.O.;

"Mutations in the csgD promoter associated with variations with the csgD promoter associated with variations expression in certain strains of Escherichia coli 0157:H7."

Environ. Microbiol. 67:2367-2370(2001).
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28-FEB-2003
28-FEB-2003
28-FEB-2003
                                               MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
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Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
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28-FEB-2003 (Rel. 41, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
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01-CCT-1996 (Rel. 34, Last sequence upda
28-FEB-2003 (Rel. 41, Last annotation up
Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
Escherichia coli, and
Escherichia coli O157:H7.
Bacteria, Proteobacteria, Gammaproteobac
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P39828;
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SEQUENCE FROM N.A.
STRAIN-K12 / MC4100;
MEDLINE-96414468; PubMed-8817489;
Hammar M., Arngvist A., Bian Z., Olsen A.,
"Expression of two csg operons is required fibronectin- and congo red-binding curli po
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-I- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CUI COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GITTMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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SEQUENCE FROM N.A.
STRAIN=0157:H7 / RIMD 0509952;
STRAIN=-1166231; PubMed=1155
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an email to license@isb-sib.ch
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MEDLINE=21156231; PubMed=11258796;
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Hayashi T., Makino K., Ohnishi M., Murata T., Tanaka M., Tobe T
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCC 700927;
STRAIN-0157:H7 / ED1933 / ATCC 700927;
STRAIN-0157:H7 / ED1933 / D.,
MEDLINE-21074935; PubMed-11206551;
MEDLINE-21074935; PubMed-11206551;
Merian N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
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Escherichia coli can be achieved in vivo by sigma
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STRAIN=K12
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Welch R.A., Blattner F.R.,
"Genome sequence of entero
Nature 409:529-533(2001).
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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., Rr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       corresponding to the 12.7 DNA Res. 3:137-155(1996).
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1. Microbiol. 13:1021-1032(1994).

1. FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLICULED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TELERONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENTS.
                                                                                                                            SIMILARITY: BELONGS
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ka M., Tobe .
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EMBL; D90741; BAA35831.1; --
EMBL; AE005315; AAC55787.1; --
EMBL; AE005315; AAC55787.1; --
EMBL; AP002554; BAB34842.1; --
PIR; C90806; C90806.
PIR; C90806; C90806.
PIR; G85665; G85665.
PIR; S70787; S70787.
ECOGene; EG12621; C69B.
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SIGNAL
  Ice nu
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16-OCT-2001 (Re
Ice nucleation
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                                          PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 49.
                                                                                                                                                                                                                          entities requires a license agreement (So or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
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FEBS Lett. 258:297-300(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-90092494; PubMed=2599095;
Abe K., Watabe S., Emori Y., Watanabe M., Arai S.
"An ice nucleation active gene of Erwinia ananas.
to those of Pseudomonas species and regions requi:
                                                                                                                 [nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Ice nucleation proteins enable bacteria to nuclearison in supercooled water:
SUBCELLULAR LOCATION: Outer membrane (By similarity).
DOMAIN: CONTAINS MANY IMPERFECT REPEATS OF THE CONSENSUS
OCTAPEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
SIMILARITY: Belongs to the bacterial ice nucleation prote
                                                                                                                                                          ; X17316; CAA35194.1;
S07053; S07053.
                                                                                                                                                                                                                                                                                                                                                                                                                family.
                                                                                                                                       P06620;
                                                                                       PF00818; Ice_nucleation;
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IPR000258; ICe_
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Repeat;
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sobacteria; Gammaproteobacteria;
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MINOR CURLIN SUBUNIT.
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  OCTAPEPTIDE
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Best Local
                                                                                                                                                                                                                                                                                                     J. Bacteriol. 185:2330-2337(2003).

-I- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLICOLLED SURPACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TEMPERONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi st
and CT18.";
    EMBL;
                                                                   between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple enterica serovar Typhi CT18."; Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Minor curlin subunit precursor.
CSGB OR STY1180 OR T1777.
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                                                                                                                                                                                                                                                                                         CURLIN MONOMERS
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    AL627269;
AE016840;
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  CAD08267.1;
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Minor curlin subunit precursor (Fimbrin SEF17
CSGB OR AGFB OR STM1143.
Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fimbria;
SIGNAL
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                   McClelland M., Sanderson K.E., Spieth J., Clifton S.W. Courtney L., Porwollik S., Ali J., Dante M., Dt F., Ali J., Dante M., Dt F., Ali J., Dante M., Dt F., Ali J., Bonte M., Grewal N., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Ni Waterston R., Wilson R.K.;
                                                                                                                                                                                    MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., D
"Salmonella enteritidis agfBAC op
                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=S.typhimurium; STRAIN=SR-11; MEDLINE=98117058; PubMed=9457880; Romling U., Bian Z., Hammar M., Sierralta W.D., Normar Romling U., Bian Z., Hammar M. Seierralta W.D., Normar "Curli fibers are highly conserved between Salmonella Escherichia coli with respect to operon structure and J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SALTY
                                                                                                                                                                                                                                                                                                                                                                   SPECIES=S.typhimurium; STRAIN=LT2 / MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterobacteriaceae;
NCBI_TaxID=602, 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella typhimurium, and Salmonella enteritidis.
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                                                                                                                                                                                                                                                                 Nature 413:852-856(2001).
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                                                                                     COILED SURFACE STRUCTURES THAT ASSEMBLE TEMPERATURES BELOW 37 DEGREES CELSIUS. CIFIBRONECTIN. THE MINOR SUBUNIT IS THE MUCURLIN MONOMERS.
                                                                                   SIMILARITY: BELONGS
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17; Mismatches
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S., Layman D.,
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Q47879;
01-NOV-1997
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-!- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO -!- SIMILARITY: Belongs to the bacterial ice nucleation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      StyGene; SGIUbUV; LOGI-
Fimbria; Signal; Complete proteome.
21 POTENTIAL.
                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94264407; PubMed=7764866; Michigami Y., Watabe S., Abe K., Obata H., Ar "Cloning and sequencing of an ice nucleation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ002301; CAA05316.1; --
EMBL; AE008749; AAL20073.1; --
EMBL; U43280; AC43598.1; --
PIR; JC6040; JC6040.
        InterPro, IPRO00258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 51.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 34.
                                                                            EMBL; D14992; BAA03636.1; PIR; JC2143; JC2143.
                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                   Biosci. Biotechnol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pantoea ananas (Erwinia uredovora)
Bacteria; Proteobacteria; Gammaprot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                    entities requires a license agreement
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                                                                 P06620; 1INA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNRAKVDQ--AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
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                    Query Match
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HSSP; P06620; IINA.
InterPro; IPR000258; Ice_nucleatn.
InterPro; IPR000258; Ice_nucleation; 65.
Pfam; PF00818; Ice_nucleation; 65.
PRLNTS; PR00327; ICEMUCLEARIN.
PROSITE; PS00314; ICE_NUCLEARIN, 45.
Ice_nucleation; Repeat; Outer_membrane.
DOMAIN 162 1217 OCTAPEFTIDE
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SEQUENCE
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                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Ice nucleation proteins enable k crystallization in supercooled water. SUBCELLULAR LOCATION: Outer membrane. DOMAIN: CONTAINS 126 IMPERFECT REPRAYS OF A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE A PERIODICITY IS SUPERIMPOSED.
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                                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute.
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Best Local Similarity

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RESULT 10
ICEN XANCT
ID TICEN
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Best Local S
Matches 45
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01-NOV-1990
16-OCT-2001
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P18127;
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                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                  Pfam; PF00818; Ice nucleation; 81.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE NUCLEATION; 57.
                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                              EMBL; X52970; CAA37140.1;
HSSP; P06620; 1INA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao J., Orser C.S.; "Conserved repetition in the ice nucleation
                                                                                                                                                                                                                                                          InterPro; IPR000258; Ice nucleatn.
                                                                                                                                                                                                                                                                                                                                                     or send
                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91080859; PubMed=2259339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xanthomonas campestris (pv. translucens).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (anthomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTYSTAILIZATION IN SUPERCOOLED WATER.
SUBCELLULAR LOCATION: OUTER membrane (By similarity).
SUBCELLULAR LOCATION: OUTER membrane (By similarity).
DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
OCTAPEPTIDE A.G.Y.G.S.T.L.T; FURTHER ON A 16-RESIDUE AND A
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
MISCELLANGEDUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE
NUCLEATION PROTEIN DISPILAYS A SYMMETRY RELATED TO THAT OF ICE.
SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                     nucleation;
UENCE 1567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Ice nucleation proteins enable
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                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                     an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSTAGADSSLIAGYGSTQTAGYNSILTAGYGSTQTAQENSDLTTG-YGSTSTAGYDSSLI
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                                      GSTGTAGADSTL-IAGYGSTQTAGSDSSLT-----AGYGSTQTARQGSDITAGYGS
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Genet. 223:163-166(1990)
   ·GQGADNSTIE----LTQN-GFRNNATI----DQWNAKNSDITVGQYG-----GNNAALV
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(Rel. 16, Last sequence up
(Rel. 40, Last annotation
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                                                                                                            Conservative
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                                                                                                                              Score 102.5;
Pred. No. 0.
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RESULT 11
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OMRKA3; Q9KKA3; Q9KKA5;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide).
                                                                              EMBL; AE008659; AAL03623.1;
EMBL; AF123721; AAF34124.1;
EMBL; AF123726; AAF34129.1;
EMBL; AF149110; AAD39533.1;
                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (By similarity).

-!- SUBCELLULAR LOCATION: Cell wall. This bacterium layer with hexagonal symmetry (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The rickettsial outer membrane protein A and B genes of Rickettsia australis, the most divergent rickettsia of the spotted fever group. Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By
                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                      layer with hexagonal symmetry (By similarity).
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Phylogenetic analysis of members of the genus Rickettsia using gene coding the outer-membrane protein rOmpB (ompB)."; int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Indian tick typhus, and Malish 7; MEDLINE=20393643; PubMed=10939649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., R
Samson D., Roux V., Cossart P., Weissenbach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=Malish 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                         entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Malish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 353-1655 FROM N.A.
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Samson D., Roux V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 33-1649 FROM N.A.
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                                                            E97835; E97835
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P5152; Q9XZU4;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
Ovo protein (Shaven baby protein).
OVO OR SVB.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                       STRAIN=Oregon-R; PubMed=1712294; MEDLINE=9129102; PubMed=1712294; Mevel-Ninio M.T.M., Terracol R., Kafatos "The ovo gene of Drosophila encodes a zir for female germ line development."; EMBO J. 10:2259-2266(1991).
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FUNCTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF I
LINE CELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION
SUBCELLULAR LOCATION: Nuclear (potential).
DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND
ACCUMULATES IN NURSE CELLS DURING OOGENESIS. STORED IN 7
BUT IS RAPIDLY LOST IN THE EMBRYOS EXCEPT FOR ITS CONTIN
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PIR; A56038; A56038.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restrest to the by non-profit institutions as long as its content if if and this statement is not removed. Usage by and ities requires a license agreement (See http://www.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sities.com/mar.isb-sit
                             119
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 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00355;
                                                                                                                                                                                                      Similarity
 NNNN---
                            GGNNAALVNQTASDSSVMVRQVGFGNNATA
                                                                                         TRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDI----TVGQY
                                                                                                                          LQNAAAAYIMSAGSG-----
                                                                                                                                                     LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLV
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-NNNGGQTSMMGHPF-YGGNPSA
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108
152
159
339
353
361
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28.7%;
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                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                 C2H2-TYPE 1.
C2H2-TYPE 2.
C2H2-TYPE 3.
C2H2-TYPE 4.
A -> R (IN REF. 2).
A -> R (JR REF. 2).
                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                    Score 97.5; D
Pred. No. 1.1;
.2; Mismatches
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POLY-GLN.
POLY-GLN.
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POLY-GLY.
POLY-GLY.
POLY-GLY.
POLY-HIS.
POLY-ASN.
POLY-GLN.
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                                                           - LDGNNLLNFASVSNYNESNSKFHNHHHHHQH
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                             148
177
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RESULT 13 ICEV_PSESX

protein)

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RESULT 14
OMPB_RICJA
ID OMPB R
AC OO6653
DT 30-MAY
DT 30-MAY
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Best Local S
Matches 43
  OMPB RICJA
006653;
30-MAY-2000
30-MAY-2000
16-OCT-2001
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033479;
15-DEC-1998
15-DEC-1998
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 61.
PRINTS; PR00377; ICENUCLEATION; 42.
PROSITE; PS00314; ICE_NUCLEATION; 42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ001086; CAA04521.1; -. HSSP; P06620; IINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEBS Lett. 414:590-594(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97462815; PubMed=9323042;
Schmid D., Pridmore D., Capitani G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ce nucleation; Repeat; Outer membrane
OMAIN 172 1147 OCTAPEPTII
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SUBUNIT: MEMBRANE ENVIRONMENT OR AGGREGATION SEEMS TO BE
FOR ICE NUCLEATION ACTIVITY.
SUBCELLULAR LOCATION: Outer membrane (By similarity).
DOMAIN: CONTAINS MANY IMPERFECT REPEATS OF THE CONSINSUS
OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to the bacterial ice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                      AKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATA 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                       GSALAG-----VVPQWGG----GGNHN------GGGNSSGPDSTLSIYQYGSANAALYDQL
                                                                                                                                                                                                           GEDSSLTAG-YGS-----TQTAQEGSNLT--AGYGSTGTA
                                                                                                                                                                                                                                                                                                                                                VTRVVTHEMAHAGYGN-------GADVGQGADNSTIELTQNGFRNNATIDQWN
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  (Rel. 39, Created)
(Rel. 39, Last sequence up
(Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                              STANDARD;
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26.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117991 MW;
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Pred. No. 1
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WW; C9E9974CB1731E68 CRC64;
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                          update)
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                                                                      -GP63 LEICH
P15706;
01-APR-1990
01-APR-1990
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen;
CHAIN
                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell
(Major surface glycoprotein) (GP63 protein) (F
endopeptidase)
GP63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMs; TIGR01414; autotrans_barl; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR006315; Autotransport.
InterPro; IPR005546; Autotransporter.
Pfam; P03797; Autotransporter; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB003681; BAA20138.1; -.
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Rickettsiaceae; Rickettsieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rickettsia japonica.
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SUBCELLULAR LOCATION: Cell wall. This b
SUBCELL The LOCATION Cell wall. This b
layer with hexagonal symmetry.
SIMILARITY: BELONGS TO THE RICKETTSIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE
                                                                                                                                                                                                                                                                                                                              1273
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36; Conservative
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1656 AA;
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Pred. No. 2
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Leishmania chagasi. Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania. NCBI_TaxID=44271; [1]

Gaps

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"Three distinct RNAs for the surface protease gp63 are differentially repressed during development of Leishnania donovani chagasi promastigotes to an infectious form.";

RI promastigotes to an infectious form.";

RI J. Biol. Chem. 267:1888-1895(1992)...";

RC -!- FUNCTION: Has an integral role during the infection of macrophages on the mammalian host.

CC -!- FUNCTION: Has an integral role during the infection of macrophages on the mammalian host.

CC -!- FUNCTION: Has an integral role during the infection of macrophages of the mammalian host.

CC -!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 and C2 -!- and Dasic residues at P2 and P3'. A model nonapeptide is C1 and basic residues at P2 and P3'. A model nonapeptide is C2 cleaved at -Ala-Tyr-|- Leu-Lys-Lys-.

CC -!- SUBCELLUCAR LOCATION: Attached to the membrane by a GPI-anchor.

CC -!- SUBCELLUCAR LOCATION: Attached to the membrane by a GPI-anchor.

CC -!- SUBCILIARITY: Belongs to peptidase family M8.
      Query Match
Best Local :
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SIGNAL
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PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc;
Eymogen; Signal; Cell adhesion; GPI-anchor; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M80672; AAA29238.1; -.
EMBL; M28527; AAA29235.1; -.
PIR; A44951; A44951.
HSSP; P08148; 1LML.
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InterPro; IPR001577; Peptidase M8.
Pfam; PF01457; Peptidase M8; 1.
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MEDLLINB=90205976; PubMed=2320059;

Miller R.A., Reed S.G., Parsons M.;

"Leishmania gp63 molecule implicated in cellular adhesion lacks an Arg-Gly-Asp sequence.";
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MEDLINE=92112918; PubMed=1370484;
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      Similarity
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ZINC (CATALYTIC) (BY SIMILARITY).

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Db	8	Matches
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                   07x237 enterobacte
05406 galmonella
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08eih4 shewanella
08u6n9 agrobacteri
092uu8 rhizobium m
07ucz1 shigella fl
08cw64 escherichia
083ru7 shigella fl
07x244 citrobacter
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Q7x243 citrobacter
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Q8cw63 escherichia
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O1-JAN-1998 (TrEMBLrel. 05, L
O1-DEC-2001 (TrEMBLrel. 19, L
Agfa protein (Fragment).
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SEQUENCE
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Sukupolvi S.S., Lorentz R.G., Gordon J.I.,
Normark S.J., Rhen M.;
"Expression of thin, aggregative fimbriae p
                                                                                                                                                                                                                    cells.";
Infect. Immun. 65:5320-5325(1997).
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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ER 152 152
NCE 152 AA; 15401 MW;
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                                                                                       Zogaj X., Bokranz W., Nimtz M., Romling U.; "Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4158(2003).
                                                                                                                                                      STRAIN=Fec4;
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Citrobacter.
                                                                                                                                                                                                            Bacteria; Proteobacteria;
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EMBL; AJ515700; CAD56672.1; -.
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NCBI_TaxID=213763;
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  STRAIN=Fec39;
Zogaj X., Bol
                                                                                                           Bacteria; Proteobacteria;
Enterobacteriaceae; Entero
                                                                                                                                                      Enterobacter sakazakii.
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STRAIN=06:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
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152 AA;
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67.8%;
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Mismatches 30;
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Romling
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Best Local S
Matches 61
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Best Local
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Q9S3J5;
Q1-MAY-2000
Q1-MAY-2000
Q1-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
  Bacteria; Proteobacteria; Gamma
Enterobacteriaceae; Escherichia
                                                                                             Curlin
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01-NOV-1996
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                                              Escherichia coli.
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
nit monomer (Fragment).
                                                                                                                                                                                                                  PRELIMINARY;
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                        Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                   76
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Last sequence update)
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Pred. No. 1.2e
25; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 304; DB 2
Pred. No. 1e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2FD5411241A7BCB1 CRC64;
                                                                                                                                                                                                                  PRT;
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wes 34; Indels
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Best Local Similarity
                                                                                                                                                                                                                                                                                                             MEDINE-22297686; PubMed-12368813;
MEDINE-22297686; PubMed-12368813;
MEDINE-22297686; Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C. Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Teapin A., Scott J., Beanan M., Brinkac L., Daugherty S., Meyer T., Todsin A., Sott J., Beanan M., Brinkac L., Kolonay J.F., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., DeBoy R.T., Deterson J.D., Umayam L.A., White O., Wolf A.M., Vanathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8EIH4
Q8EIH4;
                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      вастетіа; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           La Ragione R.M., Collighan R.J., Woodward M.J.;
"Non-curliation of Escherichia coll 078:K80 isolates associated with
IS1 inserti on in csgB and reduced persistence in poultry infection.";
FEMS Microbiol. Lett. 175:247-253(1999).
EMBL, AJ131756; CAB45380.1; -.
                                                                                                                                                                                                                               Hypothetical protein; Complete SEQUENCE 502 AA; 52441 MW;
                                                                                                                                                                                                                                                                                          Nat. Biotechnol.
                                                                                                                                                                                                                                                                                                      Shewanella oneidensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=MR-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shewanella oneidensis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conserved hypothetical protein.
                                                                                                                                                                                                                                                             TIGR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99314153; PubMed=10386375;
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349
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                           NNAAL VNQTASDSSVMVRQVGFGN----NATAN
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NNELVAFATGEDNS I E I SQEGDANFAYVDATGN
                                                       IQGDDNDITIKQKGDSNGAEFQVWGDSNDVDLKQRGDANFATFGAYGTDN
                                                                                   VVTHE----MAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                               GDNHTGFVYALAGSENDISMEQEGSNNTAYLSMTTGDDNTVDITQDGDSN-TVGDSLIAD
                                                                                                                                             GGNHNG---
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(TrEMBLrel. 23, Last
(TrEMBLrel. 23, Last
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                                                                                                                                                                                                                                                                                          20:1118-1123 (2002) .
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89.7%;
                                                                                                                                          ------GGN------SSGPDSTLSIYQYGSANAALYDQLVTR 64
                                                                                                                                                                                                    15.5%;
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                                                                                                                                                                                     Score 121; DB 1
Pred. No. 0.086;
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Pred. No. 0.0022;
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D08CA23D6C46B62D CRC64;
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381
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RESULT

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RESULT 10
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Q92UU8
Q92UU8;
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Q92UUB;
Q92UUB;
C1-DEC-2001 (TREMBLrel. 19, C)
T 01-DEC-2001 (TREMBLrel. 25,
JT 01-OCT-2003 (TREMBLrel. 25,
DE Hypothetical glycine-rich p
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Best Local S
Matches 39
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01-JUN-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Atu4768.
ATU4768 OR AGR L 228.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria, Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium NCBI_TaxID=176299;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mull. Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markel Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S., Cielo C., Slater S., "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefacions CSB.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE=21608550; PubMed=11743193;
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Katyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
Nester F W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
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[2]
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H98144; H98144.
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AE009405; AAL45562.1; -.
AE008209; AAK88682.1; -.
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                                                                                                                                                                                                             GQFGSNHTTILTQDGNGNIAAGVQVGRGCSANVSQ 131
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                                                                                                                                                                                                                                                                                                             ALYDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITV
                                                       (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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145 AA; 14984 MW;
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                                           protein
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                                                                                                                                                                                                                                                                                                                                                                                                                            Score 114.5; DB Pred. No. 0.064;
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DEDC870E1713D51A CRC64;
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Q7UCZ1;
01-0CT-2003
01-0CT-2003
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                                                                                                                       STRAIN=2457T / ATCC 700930 / Serotype 2a;
MEDLINE=22590274; PubMed=12704152;
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., D.
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J.,
Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J.,
Schwartz D.C., Blattner F.R.;
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InterPro; IPR002016; Peroxidase.
InterPro; IPR002173; PEKB.

Pfam; PF03797; Autotransporter; 1.
PROSITE; PS00435; PEROXIDASE 1; 1.
PROSITE; PS00583; PEROXIDASE 1; 2.
PROSITE; PS00583; PEROXIDASE 1; 2.
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 2174 AA; 203314 MW; 008EB68297B44182
                                              "Complete genome sequence and comparative flexneri serotype 2a strain 2457T."; Infect. Immun. 71:2775-2786(2003).
                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gam
Enterobacteriaceae; Shigella.
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GO; GO:0004601; F:peroxidase activity; IEA.
GO; GO:0006979; P:response to oxidative stress; IEA
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Finan T.M., Weidner S., Wong K., Buhrmester J.,
Vorhoelter F.J., Hernandez-Lucas I., Becker A.,
Golding B., Puehler A.;
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Plasmid pSymB (megaplasmid 2).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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AE016981; AAP16542.1;
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  5D5D266B964014A0 CRC64;
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MEDLINE=22388234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roel Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J. Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N. Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete gen of uropathogenic Escherichia coll.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

EMBL; AE016759; AAN79778.1; -.
      SEQUENCE FROM N.A.
STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., S
Yang J., Yang F., Zhang X., Zhang
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Shigella flexneri.
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Best Local S
Matches 34
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EMBL; AJ515700; CAD56671.1; -. SEQUENCE 151 AA:
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Q8PD38;
Q1-OCT-2002
01-OCT-2002
01-JUN-2003
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Q7X244;
01-OCT-2003
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Bacteria; Proteobacteria;
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EMBL; AE015131; AAN42658.1; -.
                     NCBI_TaxID=340;
                                                                                     Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                  Ice nucleation XCC0507.
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                                                         Xanthomonadaceae;
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. 25, Last sequence upo
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f curlin monomers.
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RC STRAIN=ATCC 33913 / NCPPB 528;

RX MEDLINE=22022145; PubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Salvys M.A., Almeida N.F.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Canburgo L.B.A.,

RA Quaggio R.B., Monteiro-Vitorello C.C., Camargo L.B.A.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Clapina L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Cicarelli R.M.B., Ferreira R.C.C., Ferro M.I.T.,

RA Cormighieri E.F., Franco M.C., Greggio C.C., Ferro M.I.T.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Faria J.B., Mendado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Martins E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Martins E.C., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Findade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Gomparison of the genomes of two Xanthomonas pathogens with differing the state of the peromes of two Xanthomonas pathogens with differing RI Nature 417.44547000
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 26.3
Matches 46; Conservative
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EMBL; AB012148; AAM39823.1; -.

GO; GO:0009279; C:external outer membrane (sensu Gram-negativ. . .; IEA. InterPro; IPR000258; Ice_nucleatn.

Pfam; PF00818; Ice_nucleation; 68.

PRINTS; PR00327; ICENUCLEATION; 68.

PROSSITE; PR00327; ICENUCLEATION; 40.

Complete proteome.

SEQUENCE 1333 AA; 131306 MW; 326078458D0E4842 CRC64;
951 TÓTAGYESTLTAG-YGSTOTÁQEISWLTTGYGSTÓTÁGHGSILT--AGYGSNSTÁ 1002
                                                                     105
                                                                                                                  904 QTAGYDSFLT-----AGYGS----TQTAQSSSWLITGYGSTSTASFQSSLIAGYGS
                                                                                                                                                                                                                              856 QTAGYKSILTIGYGSTQTAQESSSLIAGY------GSSSMAGPDSSL-IAGYGST 903
                                                                                                                                                                     54 NAALYDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATID------
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                                                      -QWNAKNSDITVGQYGGNNAAL------VNQTASDSSVMVRQVGFGNNATA 148
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Search completed: March 11, 2004, 18:40:46 Job time: 31.5 secs

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Result
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Aar74625 AgfA sequ
Aab36351 AgfA::PT3
Aar74625 AgfA sequ
Aab36341 Salmonell
Aab23570 Salmonell
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664 Fibronect
663 FNB curli
118 Salmonell
118 Salmonell
124 E. coli c
122 Salmonell
127 Salmonell
137 Salmonell
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
87.5	87.5	87.5	87.5	87.5	87.5	89	89	89.5	90	91.5	92	94.5	96	96	96	102	109	109	109
11.3	11.3	11.3	11.3	11.3	11.3	11.5	11.5	11.5	11.6	11.8	11.9	12.2	12.4	12.4	12.4	13.2	14.1	14.1	14.1
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ABP69841	ABP69842	ABP66189	AAG29727	AAG29728	AAY69523	ABO23520	ABR82647	AAB36344	ABR82642	AAW32312	ABU22692	AAB36342	AAB36328	AAB36336	AAB36323	ABR82649	AAB36319	AAB36324	AAB36340
Abp69841	Abp69842	Abp66189	Aag29727	Aag29728	Aay69523	Abo23520	Abr82647	Aab36344	Abr82642	Aaw32312	Abu22692	Aab36342	Aab36328	Aab36336	Aab36323	Abr82649	Aab36319	Aab36324	Aab36340
Human	Human pol		_	Arabidops) Mycobacte	/ E. coli c	Escherich	E. coli N	Leishmani	Protein e	? Salmonell	Salmonell	Salmonell	Salmonell	B. coli V	Salmonell	Salmonell) Salmonell

ALIGNMENTS

RESULT 1 AAB36354 ID AAB3 WPI; 2000-672631/65. N-PSDB; AAC64630. White AP, 05-APR-1999; 05-APR-2000; 2000WO-CA000356 WO200060102-A2. Synthetic. Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; 26-FEB-2001 AAB36354; AAB36354 standard; 12-OCT-2000. Escherichia Salmonella enteritidis. AgfA::PT3#9 amino acid sequence (UYVI-) UNIV VICTORIA vaccine; immune Doran JL, coli. (first entry) 99US-0127888P response; protein; Collison immunogen 151 SK, ₽ SEQ ID NO:28 Kay WW;

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonalla, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) directing recombination of a recombinant gene homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 138; 139pp; English.

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RESULT 2
AAB36351
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Best Local
Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                              N-PSDB; AAC64627.
                                                                                                                                                                                                                                             WPI; 2000-672631/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36351 standard; protein; 151 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                        (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella enteritidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AgfA::PT3#6 amino acid sequence SEQ ID NO:22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                              Doran JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             response;
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                                                                                                                                                                                                                                                                                                                              Collison
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Pred. No. 2.5e-67;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                   SK,
                                                                                                                                                                                                                                                                                                                                   Kay WW
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밁 S 밁 Ś 밁 S

Disclosure; Page 137; 139pp; English

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Best Local S
Matches 144
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                                                                                                                                                                                                                                                                            Salmonella; AgfA; vaccine
                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
26-JUN-1995
                                                                                                                    26-APR-1994;
                                                                                                                                                                                               WO9425598-A2
                                                                                                                                                                                                                                      Salmonella
                                                                                                                                                                                                                                                                                                                   AgfA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       AAR74625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR74625 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
                                                                            26-APR-1993;
                                                                                                                                                         10-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA segmence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP. (KING/) KING J.
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(first entry)
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Pred. No. 3.3e-61;
0; Mismatches 0
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RESULT 4
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Salmonella AgfA protein and DNA are used in vaccine and genetic immunitation compositions, respectively, to elicit an immune response Salmonella in animals (e.g. food producing animals) and humans. (Updat on 25-MAR-2003 to correct PN field.)
The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign DI sequence which encodes a foreign epitope or antigen. Also describe
                                                                         Recombinant agfA gene having a segment replaced by a foreign DNI which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                        05-APR-1999;
                                                                                                                                                                                                                                                05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                           12-OCT-2000
                                                                                                                                                                                                                                                                                                   WO200060102-A2
                                                                                                                                                                                                                                                                                                                           Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                Salmonella; agfA; chromosomal gene replacement;
                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB36341 standard; protein; 151
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                                                     Disclosure;
                                                                                                                                                                                              (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                    vaccine; immune
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DB; AAQ87467.
                                                                                                                               2000-672631/65.
DB; AAC64617.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collinson
                                                                                                                                                                     Doran JL,
                                                  Page 135; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                        99US-0127888P
                                                                                                                                                                                                                                                                                                                                                    response; immunogen
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90.1%;
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Pred. No. 2.2e-58;
1; Mismatches 14
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                                                                                                                                                                     Kay WW
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                                                                                                                                                                                                                                                                                                                                                                fimbrin; epitope;
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  foreign DNA
30 described
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                                                                                       DNA sequence
ant AgfA
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RESULT 5
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Cd directing recombination of a recombinant gene into the chromosome of the chomologous species; (3) directing recombination of a recombinant gene combination of a recombinant gene combination of a recombinant gene composed into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino caid sequence or sequences grown on a Salmonella, E. coli or conterobacteriaceae host cell, from the host cell and introducing the coliver into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for celiciting an immune response in an animal. In a fimbrial presentation conjunction with a carrier or diluent. (I) is conjunction with a carrier or diluent. (I) is conjunction with a carrier or diluent. (I) is conjuncting an immune response in an animal. In a fimbrial presentation conjunction properties are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the complex of the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response conjunction, which may be important for directing an immune response conjunction, which may be important for directing an immune response conjunction, which may be important for directing an immune response conjunction with a sequence is given in the exemplification of the present invention
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Best Local
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  Collinson SK,
                                                                                                                                                                       03-JUN-1997
                                                                                                                                                                                                                                                                                                                                          Salmonella enteritidis
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29-SEP-1997
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                                                                                     26-APR-1993;
                                                                                                                             26-APR-1994;
                                                                                                                                                                                                                 US5635617-A
                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                 Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
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                                            (UYVI-) UNIV VICTORIA INNOVATION &
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Кау
                                                                                     93US-00054452
                                                                                                                             94US-00233788
                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                        /note= "Encoded by GCC"
WW,
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90.1%;
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Pred. No. 2.2e-58;
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RESULT 6
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Best Local Sim.
Matches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                    N-PSDB; AAC64626.
                                                   WPI; 2000-672631/65.
                                                                                                                               05-APR-1999;
                                                                                                                                                          05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                     12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                AAB36350 standard;
                                                                                                      (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                              WO200060102-A2
                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                     Escherichia
                                                                                                                                                                                                                                                                 Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                   AgfA::PT3#5 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated Salmonella gene agfA - u enteropathogenic bacteria of the
                                                                                                                                                                                                                                                                                                        Salmonella; agfA;
                                                                                                                                                                                                                                                                                                                                                             26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-309886/28.
N-PSDB; AAT74142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNPALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNAALVNOTASDSSVMVROVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                          Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fig 7; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                 99US-0127888P
                                                                                                                                                                                                                                                                                           response;
                                                                                                                                                                                                                                                                                                       chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                   acid sequence SEQ ID NO:20
                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.5%;
89.4%;
                                                                           Collison
                                                                                                                                                                                                                                                                                          immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                 151
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Pred. No. 6.6e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used for diagnosis of Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterobacteria family.
                                                                           Kay WW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 151;
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Recombinant agfA gene which encodes foreign

epitope

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antigen,

having a segment replaced by a foreign DNA sequence

05-APR-2000; 2000WO-CA000356

12-OCT-2000

expresses

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RESULT 7
AAB36353
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation or retempts the heterology and the polymer into the appression of recombinant AgfA protein which is useful for the host of the polymer into the appression of recombinant agfA protein which is useful for the heterology and the polymer into the appression of recombinant agfA protein which is useful for the heterology and the polymer into the appression of recombinant agfA protein which is useful for the heterology and the polymer into the action of the polymer into the appression of the polymer into the polymer into the appression of the polymer into the appression of the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into the polymer into 
                                                         Escherichia coli.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
                                                                                                                              Salmonella enteritidis
                                                                                                                                                                                                                      Salmonella; agfA; chromosomal gene replacement; fimbrin;
WO200060102-A2
                                                                                                                                                                                              vaccine;
                                                                                                                                                                                                                                                                                          AgfA::PT3#8
                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                         AAB36353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB36353 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 137; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 81.9
36; Conservative
                                                                                                                                                                                              immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                       amino acid sequence SEQ
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                                                                                                                                                                                        response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
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                                                                                                                                                                                                                                                                                          NO:26
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2.4e-56;
0;
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                                                                                                                                                                                                                      epitope,
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RESULT 8
AAB36355
ID AAB3
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AC AAB3
XX
DT 26-F
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DE A9fA
XX
KW Salm
KW vacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                     Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                     AAB36355 standard; protein; 151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                            AgfA::PT3#10 amino acid sequence SEQ ID NO:30.
                                                                                                       26-FEB-2001
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                                                                                                                                                                                                                                                                                             98
                                                                                                                                                                                                                                                                                                                                                                               85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128; Conservative
                                                                                                                                                                                                                                                                                                                                  98
                                                                                                                                                                                                                                                                                                                                                                                                                    61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                      RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAAL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 138; 139pp; English
                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0127888P
response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.6%;
73.6%;
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Pred. No. 5.7e-52;
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Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation
                                                                                                                                                                                                                                                                                                                                                                                                                  system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                    Sequence 151
                                                                                                                                                                                                                                                                                                                                                         against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella enteritidis.
Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYVI-) UNIV VICTORIA
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DB; AAC64631.
                                                                                                                                                                                                                                       129;
119
                                                                          61
                                                                                                                13
                                   99 NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                               Н
                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                   MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                  SDARKSETTITQSGYGNGAD-----
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                                                                                                                                                                                                                                                         Score 613; DB 3; Pred. No. 1.4e-51;
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AAB36346 ID AAB3

AAB36346 standard; protein; 151

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Salmonella;

la; agfA; chromosomal gene replacement; immune response; immunogen.

fimbrin; epitope;

AgfA::PT3#1 amino acid sequence SEQ ID

NO:12

26-FEB-2001

(first entry

vaccine;

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant Agfa, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
                                                                                                                                                   Sequence
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                                                                                                                                                                                       immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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           CC directing recombination of a recombinant gene into the chromosome of the chomologous species; (3) directing recombinant gene into the chromosome of the chomologous species; (3) directing recombinant gene into the chromosome of the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an anino acid polymer comprising a recombinant AgfA comprising separating an anino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the collisting an immune response in an animal. In a fimbrial presentation cellciting an immune response in an animal. In a fimbrial presentation consists the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and
                                                                                                                                                                                                                                                                                                                                               The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
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Escherichia coli.
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                sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF1/TAF) nucleation depended assembly system of strains of Salmonella, Bscherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing a species; replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Doran JL,
                                                                                                                                                                                                                                                                                                                 invention describes a recombinant agfA gene (I) wher
                                                                                                                                                                                                                                                                                                                                                                                                     Page 136; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid sequence
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Bequences
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80.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collison
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Pred. No. 1.3e-50;
4; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                      WPI; 2000-672631/65.
N-PSDB; AAC64628.
                                                                                                                                                                                                                                   05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                    Salmonella
                                                                                                                                                                                                                                                                                                                                                                        Salmonella; agfA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB36352 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 151
                                                                                                                                                                                                         05-APR-1999;
                                                                                                                                                                                                                                                            12-OCT-2000
                                                                                                                                                                                                                                                                                   WO200060102-A2.
                                                                                                                                                                                                                                                                                                                        Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                           vaccine; immune
                                                                                                                                                                                                                                                                                                                                                                                               AgfA::PT3#7
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                                                                                                                                                                                  (UYVI-) UNIV VICTORIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                  enteritidis
                                                                                                                                                          Doran JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                           99US-0127888P
                                                                                                                                                                                                                                                                                                                                                           response;
                                                                                                                                                                                                                                                                                                                                                                      chromosomal gene replacement;
                                                                                                                                                                                                                                                                                                                                                                                               acid sequence SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.5%;
                                                                                                                                                           Collison
                                                                                                                                                                                                                                                                                                                                                           immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 601; UB
Pred. No. 2e-50
4; Mismatches
                                                                                                                                                           SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e 601; DB 3;
                                                                                                                                                          Kay
                                                                                                                                                           M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 151;
                                                                                                                                                                                                                                                                                                                                                                         fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described

Recombinant agfA gene having a segment replaced which encodes foreign epitope or antigen, expres protein useful for eliciting immune response in

expresses recombinant se in animal.

by a

foreign

DNA sequence ant AgfA

Disclosure; Page 138; 139pp; English

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RESULT 13
AAB36348
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Best Local
WPI; 2000-672631/65
                                                                                                                                                                                                                     05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36348 standard; protein; 151 AA
                                                        White AP,
                                                                                                                                                                     05-APR-1999;
                                                                                                                                                                                                                                                                                   12-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AgfA::PT3#3
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                                                                                                                (UYVI-) UNIV VICTORIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEMAHANOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                  Doran JL,
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                                                                                                                                                                     99US-0127888P
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                                                        Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence SEQ ID NO:16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunogen.
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Pred. No. 2.5e-50;
3; Mismatches 25;
                                                     SK,
                                                     Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
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                                                                                                                                                                                                                                                                                                                                                                directing recombination of a recombinant gene into the chromosome of the Chomologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene, and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequence grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for constituting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response
                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                            Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                         against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAC64624
                                                                                                                                                                                                                                                                                              Local
121
                       121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                        121;
                                                                                        61
                                                                                                                                5
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                                                                                                                                                                                                                                                                                              Similarity
                                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                SDARKSETTITOSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDOWNAKNSDITVGQYGG
                                                                                                                                                                              MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                          MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                A,
                                                                                                                                                                                                                                                                                           73.3%;
                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                   Score 568; DB 3;
Pred. No. 3.3e-47;
4; Mismatches 26
                                        151
                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                 Length 151;
                                                                                                                                                                                                                                                                      Indels
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RESULT 14
AAB36343
ID AAB36
AC AAB36
AC AAB36
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KW vacci
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PD 12-0C
                                                                                                                            Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                            Escherichia coli CsgA amino acid sequence SEQ ID NO:7.
                                                                                                                                                                                              26-FEB-2001
                                                                                                                                                                                                                                                            AAB36343 standard; protein; 151 AA
                                                                              Escherichia coli
                                                                                                             vaccine; immune response;
                                                                                                                                                                                                                             AAB36343;
                                                                                                                                                                                             (first entry)
                                                                                                              immunogen
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12-OCT-2000

WO200060102-A2

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RESULT 15
ABR82651
ID ABR82
XX
AC ABR82
XX
DT 04-DE
XX
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XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 10,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response segainst the inserted epitope, and hybrid fimbriae are easy and the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 103; Conserv
                 E. coli CsgA
                                                         04-DEC-2003
                                                                                                                                ABR82651 standard;
                                                                                              ABR82651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a recombinant agfA gene (I) segment of the gene has been replaced by a segment of a forze sequence which encodes a foreign epitope or antigen. Also de (I) use of thin aggregative fimbriae (SEF17/TAF) nucleation assembly system of strains of Salmonella, Escherichia coli a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-672631/65.
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                                                                                                                                                                                                                                                 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                               MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                           GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                                                                                                                                                                                                                                                           MKLLKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGGNNSGPNSELNIYQYGGGNSALALQ
                                                                                                                                                                                                                                                                                                  TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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               subunit 15 kDa protein
                                                     (first entry)
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                                                                                                                                protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 509; DB
Pred. No. 1.8e
15; Mismatches
                                                                                                                                ⋛
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 151; .8e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i foreign DNA
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Matches
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                                                                                                                                                                                                                                                                            The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABR02642, ABR0264349. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli 15 kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmor or Shigella infections.
                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 41-42; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bjoerck L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2002; 2002GB-00002275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2003; 2003WO-EP000943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HANS-) HANSA MEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasma
                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2003-646136/61.
 121
                              121
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                                                                                                                                                                                      102;
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                                                                                                                                                    1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; immune response; antibacterial; vaccine; gene therapy.
                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACF36153
                         NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
                                                            TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
                                                                                                                      MKLLKVEAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
                                                                                       SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                               151 AA;
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olsen A,
                                                                                                                                                                                                 67.5%;
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                                                                                                                                                                                  15;
                                                                                                                                                                                                 Score 504; DB 7;
Pred. No. 5.5e-41;
                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herwald H;
151
                                                                                                                                                                                                             Length 151;
                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella
                                                                                                                                                                                  Gaps
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Search completed: March 11, 2004, 18:33:46 Job time: 46.9 secs

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Minimum
Maximum
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Maximum Match 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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775
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1 (cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/backfIles1.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-233-788A-57

US-08-233-788A-3

US-09-28-352-4764

US-09-072-596-204

US-09-072-967-204

US-09-072-967-204

US-09-252-991A-3098

US-09-252-991A-3098

US-09-252-991A-26438

US-09-252-991A-26438

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US-09-336-447A-1

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US-08-322-730A-1

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US-08-322-730A-1
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                   Sequence 204, Apple Sequence 30983, A Sequence 32096, A Sequence 32096, A Sequence 26438, A Sequence 26438, A Sequence 26438, A Sequence 1, Appli Sequence 1, Appli Sequence 280, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli Sequence 34, Appli Sequence 34, Appli Sequence 34, Appli Sequence 34, Appli Sequence 34, Appli Sequence 34, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli 
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Sequence 57, Appl
Sequence 4764, Ap
Sequence 3, Appli
Sequence 204, App
Sequence 199, App
Sequence 111, App
Sequence 204, App
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75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5
9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7
461	461	432	293	293	293	293	293	293	266	244	238	211	211	211	211	211	211
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US-08-463-667A-4	US-08-463-587A-26	US-09-403-089A-1	PCT-US94-05669A-6	PCT-US94-05669A-4	US-09-219-019-6	US-09-219-019-4	US-08-438-745-6	US-08-438-745-4	US-09-495-880A-26	US-08-553-497A-22	US-09-495-880A-42	PCT-US95-08743-34	PCT-US93-08364-16	US-09-729-597-16	US-08-907-739-16	US-08-383-619-16	US-08-899-575-34
Sequence 4, Appli	Sequence 26, Appl	Sequence 1, Appli	Sequence 6, Appli	Sequence 4, Appli	Sequence 6, Appli	Sequence 4, Appli	Sequence 6, Appli	Sequence 4, Appli	Sequence 26, Appl	-	•	Sequence 34, Appl	Sequence 16, Appl	•	•	Sequence 16, Appl	Sequence 34, Appl

ALIGNMENTS

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RESULT 1
US-08-233-788A-59
                                                                              US-08-233-788A-59
                                                                                                                CURRENT APPLICATION DATA:
APPLICATION UNMER: U5/08/233,
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: TYPE: TOTALES
Query Match
Best Local S
Matches 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Floppy Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND CO
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                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
  Conservative
                   87.5%;
89.4%;
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Score 678; DB 1
Pred. No. 4e-61;
1; Mismatches
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                                      DB 1; Length 151;
  15; Indels
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US-09-328-352-4764
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              Sequence 4764, Application US/09328352 Patent No. 6562958
GENERAL
                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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REGISTRATION NUMBER: 35,570
REFERENCE DOCKET NUMBER: 921
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 26-APR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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INFORMATION:
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                                                                                                                             DQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITYGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                        VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADY
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                                                                                                                                                                   VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
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amino acid
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Collinson, Karen S.
Clouthier, Sharon C.
NVENTION: METHODS AND COMPOSITIONS FOR DETECTION
NVENTION: OF SALMONELLA
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William W.
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                                                                                                                                                                                                                                 Mismatches
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GENERAL INFORMATION:
APPLICANT: Kunio
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SEQ ID NO 4764
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                                   TELEFAX: (212)953-7733
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Acinetobacter baumannii
                                                                                                                                          AFFILING DATE: 15-00.
FILING DATE: 15-00.
ATTORNBY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
NAME: C. Bruce Hamburg
22,389
                                                                                                                                                                                                           FILING DATE: May 28, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-
FILING DATE: 15-July-1996
                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: Microsof SOFTWARE: Word Perfect 6.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
                                                                                             TELEPHONE: (212) 986-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: JAPAN
ZIP: 514-01
                     LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 SGSALAGVVPQWGGGGNHNGG-GNSSGPDSTLSIYQYG--
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mie-prefecture
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                                                                           (212) 953-7733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KUNIÓ NAKASHIMA et al.

KUNIÓN NAKASHIMA ET BLIDE GENE CDNA, VECTOR

ENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR

ENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID

ENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCI
                                                                                                                                                                                                                                                                                                                                                          E: Diskette, 3
IBM Compatible
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                                                                                                                                                                                                                                                                                                                                            Microsoft Windows
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Pred. No. 4.
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                                                                                                                                                                                                                                                                                                                                                                                  storage
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                                                                                                                                                                                          US-09-056-556-204
                                                                                                                                       Query Match
Best Local S
                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 20.
SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino
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GENERAL INFORMATION:
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Best Local (
                                                                                                                                                                                                                                                                                                                            NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/056,556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
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LOCATION: from 1 to 738
IDENTIFICATION METHOD: E (by experiment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDRESSEE:
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LICANT: Dillon, Davin C.
LE OF INVENTION: COMPOUNDS AND METHODS
                                                     464 GSGNIGVFNVGSGSLGNYNIGSGN------LGIYNIGFGNVG-------DYNV 503
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74 GYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGN-----
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l Similarity 35.5%;
27; Conservative
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                                                                                                                                       Similarity
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                                                                                                                                     10.8%; Score 84; DB 4; Length 943; 24.7%; Pred. No. 5.1;
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Pred. No. 3.3;
4; Mismatches 22;
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NAME: MAKE DAVID 1

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 2101

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TO C00 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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NAME: Maki, David J.
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                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                              504 GFGNAGDFNQ----
                                                               554 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN
                                                                                              122 --- NAALVNQTASDSSVM---- VRQVGFGNNATAN 149
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Houghton, Raymond
Vedvick, Thomas S.

Park Daniel R.
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Hendrickson, Ronald C.
VENTION: COMPOUNDS AND
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Dillon, Davin C.
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Pred. No.
                                                                                                                              -GFANTGNNNIGFANTGNNNIGIGLSGDNQQGFNIASGWNS
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LENGTH: 943
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CURRENT FILING DATE: 2000-01-03
PRIOR APPLICATION UNMBER: 08990823
PRIOR FILING DATE: 1997-12-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Nano, Fr.
TITLE OF INVENTION:
TITLE OF INVENTION:
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                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: FILING DATE: 05-MA
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o. 6592877
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/ENTION: COMPOUNDS AND
/ENTION: AND DIAGNOSIS
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Vedvick, Thomas S.
Twardzik, Daniel R.
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Dillon, Davin C.
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 05-MAY-1998
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               US/09/072,967
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                                                                                                                                                                                                                                                                                         METHODS FOR IMMUNOTHERAPY OF TUBERCULOSIS
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                                                                                       TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                           REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 79
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: ___ STREET: ___ York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: No. 62 CLASSIFICATION:
                                                                                                                           TELEFAX:
                  STRANDEDNESS
                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
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COPOLOGY:
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STRANDEDNESS:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 GYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGN----- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS 73
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                                                                                                                         (212) 869-8864
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20.1%; Pred. No. 3.3;

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US-09-252-991A-32096
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LENGTH: 558
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Patent No. 6551795
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Best Local Similarity
Query Match
                                                                                                           SEQ ID NO 32096
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                    APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                NUMBER OF SEQ ID NOS:
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                                                       ORGANISM: Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
                                                                                           LENGTH: 339
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                                                                                                                                                                                                                                                                                                                                                                     Application US/09252991A
                                                                                                                                                                             UMBER: US 60/074,788
1998-02-18
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Score 80;
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Length 339;
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                 TYPE: PRT
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RESULT 13
US-09-336-115C-6
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                                             SOFTWARE: FastSEQ for Windows Version SEQ ID NO 6
LENGTH: 745
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LENGTH: 1207
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Patent No. 6610836
                                                                                                                                                 APPLICANT: Guy, Bruno
TITLE OF INVENTION: LT and CT in Parenteral Immunization
TITLE OF INVENTION: Methods Against Helicobacter Infect:
FILE REFERENCE: 06132/055002
CURRENT APPLICATION NUMBER: US/09/336,115C
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: US 09/100,258
PRIOR PILING DATE: 1998-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/489,039A CURRENT FILING DATE: 2000-01-27 PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR FILING DATE: 1999-01-29 NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GATY BREEON Et. al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Weltzin,
APPLICANT: Guy, Br
                                                                                                                                 NUMBER OF SEQ ID NOS: 24
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ORGANISM: Helicobacter pylori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 YG--GNNAALVNQTASDSSVMVRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          482 GPVMQSQPAYNHNQFSGALANGAESMLSTFSLGSTLASGVSSAQALQSQKSEAFQSTLGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 AAAVSNGQYSTAGSAASQTSTGNTTVNSANYAYG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFSDGVSQDQAYSRLSNIGRNVSSQNTAQSQLINQQAKNFMDKFQVDD----SHSDAVKGA 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVVPQWGGGGNHN--GGGNSSGPDSTLSIYQYGS----ANAALALQSDARKSETTITQS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TV----GOYGGNNAALVNQTASDSSVMVRQVGFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVSNFGTL--NNASVSGSIKDASGNVGVNVAAGDNNQQANAAALASADASFVFGTATAS- 114
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Pred. No. 18;
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RESULT 15
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US-09-252-991A-26438
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                                                         Sequence 4, Application Patent No. 6669940 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 26438
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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APPLICANT: NAGARAJA, T. G.
APPLICANT: STEWART, GEORGE C.
APPLICANT: NARAYANAN, SANJEEV K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Marc. J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY:
LOCATION:
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ORGANISM: Pseudomonas aeruginosa
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NAME/KEY: VARIANT
LOCATION: 721
COTHER INFORMATION: Xaa = Any Amino
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                                                                                                                                                                                                                              122 NAALVNOTA-SDSSVMV-ROVG--FGNNATAN 149
                                                                                                                                                                                                                                                                   989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 RNNATIDOW-NAKUSDITVGQYGGNNAALVNOTASDSSYMVRQVGFGNNAT 147
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                                                                                                                                                                                         NAAINNASAHGDVSLQAGRYLGGLIGHNQAGN 1076
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20.5%; Pred. No. 1:
                                                                                              US/09841786
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Pred. No. 25;
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SEQ ID NO 4
LENGTH: 714
TYPE: PRT
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                            Query Match
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PRIOR APPLICATION NUMBER: 09/558,257
PRIOR FILING DATE: 2000-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/841,786
CURRENT FILING DATE: 2001-04-24
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: RECOMBINANT FUSOBACTERIUM NECROPHORUM LEUKOTOXIN TITLE OF INVENTION: VACCINE AND PREPARATION THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                             Local
151
                                     103 IDQWNAKNSDITVGQY 118
                                                                        92 NANKFKVNALSGGTQVAAGAGLEAVKESG-GQGKSYLLGTSASINLVNNEVSAKSENNTV 150
                                                                                                                                                  35 VTSSDSTFVGA---WGGSAALQWNHIGSGNSNISAGLAGAAAVNNIQSKTSALVKNSDIR 91
                                                                                                                                                                                      12 IVVSGSALAGVVPQWGGGG----NHNGGGN---SSGPDSTLSIYQYGSANAALALQSDAR
                                                                                                                                                                                                                           31;
                                                                                                                                                                                                                                           Similarity
AGESESQKMDVDVTAY 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHENGAPPA, M. M.
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                             10.1%; Score 78.5;
22.8%; Pred. No. 13;
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                                                                                                               TTITQSGYGNGADY---DQLVTRVVTHEMAHAFRNNAT 102
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Search completed: March 11, 2004, 18:44:54 Job time: 13.4 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                               87.5
87.5
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seq length: 2000000000
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         protein search, using sw model
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/cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*

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       6/ptodata/1/pubpaa/US07_PUBCOMB.pep:
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                                                                                    US-09-996-634-131

US-09-997-182-131

US-09-997-181-131

US-10-193-002-199

US-10-193-002-199

US-10-084-843-204
                                                                                                                                                                             US-09-793-306-146
US-09-880-748-905
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US-09-730-374-3
                                                      US-09-813-214A-9
US-09-738-626-4894
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Sequence 146, App
Sequence 131, App
Sequence 131, App
Sequence 131, App
Sequence 199, App
Sequence 204, App
Sequence 9, Appli
Sequence 4894, Ap
Sequence 9134, Ap
Sequence 1847, Ap
Sequence 1847, Ap
                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                           Sequence 21, Appl
Sequence 3, Appli
Sequence 20638, A
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6	80	10.3	253	10	US-09-880-748-2098	Sequence 2098, Ap
7	79.5		278	ø	09-810-264-2	28, App
8	9	10.3	745	8	-08-834-	σ
9	79		65	9	-09-996-194-	_
õ	78.5		486	15	US-10-369-493-20619	O
21	78.5	•	714	9	09-841-786-4	4, Appli
22	78.5	10.1	3241	9	US-09-841-786-1	Ļ
ຜ	78		892	10	US-09-952-267-5	æ
24	77.5		438	14	761-	ø
5	77.5	10.0	518	9	US-09-976-297-2	2, App
6	77.5	•	562	14	US-10-156-761-13039	Sequence 13039, A
27	77.5		1621	14	US-10-185-990-10	
8	77.5	•	1626	14	-10-185-990-	ш
9	77		250	14	-10-072-301-	,
ö	77	9.9	250	14	US-10-072-301-29	29,
ĭ	77	9.9	250	14	US-10-071-866-21	21,
2	77	9.9	250	14	US-10-071-866-29	æ
ü	77		250	15	US-10-360-828-21	e 21,
4	77	9.9	250	15	-828-	e 29,
š	77	9.9	255	10	US-09-880-748-1153	115
õ	77		255	10	-748-186	e 186
37	77	9.9	257	10	US-09-880-748-1494	e 1494,
8	77	•	271	14	US-10-156-761-11721	e 11721,
9	77		1046	15	69-493-	æ
6	76.5	9.9	251	10	0-748-	Sequence 71, Appl
Ħ	76.5		809	14	US-10-156-761-13874	e 1387
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US-09-820-843A-21
VS-09-820-843A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 21
LENGTH: 354
TYPE: PRT
ORGANISM: M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                   Matches
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CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
OTHER INFORMATION: gi 1781260
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
OTHER INFORMATION: PPE
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115 VGQYGGNNAALVNQTASDSSVMVRQV---GFGNNATAN 149
                                                                                                                                                   200
                                                               258 SGFGHNDPÅGSGNSGIQNSGFGNS-------GYVNTSTTSMFGGNSGVLN
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                                                                                                       AALALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDIT 114
                                                                                                                                                   AGDVNSGVGNAGDVNTGLGNSGNINTGGFNPGTLNTGFFSAMTQAGPNS--GFFNAGTGN
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                                                                  US-10-369-493-20638
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  Best Local Similarity
                                                                                                                                                                                                                                           SEQ ID NO 20638
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APPLICANT: Lust, John A.
APPLICANT: Donovan, Kat
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                         Query Match
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Patent No. US20010031261A1
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2002-02-21 NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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PRIOR APPLICATION NUMBER: 60/088,277
PRIOR FILING DATE: 1998-08-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/730,374
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: PCT/US99/12512
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TITLE OF INVENTION: USE OF GENETICALLY ENGINEERED ANTIBODIES
TITLE OF INVENTION: TO CD38 TO TREAT MULTIPLE MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
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                                                                                    PEATURE:
NAME/KEY: unsure
LOCATION: (1).. (445)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                         ORGANISM: Rhodopseudomonas palustris
                                                                                                                                                                                                    LENGTH: 445
TYPE: PRT
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11.3%;
26.3%;
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Pred. No. 0.95
9; Mismatches
Score 87.5;
Pred. No. 2;
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0.95;
                      DB 15;
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US-09-793-306-146
Sequence 905, Application US/09880748
publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1
SQ ID NO 146
LENGTH: 597
TYPE: PRT
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Sequence 146, App
Sequence 146, App
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PRIOR FILLING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 014058-008740US
CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT FILING DATE: 2001-02-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIILE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
IIILE OF INVENTION: of Tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE: OTHER INFORMATION: Description of Artificial Sequence: mTTC#3-His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                 NAGTLN
                                                                                                                                                                                                                                                                                                                                                           TRVVTHEMAHAFRNNATIDQ--WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                FGNSGNNNIGFFNSG-NNNVGFFNSGNNNFGFGNAGD-
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Corixa Corporation
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Pred. No. 3.
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FILING DATE: 2000-06-15

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                                                                                                                                                                                                     ; ORGANISM: Mycobacterium tuberculosis
US-09-996-634-131
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US-09-880-748-905
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Best Local Similarity 23.0
29; Conservative
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                                                                                                                                                   Query Match
Best Local Similarity
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Patent No. US2002017268471
                                                                                                                                     Matches
                                                                                                                                                                                                                                                                       SEQ ID NO 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/996,634
CURRENT FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 169
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/447,135 PRIOR FILING DATE: 2000-01-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 61260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Nano,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 3239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2000-10-17
APPLICATION NUMBER: 60/276,248
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/000,254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/240,816
                                                                 571 GSGNIGVFNVGSGSLGNYNIGSGN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 TLSCRASOSIRSNYLAWYQQKSGQAPRLLIYDVSSRATGIPDRFSGSGSGTDFTLTISRL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 ILTGYYMGSAFDOWGRGTMVTVSSGGGGSGGGGGGGGGGALEIVMTQSPGTLSLSPGERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89
                               74 GYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGN------
                                                                                                 16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 VVSGSALAGVVPQWG------GGGNHNGGGNSSGPDSTLSI------
                                                                                                                                   38;
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23.0%;
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--GFANTGNNNIGFANTGNNNIGIGLSGDNOOGFNIASGWNS
                                                                                                                                                   Score 84; DB 9; Length 943
Pred. No. 11;
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Pred. No. 1.7
                                                                                                                                   Mismatches
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                                                                 -LGIYNIGFGNVG-----
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                                                               ----- DYNV 610
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                                                                                                                                                                                                                                                                                                                                                          ; Sequence 131, Applica
; Publication No. US200
; GENERAL INFORMATION:
; APPLICANT: Nano, Fra
                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-997-181-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Pa
SEQ ID NO 131
LENGTH: 943
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Best Local Similarity
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                                                                                                                            PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/997,181
CURRENT FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding TITLE OF INVENTION: immunostimulatory Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
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CURRENT FILING DATE: 2001-11-28
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                                             SOFTWARE:
                                                                 NUMBER OF SEQ ID NOS: 169
                                                                                     PRIOR FILING DATE: 1995-06-15
                                                                                                        PRIOR APPLICATION NUMBER: 60/000,254
                                                                                                                                                                                                                                                                                               FILE REFERENCE: 61257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     611 GFGNAGDFNQ
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                                         Patentin
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Pred. No.
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-193-002-199
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US-10-193-002-199
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     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 199, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
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Best Local Similarity 24.7
Matches 38; Conservative
                                                                                                                           INFORMATION FOR SEQ ID NO: 199: SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
4900 Columbia Center,
                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/072,596
PILING DATE: 05-MAY-1998
ATTORNEY,AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.4
                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PStentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/193,002
PILING DATE: 10-Jul-2002
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            661 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN 694
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                                                                                                              TYPE: amino acid
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                                                                                              STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
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IVENTION: COMPOUNDS AND METHODS

TUBERCULOSIS
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Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Campos-Neto, Antonia
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     10.8%;
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Pred. No. 11;
12; Mismatches
   Score 84;
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                                                          199:
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 DB 14;
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Length 943;
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Query Ma Best Lo Matches	RESULT US-10- US-10- US-10- US-10- US-10- US-10- US-10-	Qy Db	2y 2y 2y	Best Matc
ry Match 10.8%; Score 84; DB 14; Length 943; it Local Similarity 24.7%; Pred. No. 11; ches 38; Conservative 12; Mismatches 54; Indels 50; Gaps	INT 10 10-084-3.204 Sequence 204, Application US/10084843 Publication No. US20030143243A1 GENERAL IMPORMATION: APPLICANT: Reed, Steven G. Skeiky, Yasir A.W. Dillon, Davin C. Campos-Neto, Antonio Houghton, Raymond Vedvick, Thomas S. Twardzik, Daniel R. Lodes, Michael J. Lodes, Michael J. Foreward Adminish Compounds and METHODS FOR IMMUNOTHERAPY NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS: ADDIAGNOSIS OF TUBERCULOSIS CORRESPONDENCE ADDRESS: ADDIAGNOSIS OF TUBERCULOSIS CORRESPONDENCE ADDRESS: ADDRESSES: SEED and BERRY LLP STREET: 6300 COlumbia Center, 701 Fifth Avenue CITY: Seattle STRIT: Washington COUNTRY: USA ZIF: 98104-7092 COMPUTER READALE FORM: MEDIUM TYPE: Floppy disk COMPUTER READALE FORM: MEDIUM TYPE: Floppy disk COMPUTER: NEADLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READALE FORM: MEDIUM TYPE: Floppy disk COMPUTER: NEADLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: NEADLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: NEADLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: NEADLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: NEADLE FORM: MEDIUM TYPE: Floppy disk MEDIUM TYPE: Floppy disk COMPUTER: NEADLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: NEADLE FORM: MEDIUM TYPE: Floppy disk MEDIUM TYPE: Floppy disk COMPUTER: NEADLE FORM: MEDIUM TYPE: Floppy disk MEDI	122NAALVNQTASDSSVMVRQVGFGNNATAN 149	16 GSALAGVVPQWGGG-CNHN-GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS	Best Local Similarity 24.7%; Pred. No. 11; Matches 38; Conservative 12; Mismatches 54; Indels 50; Gaps
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16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS 73

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; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-813-214A-9
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US-09-813-214A-9
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                                             TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4894, Application US/09738626 Publication No. US20020197605A1
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APPLICANT: Tucker, Kenneth
APPLICANT: Plosila, Laura
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Patent No. US20020177200A1
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/813,214A CURRENT FILING DATE: 2000-03-20
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TITLE OF INVENTION: MORAXELLA CATARRHALIS OUTER MEMBRANE PROTEIN-106 POLYPEPTIDE,
TITLE OF INVENTION: SEQUENCE AND USES THEREOF
FILE REFERENCE: 7969-089-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 20
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                               APPLICATION NUMBER: JP 00/280988
                FILING DATE:
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TATEISHI, NAOKO
SENOH, AKIHIRO
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OCHIAI, KEIKO
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ANDO, SEIKO
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NOS:
                                                                                                                                                                                                                  MASATO
             2000-08-03
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25.8%; Pred. No.
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Marry S.
APPLICANT: Goldman, Marry S.
APPLICANT: Goldman, Marry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION MIMBER: US 105-04-03
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER: TITLING DATE: 2002-02-21
                                                                                                                                                                                                                                        RESULT 14
US-09-880-748-1847
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Sequence 1847, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind
FILE REFERENCE: pF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
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SEQ ID NO 9134
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LENGTH: 224
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Best Local (
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Chloroflexus aurantiacus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
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Pred. No. 3
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Pred. No. 18;
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US-09-880-748-1201
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; ORGANISM: Homo sapiens
US-09-880-748-1201
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PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1201
LENGTH: 252
                                                                                                                                                                                                                                                                               Query Match 10.3%; Score 80; DB: Best Local Similarity 27.3%; Pred. No. 5.4; Matches 42; Conservative 12; Mismatches
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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SEQ ID NO 1847
LENGTH: 246
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-09-880-748-1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/277,379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/276,248 PRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 10.3%;
Local Similarity 31.1%;
nes 28; Conservative
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FILING DATE: 2000-10-17
APPLICATION NUMBER: 60/276,248
FILING DATE: 2001-03-16
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217 ITGLQGEDEADYYCQ-SFDTSLGVRVFGGGTQLT 249
                                            115 - VGQYGGNNAALVNQTASDSSVMVRQVGFGNNAT 147
                                                                                              164 GSGSNIGAGYD
                                                                                                                                                                                        114 WGKGTLVTVSSGGGGGGGGGGGGG------GSAQAVLTQPSSVSGAPGQRVTISCT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 TOPSSVSGAPGORVTISCTGSSSNIGADYD 167
                                                                                                                                        74 GYGN--GADYDQLVTRVVTHEMAH-----AFRNN----ATIDQWNAKNSDIT---- 114
                                                                                                                                                                                                                                     26 WG-----GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD---ARKSETTITQS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 ALQSD---ARKSETTITQSGYGN--GADYD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 AADTAVYFCATGKEGYNDNWGRGTMVTVSSGGGGSGGGGGGGGGG
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                                                                                            ---VHWYOHLPGTAPKLLIFGNNNRPSGVPDRFSGSKSGTSASLA 216
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                                                                                                                                                                                                                                                                                                                              DB 10; Length 252;
                                                                                                                                                                                                                                                                                    50;
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                                                                                                                                                                                                                                                                                    9;
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Search completed: March 11, 2004, 19:18:40 Job time : 25.6 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2004, 18:24:14; Search time 10.3 Seconds (without alignments) 1410.186 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-543-407-28 775 1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151

45	44	43	42	41	40	39	38	37	36	3 5	34	ω u	32	31	30
82.5	82.5	82.5	83	83	83.5	84	84	84	84	84	84.5	84.5	84.5	85	85
10.6	10.6	10.6	10.7	10.7	10.8	10.8	10.8	10.8	10.8	10.8	10.9	10.9	10.9	11.0	11.0
945	940	770	343	277	582	3300	1608	599	599	586	978	928	646	1341	1052
N	N	N	N	N	N	N	N	N	N	N	N	N		N	N
T21998	D89723	T51024	T05221	AB1390	F70675	D70575	A28182	A44951	B42049	T26667	D81411	C81265	819916	H98323	AF2959
hypothetical prote	protein F39D8.1b [related to C2H2 zi	hypothetical prote	hypothetical cell	probable PPE prote	probable PPE prote	hemolysin A - Serr	leishmanolysin (EC	leishmanolysin (EC	hypothetical prote	probable lipoprote	probable lipoprote	leishmanolysin (EC	hypothetical prote	conserved hypothet

ALIGNMENTS

ß &	B 8	Ma Be	C; Fu A; De A; No C; Ke F; 1- F; 21	A; Re A; Re A; Ge	A;Re A;Ro A;Ro A;Ro	A;Re A;Ac A;Re A;Cr	RESULT JC6039 fimbri C;Spec C;Date C;Acce R;C011 J. Bac A;Tit1
61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120	1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60 	Query Match 88.1%; Score 683; DB 2; Length 151; Best Local Similarity 90.1%; Pred. No. 1.4e-51; Matches 136; Conservative 1; Mismatches 14; Indels 0; Gaps 0;	C;Function: A;Description: major component of thin aggregative fimbriae A;Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator C;Reywords: fimbria F;1-20/Domain: signal sequence #status predicted <sig> F;21-151/Product: fimbrin protein agfA #status experimental <wat></wat></sig>	A;Contenes: 2/855 A;Accession: A44898 A;Status: preliminary A;Molecule type: protein A;Residues: 21-33 <c03> A;Note: sequence extracted from NCBI backbone (NCBIP:45936) C;Genetice: A;Gene: agfA</c03>	A; Molecule type: Protein A; Molecule type: Protein A; Molecule type: Protein A; Residues: 21-52 <co2> A; Residues: 21-52 <co2> A; Reperimental source: strain 27655-3b A; Note: the authors translated the codon ACG for residue 44 as Ile R; Collinson, S.K.; Emody, L.; Muller, K.H.; Trust, T.J.; Kay, W.W. J. Bacteriol. 173, 4773-4781, 1991 A; Title: Purification and characterization of thin, aggregative fimbriae from Salmonell. A; Reference number: A44898; MUID:91310586; PMID:1677357</co2></co2>		RESULT 1 JC6039 JC6039 Identify and protein agfA precursor - Salmonella enteritidis C;Species: Salmonella enteritidis C;Date: 31-Dec-1996 #sequence revision 31-Dec-1996 #text_change 08-Oct-1999 C;Accession: JC6039; PC6015; Ā44898 C;Accession: JC6039; PC6015; Ā44898 J. Bacteriol. 178, 662-667, 1996 J. Bacteriol. 178, 662-667, 1996 A;Title: Salmonella enteritidis aqfBAC operon encoding thin, aggregative fimbrise.

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A;Experimental source: strain Ki2, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library,
R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland,
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 01-Mar-2002 C;Accession: S70788; G64846; S31202; S34560; S34559 R;Hammar, M.; Arngvist, A.; Bian, Z.; Olsen, A.; Normark, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                curlin protein csgA precursor - Escherichia coli (strain K-12) N;Alternate names: csgA protein; major curlin protein C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete MB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                      R;Hammar, M.; Arnqvist, A.; Bian, Mol. Microbiol. 18, 661-670, 1995 A;Title: Expression of two csg open
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           딩
                                                                                                                                  A;Status: nucleic acid sequence
                                                                                                                                                     A; Accession: G64846
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                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-151 < HAM>
                                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic
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C;Accession: AI0635
R;Parkhill, J.; Dougan, G.; Jan
th T.: Connerton, P.; Cronin,
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A; Residues: 1-151 < PAR>
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A;Accession: AI0635
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Matches 136
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in, A.;
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Pred.
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No. 1.4e-51;
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                                                                                                                                  translation
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ries, R.M.; Dowd
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Salmonella enterica
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, L.; White,
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Riley, M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S31202
                 QSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYG
                                                                                            MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL
                                                         MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAL
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A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                            DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A:Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                      R;Hayashi, T.; Makino, gasawara, N.; Yasunaga,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; McCcccc
A; Molecule type: DNA
A; Residues: 1-6,'V', 8-151 <OLS1>
A; Residues: 1-6,'V', 8-151 <OLS1>
                                                                                                                                                                                                                                                                                                                                                                                                          curlin major subunit CsgA [imported] - Escherichia C;Species: Escherichia coli
                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-152 < HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Description: major component of wild-type curli; A; Note: curli are thin, coiled fibers expressed on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-133,'RQRDSGWLW' <OLS3>
A;Residues: 1-133,'RQRDSGWLW' <OLS3>
A;Cross-references: EMBL:LO4979; NID:g290424;
A;Experimental source: strain K-12, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Olsen, A.N.; Arnqvist, A.M. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 21-42; 44-50 < OLS2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: The RpoS sigma factor relieves H-NS-mediated transcriptional repression A;Reference number: S31202; MUID:93211294; PMID:8459772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S34559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers 7;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                 Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                      ;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                          T.; Makino, K.; Ohnishi,
N.; Yasunaga, T.; Kuhara,
                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDARKSETTITOSGYGNGADYDOLVTRVVTHEMAHAFRNNATIDOWNAKNSDITVGOYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKLLKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                               GB:BA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154
e: strain O157:H7, substrain ŘIMD 0509952
                    62.9%;
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Score 487.5;
Pred. No. 7.6e
16; Mismatches
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Pred. No. 1.1e-36;
5; Mismatches 33
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                    .6e-35;
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W3110
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Shinagawa,
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-2174 <KUR>
A;Cross-references: GB:AL591985; PIDN:CAC49389.1; PID:g15140875; GSPDB:GN00167
A;Cross-references: GB:AL591985; PIDN:CAC49389.1; PID:g15140875; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
A;Experimental source: strain 1021, megaplasmid pSymB
A;Experimental source: strain 1021, megaplasmid pSymB
A;Galibert, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE005174; NID:g12514574; PIDN:AAG55788.1; GSPDB:GN00145; UWGP:Z1
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
                                                                                       Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Ehebault P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; hebault P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; A;Title: The composite genome of the legume symbiont Sinorhizobium meli
                                                                                                                                                                                                                                                                                                                                                                                                    R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: H85665
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein csgA [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                   A; Reference number: A96039; MUID: 21368234; PMID: 11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical glycine-rich protein [imported] - C; Species: Sinorhizobium meliloti
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                                             Contents: annotation
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;Accession: E95965
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                         Genetics:
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Best Local Similarity
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SMb21548
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Pred. No. 7.0
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                                                                                                                K.; Yeh, K.
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A;Gene: cnjB
A;Genetic code: SGC5
A;Introns: 85/3; 136/1; 157/3; 201/2; 25
A;Introns: 85/3; 136/1; 157/3; 201/2; 25
C;Reywords: zinc finger
F;114-1450/Region: glycine-rich
F;1451-1464/Region: zinc finger CCHC mot
F;1478-1491/Region: zinc finger CCHC mot
F;1530-1514/Region: zinc finger CCHC mot
F;1530-1543/Region: zinc finger CCHC mot
F;1530-1563/Region: zinc finger CCHC mot
F;1530-1563/Region: zinc finger CCHC mot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 21, 4610-4614, 1993
A, Title: Retroviral-type zinc fingers and glycine-rich repeats A, Reference number: S42135; MUID:94051569; PMID:8233798
A, Molecule France.
                                                                                                                                                                                                             F;1579-1592/Region:
F;1602-1615/Region:
F;1626-1748/Region:
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R;Martindale, D.W.; Taylor, F.M.
Nucleic Acids Res. 16, 2189-2201, 1988
A;Title: Multiple introns in a conjugation-specific gene A;Reference number: S03650; MUID:88189811; PMID:3357771
A;Accession: S03650
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S42136
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A;Residues: 236-250,'I',252-255,'N',257-773
A;Cross-references: EMBL:X06462
C;Genetics:
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C;Date: 19-Mar-1997 #sequence revision
C;Accession: $42.136; $42.135; $03650
R;Taylor, F.M.; Martindale, D.W.
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A; Residues: 1164-1174; 1179-1198; 1233-1252; 1285-1293; 1297-1309; 1316-1326; 1331-1341; 1343-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-1748 <TAY>
A;Cross-references: EMBL:L03710; NID:g161751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: S42136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, A;Reference number: S42136
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                                                                                                                                          Best Loc
Matches
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                                                                                                                                          36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 AIVVSGSALAGVVPQ--WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR---K 65

    Tetrahymena thermophila

                                                                                                                                                            Similarity
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                                   DQLVTRVVTHEMAHAFRINIAT I DQWNAKNSDI TVGQYGGNNAAL VNQTASDSSVMVRQVG
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                                                                     QFGGGGNSNGGQSWGTSSGSDWN-----
                                                                                                        QWGGGGNHNGG---GNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADY
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                                                                                                                                                          Score 97;
Pred. No.
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Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70825
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R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W. J. Bacteriol. 178, 662-667, 1996
A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative A;Reference number: JC6039; MUID:96146512; PMID:8550497
                                                                                                       A;Cross-references: GB:AL021958; GB
A;Experimental source: strain H37Rv
C;Genetics:
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                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-645 < COL>
                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                  R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho
                                                                                                                                                                                                                                                                                                                                                                                                             probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
C;Accession: F70825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: minor component of thin aggregative A; Note: fimbriae bind to fibronectin, plasminogen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: agfB
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A; Residues: 1-151 < COL>
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C;Species: Salmonella enteritidis
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
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Best Local S
Matches 35
                                                                                     ;Gene:
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                      Query Match
Best Local
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                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETT 69
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                    12.1%;
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14;
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Score 94; DB:
Pred. No. 2;
14; Mismatches
                                                                                                                                                    GB:AL123456; NID:g3261536; PIDN:CAA17522.1; PID:e12532
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Pred. No. 0.
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  42;
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tissue plasminogen
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                                        Length 645;
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50;
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C;Superfamily: leishmanolysin
C;Keywords: blocked carboxyl end; cell adhesion; glycoprotein;
F;1-39/Domain: stignal sequence #status predicted <SIG>
F;40-100/Domain: activation peptide #status predicted <AITP>
F;101-577/Product: leishmanolysin #status experimental <MATP>
F;101-577/Product: leishmanolysin #status experimental <MATP>
                                                                                                                                                               F;578-602/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;488-264,268,334/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #sta
F;100-101/Cleavage site: Val-Val (autolytic) #status experimental
F;125-142,191-230,314-386,393-455,406-425,415-489,466-510,515-565,535-558/Disulfide
F;264,268,334/Binding site: zinc, catalytic (His) (active) #status experimental
F;265/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Experimental source: strain LEMS13
R,Schlagenhauf, E.; Etges, R.; Metcalf, P.
submitted to the Brookhaven Protein Data Bank, March 1997
A,Reference number: A68135; PDB:1LML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Bouvier, J.; Bordier, C.; Vogel, H.; Reichelt, R.; Et; Mol. Biochem. Parasitol. 37, 235-248, 1189
A;Title: Characterization of the promastigote surface p; A;Reference number: A60648; MUID:90114330; PMID:2608099
                                                                                                               F;577/Modified site: GPI-anchor ethanolamine amidated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Description: catalyzes the hydrolysis of peptide bonds between two \hat{\mathbf{A}}_1, Note: the activated form can activate the proenzyme form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Contents: annotation; X-ray crystallography, 1.86 angstroms, A;Note: strain LRC-L119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 101, 'E', 103-118, 'SV', 121-123 <BOU>
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J. Exp. Med. 167, 724-729, 1988

A;Title: Molecular cloning of the major surface antigen

A;Reference number: A27598; MUID:88154764; PMID:3346625
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C;Accession: PL0221; A27598; A60648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leishmanolysin (EC 3.4.24.36) precursor N;Alternate names: promastigote surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:Y00647; NID:g9554; PIDN:CAA68673.1; A;Note: this is a revision to the sequence from reference.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Button,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Contents:
                                                      Query Match
                                                                                                                                             300,407/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complex: homodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Leishmanīa major
                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294
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                           Similarity
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Score 91.5; DI
Pred. No. 3;
2; Mismatches
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                                                         DB 1;
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A27598
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81 YDQLVTRVVTHEMAHAF-

----RNNATIDOWNAKNSDITV-

12;

Indels

21;

Gaps

2

for

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YDQLVTRVVTHEMAHALGFSGPFFEDARIVANVPNVRGKNFDVPVINSSTAVAKAREQYG

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A; Experimental C; Genetics: A; Gene: PPE
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell A;Title: Deciphering the biology of Mycobacterium tuberculosis from the A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70663
A;Status: preliminary; nucleic acid sequence not shown; translation not A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: C86266
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; De ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; M Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUJD:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003
C;Accession: B70663
C;Accession: B70663
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hornor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Squares, S.
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A;Cross-references: GB:Z83860; GB:AL123456;
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A; Residues: 1-573 <STO>
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                                                                     Query Match
Best Local S
Matches 31
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Best Local S
Matches 36
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;Species: Arabidopsis thaliana (mouse-ear cress)
;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001
;Accession: C86266
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                                                                       l Similarity
31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
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SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG
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                                                                                                                                                                                                                  source: strain H37Rv
                                                                          Conservative
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26.9%;
                                                                                           11.7%;
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                                                                     Score 91; DB 2
Pred. No. 3.4;
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 91; DB
Pred. No. 3.2;
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                                                                                                                                                                                                                                        NID: 93261681;
                                                                                                                    2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
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                                                                                                                    Length 615
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                                                                                                                                                                                                                                        PIDN: CAB06165.1;
                                                                                                                                                                                                                                                                                                                                                          ; Barrell, B.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S.; Khaykin, E.; Kim, S.; Maiti, R.; Marzia
                                                                          46;
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                                                                                                                                                                                                                                                                                                                                                                                genome
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NyAlternate names: csgB protein; curlin nucleation component; mi C;Species: Escherichia coli C;Species: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change C;Accession: S70787; F64846 Time 7 . Olean A . Normark. S.
RESULT
C90806
                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: minor component of wild-type curli; interaction between CsgA and CsgB tri A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-21/Domain: signal sequence #status predicted <SIG>F;22-151/Product: minor curlin chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: the nucleotide sequence was submitted to the EMBL Data Library, R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S. Mol. Microbiol. 18, 661-670, 1995
Mol. Microbiol. 18, 661-670, 1995
A;Title: Expression of two csg operons is required for production A;Reference number: S70783; MUID:96414468; PMID:8817489
A;Accession: S70787
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A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F64846
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                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74125.1; PID:g1787278
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-151 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-151 < HAM>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 DSSVMVRQVGFGNNATAN
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                                                                                                                                                            RNNATIDOWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                    SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAF
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                                                                                                                                                                                                                                                                                                                                                11.5%; Score 89.5; DB 2; 28.1%; Pred. No. 0.92;
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minor curlin subunit precursor CsgB [impo C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18 C;Accession: C90806 R;Hayashi, T.; Makino, K.; Ohnishi, M.; K gasawara, N.; Yasunaga, T.; Kuhara, S.; S DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of ente

M.; Kurokawa, K S.; Shiba, T.;

K.; Ishii,

Hattori,

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K.; Yokoyama, K.; M.; Shinagawa, H.

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18-Jul-2001

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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: G85665
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A;Molecule type: DNA
A;Molecule type: CNA
A;Residues: 1-151 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:g13360879; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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A;Accession: C90806
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A;Residues: 1-151 <STO>
A;Cross-references: GB:AE005174; NID:g12514573; PIDN:AAG55787.1; GSPDB:GN00145; UWGP:Z1
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.5%; Score 89.5; DB 2; Length 151; Best Local Similarity 28.1%; Pred. No. 0.92; Matches 32; Conservative 15; Mismatches 62; Indels
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Best Local Similarity
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                                                                                                                                                                                                              SNRAKIDOTGDYNL-AYIDOAGSANDASISOGAYGNTAMIIOKGSGNKANITOY 129
                                                                                                                                                                                                                                                                                                             RNNATIDOWNAKUSDITYGOYGGNNAALVNOTASDSSVMYROVGFGNNATANOY 151
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28.1%; Pred. No. 0.92;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
                                                                                                    Database :
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein -
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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775
1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   March 11, 2004, 18:14:48; Search time 6.3 Seconds (without alignments) 1248.031 Million cell updates/sec
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                                                                                               SwissProt_42:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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SUMMARIES

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000	10.1	999		10.3				٠	٠	•	10.8	٠	10.9	•	11.2	11.3				11.5	11.8	12.2	62.9	65.7	88.1	Query
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ICEK_PSESX ICEV_PSESX	IMD ARTGO SPT5_YEAST	NSP1_YEAST	YF48 MYCTU	CEAK_ECOLI	YBIL_ECOLI	OMB2_NEIMB	OVO_DROME	HME1_HUMAN	OMPB_RICJA	ALE7_AZOVI	HLYA_SERMA	GP63_LEICH	GP63_LEIME	GP63_LEIDO	CSGB_SALTI	ICEN_ERWHE	ICEN_PANAN	ICEN_XANCT	ICEA PANAN	CSGB_ECOLI .	GP63_LEIMA	CSGB SALTY		CSGA ECOLI	CSGA_SALTY	ID
O30611 pseudomonas P23226 drosophila O33479 pseudomonas			P09815 pseudomonas O10778 mycobacteri	Q47502 escherichia	escherichi		P51521 drosophila	٠×		Q9zfg9 azotobacter					salmone	P16239 erwinia her			P20469 pantoea ana	P39828 escherichia		P55226 salmonella		P28307 escherichia	P55225 salmonella	Description

45	44	43	42	41	40	39	38	37	36	35	34
75.5	75.5	75.5	76	76	76	76	76.5	76.5	77	77	77
9.7	9.7	9.7	9.8	9.8	9.8	9.8	9.9	9.9	9.9	9.9	9.9
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COAA BPFD	OMS1_SALTI	HCY_NATPH	C3G_DROME	SCWB_YEAST	P35_MYCPE	HFAA_CAUCR	YFCU_ECOLI	Y442_MYCTU	ACMA_LACLA	P33_MYCPE	CORA_MEDSA
P03661	Q56110										Q07202
bacterioph	salmonella	natronomon	drosophila	saccharomy	mycoplasma	caulobacte	escherichia	mycobacter	lactococcu	mycoplasma	medicago B

ALIGNMENTS

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[4] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931; SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931; MEDLINE=22531367; PubMed=12644504; MEDLINE=22531367; PubMed=12644504; Deng W., Liou SR., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;	SECUENCE FROM N.A. SPECIES=S.typhi; STRAIN=CT18; SPECIES=S.typhi; STRAIN=CT18; MEDLINE=21534947; PubMed=11677608; Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Peltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi (CT18."; Nature 413:848-852(2001).	SEQUENCE FROM N.A. SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677509; MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2."; Nature 413:852-856(2001).	Salmonella typhi, and Salmonella enteritidis. Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella. NCBI_TaxID=602, 601, 592; [1] SEQUENCE FROM N.A. SPECIES=S.typhimurium; STRAIN=SR-11; SECIES=S.typhimurium; STRAIN=SR-11; MEDLINE=98117058; PubMed=9457880; ROMILINE=98117058; PubMed=9457880; ROMILINE=98117058; PubMed=9457880; ROMILINE=98117058; PubMed=9457880; SECIES=S.typhimurium and STRAIN=SR-11; MEDLINE=98117058; PubMed=9457880; SECIES=S.typhimurium and SECIES=S.typhimur	ULT 1 A SALTY CSGA SALTY STANDARD; PRT; 151 AA. P5525; 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Major curlin subunit precursor (Fimbrin SEF17). CSGA OR AGFA OR STM1144 OR STY1181 OR T1776. Salmonella typhimurium.

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Matches
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EMBL; AE008749; AAL20074.1; --
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                                                                                                                                                                                                                           CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriol. 173.4773-4781(1991).
- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI, CURLI AS COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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STRAIN=K12 / YMEL;
MEDLINE=93023873; PubMed=1357528;
Arnqvist A., Olsen A., Pfeifer J., Rt
"The Crl protein activates cryptic gr
fibronectin binding in Escherichia cr
Mol. Microbiol. 6:2443-2452(1992).
MEDLINE=91310586; PubMed=1677357; Collinson S.K., Emoedy L., Trust T "Purification and characterization"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.,
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose I
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"The RpoS sigma factor relieves H-NS-mediated transcriptional repression of csgA, the subunit gene of fibronectin-binding cscherichia coli.";
Mol. Microbiol. 7:523-536 (1993).
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Hammar M., Arnqvist A., Bian Z., Olsen A., Normark
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Best Local Sim:
Matches 103;
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Q93U24;
28-FEB-2003
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CSGA OR Z1676 OR ECS1420.
Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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                                Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J. Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamous Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=0157:H7 / ATCC 43895;
MEDLINE=21218556; PubMed=11319125;
MIDLINE=21218556; PubMed=11319125;
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                                                                                                                                                                                                                                                                                                                   STRAIN=0157:H7 / EDL933 / ATCC 700
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1; X90754; CAA62282.1; -.
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an email to license@isb-sib.ch).
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(Rel. 41, Last annotation)
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                                                 Escherichia coli O157:H7.";
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01-OCT-1996 (Rel. 34, Last Sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEF17
CSGB OR AGFB OR STM1143.
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MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino K., Ohnishi M., Murata T., Tanaka M., Tobe T Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunac Kuhara S., Shiba T., Hattori M., Shinagawa H.;

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).
   Romling U., Bian Z., Hammar M., Sierralta W.D., Normark "Curli fibers are highly conserved between Salmonella ty Escherichia coli with respect to operon structure and re
                                                                                                        SEQUENCE FROM N.A.
SPECIES=S.typhimurium; STRAIN=SR-11;
MEDLINE=98117058; PubMed=9457880;
                                                                                                                                                                                                                                                                                                                                                             Salmonella typhimurium, and Salmonella enteritidis.
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Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS
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Best Local
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P08148; P15906;
01-AUG-1988 (Rel
01-APR-1990 (Rel
       01-AUG-1988 (Rel. 08, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell
(Major surface glycoprotein) (GP63 protein) (1
                                                                                                          LEIMA
endopeptidase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ002301; CAA05316.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran
"Salmonella enteritidis agfBAC operon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=S.typhimurium; STRAIN=LT2
MEDLINE=21534948; PubMed=11677609;
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SIMILARITY: BELONGS
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COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND T
FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPON
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2; SG10609; csgB.
2; Signal; Complete proteome.
21 POTENTIAL.
21 MINOR CURLIY
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                                                                                            STANDARD;
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Pred. No. 0.19
L7; Mismatches
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Zymogen;
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U entitles requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The crystal structure of the Leishman.leishmanolysin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95406217; PubMeq=/o/////,
Schlagenhauf E., Etges R., Metcalf P.;
"Crystallization and preliminary X-ray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schneider P., Ferguson M.A.J., McConville M.J., Homans S.W., Bordier C., "Structure of the glycosyl-phosphatidylinositol
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PROSITE; PS00142; ZINC_PROTEASE; 1.
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InterPro; IPR001577; Peptidase M8.
Pfam; PF01457; Peptidase M8; 1.
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SIMILARITY: Belongs to peptidase family M8.
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Biol. Chem. 265:16955-16964(1990)
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1LML; 17-SEP-97.
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171:589-589(1990)
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Matches 25
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SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., I
Gregor J., Davis N.W., Kirkpatrick H.A., Gc
Mau B., Shao Y.;
"The complete genome sequence of Escherichi
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SEQUENCE FROM N.A.
SETRAIN=K12 / MC4100;
STRAINE-96414468; PubMed=8817489;
MEDLINE-96414468; PubMed=8817489;
Hammar M., Arnqvist A., Bian Z., Olsen A., Normark S.;
"Expression of two csg operons is required for production of "Expression of two csg operons is required for production of "Expression of two csg operons is required for production of "Expression of two csg operons is required for production of "Expression" and congo red-binding curli polymers in Escherichia
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 83334;
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nilarity 41.7%;
Conservative
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Pred. No. 1.6;
2; Mismatches
    of Escherichia coli K-12.";
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                     C.A., Perna N.T., Burland V.D., Rode C.K., Mayhew G.F., A., Goeden M.A., Rose D.J.,
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Ikemoto K., Inada T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
"A 718-kh nun ~~~~~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escher
O157:H7 and genomic comparison with a laboratory stra
                                                                                                                                                                                                                                                                                                                                                                      Arnqvist A., Olsen A., Normark S.;

"Sigma S-dependent growth-phase induction of the csgBA promoter in Escherichia coli can be achieved in vivo by sigma 70 in the absence of the nucleoid-associated protein H-NS.";

Mol. Microbiol. 13:1021-1032(1994).

-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWT TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                            PIR; C90806; C90806.
PIR; G85665; G85665.
PIR; S70787; S70787.
                                                                                                             EMBL;
                                                                                                                                            EMBL; X90754; CAA62281.1; -. EMBL; AE000205; AAC74125.1; EMBL; D90741; BAA35831.1; -.
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                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
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                              Fimbria;
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"A 718-kb DNA sequence of the Escherichia
Corresponding to the 12.7-28.0 min region
DNA Res. 3:137-155(1996).
                              EcoGene; EG12621;
Fimbria; Signal; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95157246; PubMed=7854117;
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                                                                                                            AE000205; AAC74125.1; -. D90741; BAA35831.1; -. AE005315; AAG55787.1; -. AP002554; BAB34842.1; -.
                                                                                                                                                                                                          s requires a license agreement (San email to license@isb-sib.ch).
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MINOR CURLIN
                  POTENTIAL
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or J., Kirkpatrick H.A.,
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on the lin
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T., Tanaka
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ry strain K-12.";
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M., Tobe T.,
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Matches 32
                                                                                                                                                                              Pfam; PF00818; Ice_nucleation; 69.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 49.
                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abe K., Watabe S., Emori Y., Watanabe M., Arai S., "An ice nucleation active gene of Erwinia ananas. to those of Pseudomonas species and regions requir
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P20469
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                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleation activity.";
FEBS Lett. 258:297-300(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Ga
Enterobacteriaceae; Pantoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991
16-OCT-2001
                                                                                                                                       Ice nucleation; Repeat; Outer membrane.
DOMAIN 162 1281 OCTAPEPTIDE PERIODICITY.
SEQUENCE 1322 AA; 131094 MW; 89B0EE24AA837039 CRO
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Bacteria; Proteobacteria; Gammaproteobacteria;
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SUBCELLULAR LOCATION: Outer membrane (By similarity).
DOMAIN: CONTAINS MANY IMPERFECT REPEATS OF THE CONSEN
OCTAPEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE
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AHAFRNNATIDQWNAKNSDITVGQYG---
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Pred. No. 5.9;
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enable bacteria to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                             ---GYNSILTAGYGS---
                                                                                                                                                                                                                                                                                                                                     There are no restrictions ong as its content is in
 GNNAALV----NQTASDSSVMVRQVGFG
                                                                                               .9;
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                                                                                  26;
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                                                                                                                                                                                                                                                                                                                                                                                                                        nucleation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                              Length 1322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence similarity
                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONSENSUS
                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151;
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                                                                                  Gaps
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RESULT 8
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                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wanthomonas campestris pv. translucens.";

MO1. Gen. Genet. 223:163-166 (1990).

-I- FUNCTION: Ice nucleation proteins enable bacteria to nucleat crystallization in supercooled water.

-I- SUBCELLULAR LOCATION: Outer membrane (By similarity).

-I- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-L-T; FUNTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUGGESTED IN WHICH THE NUCLEARION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF IC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICEN XAX
P18127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XANCT
                                                                                                                                                                                                                                                                           Pfam; PF00818; Ice nucleation; 81.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE NUCLEATION; 57.
PROSITE; PS00314; ICE NUCLEATION; 57.
PROSITE; PS00314; ICE NUCLEATION; 57.
PROSITE: CONST.
                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xanthomonas campestris (pv. translucens).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000258; Ice_nucleatn.
Pfam: PF00818; Ice_nucleation; 81.
                                                                                                                                                                                                                                                                                                                                                                    EMBL; X52970; CAA37140.1; -. HSSP; P06620; 1INA.
                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhao J., Orser C.S.;
"Conserved repetition in the ice nucleation gene inaX from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91080859; PubMed=2259339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xanthomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ice nucleation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the bacterial ice nucleation
                               103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XANCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      967
                                                                  264
                                                                                                 60
                                                                                                                                                                                                  47;
                                                                                                                                                                                                                  Similarity
A----RKGSDITAG-YGSTGTAGSDSALIAGYGSTQTAGSESSLT--AGYGSTQTARK 374
                               IDOWNAKNSDITVGQYG-----GNNAALV-----NQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                VYGSTLTGADQSRLVAGYGSTETAGDHSDLIAGYGSTGTAGSDSSI-LAGYGSTQTAAGR 263
                                                                                                                                                              VSGSALAG-----VVPQWGG----GGNHN------GGGNSSGPDSTLSIYQYGSANAALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSQTARE 1020
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                                                                STLTAGYGSTQTAQEGSRLTSGYGSTATSGSDSAVISGYGSTQTAGSESSLTAGYGSTQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TQTGQENSDLTTG-YGSTSTAGYESSLIAGYGSTQTASFKSTLM--AGYG 1013
                                                                                                                                                                                                                                                                   1567 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 16, Created)
(Rel. 16, Last sequence up)
(Rel. 40, Last annotation
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150
                                                                                               SDARKSETTITQSGYG----NGAD-----YDQLVTRVVTHEMAHAFRNNAT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xanthomonas
                                                                                                                                                                                                                11.5%;
                                                                                                                                                                                                                                                                   152548 MW;
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                                                                                                                                                                                                  23;
                                                                                                                                                                                               Score 89.5; D
Pred. No. 7.2;
23; Mismatches
                                                                                                                                                                                                                                                                   C8B451D959ECAD63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
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                                                                                                                                                                                                  59;
                                                                                                                                                                                                                                Length 1567;
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RESULT 9
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RESULT 10
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Best Local (
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16-OCT-2001
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Q47879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: Ice nucleation proteins enable bacteria to nucleate crystallization in supercooled water.
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- DOMAIN: CONTAINS IMPERFECT REPEATS OF A CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RES
                                                                                                                                                                                                                                                                                                         InterPro; IPR000258; Ice_nucleatn.
Pfam; Pf00818; Ice_nucleation; 51.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 34.
ICe_nucleation; Repeat; Outer_membrane.
DOMAIN 162 993 OCTAPEPITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERIODICITY IS SUPERIMPOSED.

-!- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF IC-!- SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94264407; PubMed=7764866; Michigami Y., Watabe S., Abe K., Obata H., An "Cloning and sequencing of an ice nucleation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PANAN
                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pantoea ananas (Erwinia uredovora).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; JC2143; JC2143.
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D14992; BAA03636.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biosci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uredovora."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ce nucleation
                                                                                                                                                                                                                                                 Local Similarity
                                              244
                                                                                                                                                                                                                                                                                                                                                                                                      P06620; 1INA.
                                                                                                                                                                                                  12 IVVSGSALAGVVPQW--GGGGNHNGGGNSS-----GPDSTLSIYQYGSANAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biotechnol. Biochem.
                                                                                                                                     ALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pean Bioinformatics Institute. There are no restrictions on non-profit institutions as long as its content is in no
                                              YGSTGTAGDDSSLIAGYGSTQTAGEDSSLT--AGYGSTQTAQK 284
                                                                                                          ----GEESSQMAGYGS---
                                                                                                                                                                     IATYGSTLSGTHQSQLIAGYGSTETAGDSSTLIAGYGSTGTAGSDSTL-VAGYGSTQTA-
                                                                                                                                                                                                                                                                                              1034 AA;
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 35, Created)
(Rel. 35, Last sequence up)
(Rel. 40, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                         GNNAALV-----NOTASDSSVMVRQVGFGNNATANO 150
                                                                                                                                                                                                                                               11.3%;
                                                                                                                                                                                                                                                                                              103378 MW; FA222523D333EADD CRC64;
                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58:762-764(1994).
                                                                                                                                                                                                                                                 Score 87.5;
Pred. No. 6.
                                                                                                                                                                                                                                                                                                              OCTAPEPTIDE PERIODICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                             DB 1;
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active
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                                                                                                                                                                                                                                                             Length 1034;
                                                                                                                                                                                                                                  Indels
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                                                                                                          --TOTGMKGSDLTAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Erwinia
                                                                                                                                                                                                                                  63;
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ICEN_ERWHE
ID ICEN_E
AC P16239

TICEN ERWHE P16239;

STANDARD;

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RESULT 11
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Best Local S
Matches 41
28-FEB-2003 (Rel. 41,
10-OCT-2003 (Rel. 42,
Minor curlin subunit p
CSGB OR STY1180 OF T
                           CSGB SALTI
Q8Z7M3;
28-FEB-2003
28-FEB-2003
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                    INA.

InterPro; IPRO0258; Ice nucleatn.

Pfam; PF00818; Ice nucleation; 65.

PRINTS; PR00327; ICENUCLEATN.

PROSITE; PR00321; ICE NUCLEATION; 45.

PROSITE; PS00314; ICE NUCLEATION; 45.

ICE nucleation; Repeat; Outer membrane.

DOMAIN 162 1217 OCTAPEPTID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M26382; AAA24823.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 herbicola, Pseudomonas fluorescens and Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Warren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90152370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
Enterobacteriaceae; Panto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erwinia herbicola.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The consensus sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1990
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTYSTABLIZATION IN SUPERCOOLED WATER.
SUBCELLULAR LOCATION: OUTER membrane.
DOMAIN: CONTAINS 126 IMPERFECT REPEATS OF A CON
A-G-Y-G-S-T-X-T, FURTHER ON A 16-RESIDUE AND A
PERIODICITY IS SUPERIMPOSED.
MISCELLANBOUS: A STRUCTURAL MODEL IS SUGGESTED
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED
SIMILARITY: Belongs to the bacterial ice nuclea
family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Ice nucleation proteins enable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleation
                                                                                                                                           244
                                                                                                                                                                   118
                                                                                                                                                                                                                                                                                                                                                                                                                                           JQ0188; JQ0188.
                                                                                                                                                                                                                                            161
                                                                                                                                                                                                                   58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85:239-242 (1989)
                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                                                                                            41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G.J.,
                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                           ALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQ
                                                                                                                                                                                                                                      IATYGSTLSGTHQSQLIAGYGSTETAGDSSTLIAGYGSTGTAGADSTL-VAGYGSTQTA-
                                                                                                                                                                                                                                                                IVVSGSALAGVVPOW--GGGGNHNGGGNSS----
                                                                                                                                      YGSTGTAGDDSSLIAGYGSTQTAGEDSSLT--AGYGSTQTAQK
                                                                                                                                                                                          ----GEESSQMAGYGS----
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                                                                                                                                                                                                                                                                                                                                            1258
                                                                                                                                                                                                                                                                                          Conservative
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(Rel. 14,
(Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corotto
                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                            ΑĄ,
                                                                                                                                                            -GNNAALV----NOTASDSSVMVRQVGFGNNATANQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein.
                          41, Created)
41, Last sequence up
42, Last annotation
      It precursor T1777.
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                                                                                                                                                                                                                                                                                                     11.3%;
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Pred. No. 8
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                                                                            PRT;
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O A REGIONAL 48-RESIDUI
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syringae.";
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SIGNAL 1 21 POTENTIAL.
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-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.

COILED SUMFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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STRAIN=172 / ATCC 700931;
STRAIN=172 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew
Deng W., Kodoyianni V., Schwartz D.C., Bla
Burland V., Kodoyianni V., Schwartz D.C., Bla
"Comparative genomics of Salmonella enterica
and CT18.";
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K. Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
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Bacteria; Proteobacteria;
Enterobacteriaceae; Salmor
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SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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Pred. No. 0.89;
17; Mismatches
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.C., Blattner
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F.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001577; PeptIdase M8; 1
Pfam; PF01457; PeptIdase M8; 1
PRINTS; PR00782; LSHMANOLYSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of Leighmania donovani.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92107220; PubMed=1762629; Webb J.R., Button L.L., McMaster R.W. "Heterogeneity of the genes encoding
                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Glycoprotein; Metal-binding;
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Leishmanolysin precursor (EC 3.4.24.36) (Cell
(Major surface glycoprotein) (GP63 protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Parasitol. 48:173-184(1991).

FUNCTION: Has an integral role during the infection of in the mammalian host.

CATALYTIC ACTIVITY: Preference for hydrophobic residues P1' and basic residues at P2 and P3'. A model nonapept: cleaved at -Ala-Tyr-|-Leu-Lys-Lys-Lys-COFACTOR: Binds I zinc ion per subunit (By similarity) SUBCELLULAR LOCATION: Attached to the membrane by a GP. SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M60048; AAA29244.1;
P08148; 1LML.
                                                                                                   Similarity
YDQLVTRVVTHEMAHALGFSVVFFRDARILESISNVRHKDFDV
                                     YDQLVTRVVTHEMAHA-----
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L.L., McMaster R.W.;
                                                                                                                                                                                                        62950
                                                                                              11.1%;
48.8%;
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LEISHMANOLYSIN.
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                                   FRNNATIDO-WNAKNSDITV 115
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RESULT 13
GP63_LEIME
     MEDLINE-314206; PubMed=8426614;
Medina-Acosta E., Karess R.E., Russell D.G.;
"Structurally distinct genes for the surface protease
"Structurally distinct genes for the surface protease
mexicana are developmentally regulated.";
Mol. Blochem. Parasitol. 57:31-46(1993).
-!- FUNCTION: Has an integral role during the infection the mammalian host.
-!- CATALYTIC ACTIVITY: Preference for hydrophobic repring and basic residues at P2 and P3'. A model non cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995
01-NOV-1995
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _LEIME
GP63_LEIME
P43150;
                                                                 DISULFID
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METAL
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SIGNAL
                  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                 METĀL
                                                                                                                                                                                                                                                                                                                                                                                                 GlycoSuiteDB; P43150; -. Zn InterPro; IPR006025; Pept M Zn InterPro; IPR001577; PeptIdase_M8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X64394; CAA45733.1;
PIR; S19916; S19916.
HSSP; P08148; 1LML.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content modified and this statement is not removed. Usage by are entitles requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00782; LSHMANOLYSIN. PROSITE; PS00142; ZINC_PROTEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leishmania mexicana.
Eukaryota; Euglenozo
NCBI_TaxID=5665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endopeptidase)
GP63-C1.
                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                    PROPEP
                                                                                                                                                                                                                                                                                                                                                     Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leishmanolysin
(Major surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; M08.001; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=MNYC/BZ/62/M379;
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                                                                                                                                                                                                                                                                                                                                   Signal;
                                                                                                                                                                                                                                                                                                                                                     Metalloprotease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euglenozoa;
   (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel.
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1. 32, Last sequence update,
el. 42, Last annotation update)
cl precursor (EC 3.4.24.36) (Ce
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   tease; Glycoprotein; Metal-binding; adhesion; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                      PROTEASE; 1.
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LEISHMANOLYSIN C1
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(See http://www.isb-sib.
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                                                                                                                                                                                                                                                                                     YSIN C1.
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Best Local S
Matches 23
 MEROPS; M08.001; -.
InterPro; IPR006025;
InterPro; IPR001577;
                                              EMBL; M80672; AAA29238.1;
EMBL; M28527; AAA29235.1;
PIR; A44951; A44951.
                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                        expressed during development of Leishmania donovani chagasi promastigores to an infectious form.";

J. Biol. Chem. 267:1888-1895(1992).
                                                                                                 entities requires a or send an email to
                                                                                                                                                                                                                                                                                                                                                        (2)
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=92112918; PubMed=1370484;
Donelson J.E., Pa
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                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE=90205976; PubMed=2320059;

Miller R.A., Reed S.G., Parsons M.;

"Leishmania gp63 molecule implicated in cellular

"Arg-Gly-Asp sequence.";
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NCBI_TaxID=44271;
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Eukaryota; Euglenoz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell
(Major surface glycoprotein) (GP63 protein) (F
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P15706;
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                                                                                                                                                                                                       in the mammalian host.

CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 and Dasic residues at P2 and P3'. A model nonapeptide cleaved at -Ala-Tyr-|-Leu-Lys-Lys-COPACTOR: Binds 1 zinc ion per subunit (By similarity).

SUBCELLULAR LOCATION: Attached to the membrane by a GPI-ar
                                                                                                                                                                                         SIMILARITY: Belongs to peptidase family MB.
                                                                                                                                                                                                                                                                                 FUNCTION: Has an integral role during
                                       P08148;
                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem.
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                                                                                               equires a license agreement (Semail to license@isb-sib.ch).
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Pept_M_Zn_BS
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-!- FUNCTION: Bacterial hemolysins are cell membranes and cause cell ruptu
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P15320;
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                                                                                                                                                                                                                                                                                                          MEDIINE-88257037; PubMed=3290200;
Poole K., Schiebel E., Braun V.;
"Molecular characterization of the hemolysin determinant
                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=SN8
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.,
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Enterobacteriaceae; Serrat
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Hydrolase; Metalloprotease; Glyco
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                                                                 ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCREQUIRES SHLB FUNCTION.
SUBCELLULAR LOCATION: Outer membrane.
SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
                                                                                                                                                                     FUNCTION: CELL-BOUND HEMOLYSIN,
                         SWISS-PROT entry
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Hemoly918; Toxin; Outer membrane; Signal.
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sp_organelle:*
sp_phage:*
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sp_virus:*
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O7x237 enterobacte
Q54069 salmonella
Q983j5 escherichia
Q89j14 bradyrhizob
Q8y106 ralstonia s
Q8x3d6 ralstonia s
Q8x3d6 ralstonia s
Q8x3d6 ralstonia s
Q8x1d3 shewanella
Q8eila shewanella
Q92uu8 rhizobium m
Q8eil4 shewanella
Q89j13 bradyrhizob
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Q7x240 citrobacter
Q8cw63 escherichia
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P95248 mycobacteri .	6 P95248	1	35	11.5	89	5
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Q89ji6 bradyrhizob		۳ ب	15	11.5	9	Ξ
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Q7x238 enterobacte			15:	11.5	9	9
ο	Q841Y5		128	11.7	0	8
Q8e833 shewanella			140	11.7	91	7
P95249 mycobacteri			61:	11.7	91	6
		1 16	61,	11.7	91	š
Q9saf2 arabidopsis			57:	11.7	91	4
Q7x241 citrobacter	Q7X241	2	15:	11.7	91	ü
Q25275 leishmania	Q25275	S	59	11.9	92	2
Q7v8s5 prochloroco	6 Q7V8S5	5 16	176	11.9	92.5	Ξ
O43994 leishmania	0		64	11.9	92.5	ö
O93397 cyprinus ca	13 093397		34	11.9	92.5	9
Q88hg0 pseudomonas	6 Q88HG0		15	12.0	93	8
Q8mny9 leishmania	Q8MNY9		644	12.1	93.5	27
	_		64	12.1	94	8
			64	12.1	94	55
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Q8cw64 escherichia		91 0	16	12.2	94.5	23
			1410	12.3	95	22
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Q8ewd6 mycoplasma	6 Q8EWD6		368	•	95	õ
Q94821 tetrahymena	094821		1748	12.5	97	6
Q89ji5 bradyrhizob	.6 Q89JI5	_	15		97.5	8
O33801 salmonella	033801	9	17	12.6	98	7

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O33802;
O1-JAN-1998 (TrEMBLrel. 05
1 01-JAN-1998 (TrEMBLrel. 05
1 01-DEC-2001 (TrEMBLrel. 101-DEC-2001 (Fragment).
                                                                                                                                                      EMBL; AJO
NON TER
SEQUENCE
                                                                                                                                                                                                                       MEDIINE=98053981; PubMed=9393832;
Sukupolvi S.S., Lorentz R.G., Gordon J.I.,
Normark S.J., Rhen M.;
"Expression of thin, aggregative fimbriae p
                                                                                                                                                                                                                                                                                              Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                  cells.";
                                                                                                                                                                                                             Salmonella typhimurium
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     NCBI_TaxID=602;
                                                                                                                                                                                        Infect.
  121
                                                                                                                                                                  AJ000514; CAA04151.1; -.
ER 152 152
                       61
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                                                                Similarity
                                                                                                                                                                                      Immun. 65:5320-5325(1997).
  NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                  SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG
                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                            Score 674; DB 2;
Pred. No. 1.1e-47;
2; Mismatches 15
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RESULT 3
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01-OCT-2003
01-OCT-2003
01-OCT-2003
                                                                                                                                                                                                                   Zogaj X., Bokranz W., Nimtz M., Romling U.; "Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
                                                                                                                                                                                                                                                                                       STRAIN=Fec4;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=546;
                                                                                                                                                                                                                                                                                                                                                                                Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                         Citrobacter freundii.
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"Production of Cellulose and Curli Fimbriae by Members of th
Enterobacteriacese Isolated from the Human Gastrointestinal
Infect. Immun. 72:4151-4158 (2003).
EMBL, AJ515700; CAD56672.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Citrobacter sp. Fec2.
Bacteria; Proteobacteria; Gammar
Enterobacteriaceae; Citrobacter.
                                                                                                                                                                                                     Infect.
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71.5%;
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                                                                      16;
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Pred. No. 6.5e
10; Mismatches
                                                               Score 530; DB 2;
Pred. No. 6.3e-36;
6; Mismatches 25
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Q7X237;
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STRAIN=Fec39;
Zogaj X., Bok
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                                          SEQUENCE FROM
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Enterobacteriaceae;
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                                                                                 NCBI_TaxID=28141;
                                                                                                                                                    Enterobacter sakazakii.
                                                                                                                                                                                            Curlin-csgA
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Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=06:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
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EMBL; AJ515702; CAD56678.1; -.
SEQUENCE 150 AA; 15112 MW; 5D8BBZDB72DF15F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COX J.M., Eglezos S., Woolcock J.B.;
"Virilence of Salmonella enteritidis in chickens correlates
colony morphology and expression of SEF17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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Bacteria; Proteobacteria;
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 Proteobacteria; Gammaproteobacteria; teriaceae; Escherichia.
                                                                                      (TrEMBLrel.) (TrEMBLrel.
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Best Local S
Matches 26
 Q8Y106;
Q8Y106;
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Query Match
Best Local Similarity
Matches 40; Conserv
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DNA Res. 9:189-197(2002).
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MEDLINE-99314153; PubMed-10386375;
La Ragione R.M., Collighan R.J., Woodward M.J.;
"Non-curliation of Escherichia coli O78:K80 iso."
IS1 inserti on in csgB and reduced persistence:
FEMS Microbiol. Lett. 175:247-253(1999).
EMBL; AJ131756; CAB45380.1; -...
                                                                                                                                                                                                                                 SEQUENCE 130 AA;
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Kasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yan
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Bacteria; Proteobacteria;
Bradyrhizobiaceae; Bradyrh
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01-JUN-2003
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                                                         TSNNATTLOFGATNTA-----TTLOTGSLLTV--NTAVTGQGGTTATASNTALT-GOVG
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                           GNNAALVNOTASDSSVMVROVGFGNNATANO
                                                                                 RKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQW----NAKNSDITVGQYG
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Bradyrhizobium.
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89.7%;
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Pred. No. 0.08
28; Mismatches
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Pred. No. 0.00
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EMBL; AL646601; CAD14589.1; -.
GO; GO:0004519; F:endonuclease activity; IE
GO; GO:0003676; F:nucleic acid binding; IEA
InterPro; IPR001604; Endonuclease
InterPro; IPR001604: Fil haemagg.
InterPro; IPR008619; Fil haemagg act.
Pfam; PF05594; Fil haemagg; ZO.
Pfam; PF055960; Haemagg act; 1.
PR0SITE; PS01070; NUCLEASE NON SPEC; 1.
MEDIINE=2168.879; PubMed=11823852; Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottler P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange l Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."
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01-MAR-2002 (TrEMBLrel. 20, Last sequen
01-CCT-2003 (TrEMBLrel. 25, Last annota
Probable hemaggjutinin-related protein.
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"Genome sequence of the plant pathogen Ralstonia solan Nature 415:497-902(2002).
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=GMI1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
Burkholderiaceae; Ralstoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid megaplasmid
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Probable hemagglutinin-related protein.
RSC0887 OR RS06116.
Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkh
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MEDLINE=21681879; PubMed=11823852;
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Pred. No. 5.2
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Schiex T.,
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Schiex T.,
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Q8EIH3;
01-MAR-2003
01-MAR-2003
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MEDLINE-22297686; PubMed=12368813;
MEDLINE-22297686; Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Mard N., Methe B., Clayton R.A., Read T.D., Eisen J.A., Scott J. Beanan M., Brinkac L., Daugherty S., Meyer T., Tsapin A., Scott J. Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Meller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., "Genome sequence of the dissimilatory metal ion-reducing bacterium "Cenome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                   SEQUENCE
                                                                                                                                                                                              EMBL;
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GO, GO:000376; F:nucleic acid binding; IEA.
InterPro; IPR001604; Endonuclease.
InterPro; IPR008619; Fil_haemagg.
InterPro; IPR008639; Haemagg act.
Pfam; PF05594; Fil_haemagg; ZO.
Pfam; PF05866; Haemagg; ZO.
Pfam; PF05866; Haemagg; Act.
                                                                                                                                                                Complete
                                                                                                                                                                                 TIGR;
                                                                                                                                                                                            Nat. Biotechnol. 20:1118-11;
EMBL; AE015532; AAN53942.1;
                                                                                                                                                                                                                             Shewanella
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                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shewanella oneidensis.
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Pfam; PF05860; Haemagg_act; 1.
PROSITE; PS01070; NUCLEASE_NON_SPEC;
Plasmid; Complete proteome.
SEQUENCE 3552 AA; 352934 MW; C54
                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alteromonadaceae; Shewanella.
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EMBL; AL646079; CAD17691.1; -.
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 99
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                                                                                        l Similarity
30; Conser
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                                                        SGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFR
                                                                                                                                                                proteome.
NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGN 144
                            SGRDNLIDLVQQGTANQGIVFQSGSDNS-AYVTQAGNDN----ISLVTQIGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proteobacteria;
                                                                                                                                                                                                                          oneidensis.";
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                                                                                         Conservative
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                                                                                                                                                  14811 MW; 41EC1CFA76957920 CRC64;
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                                                                                      Score 110; DB 16;
Pred. No. 0.13;
9; Mismatches 33;
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Pred. No. 5.
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Best Local
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical glycine-rich protein SMb21548.
RB0989 OR SMB21548.
RB120bium mellioti (Sinorhizobium mellioti).
Rhizobium mellioti (Sinorhizobium mellioti).
Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q92UU8;
01-DEC-2001
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01-OCT-2003
                                           SEQUENCE FROM N.A
                                                                                                      NCBI_TaxID=382;
                                                                                                                                                             Rhizobiaceae;
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PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
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Alteromonadaceae; Shewanella.
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IGR; SO1872; -.
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Pred. No. 3.
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Clayton R.A.,
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RESULT 14
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                                                                                                                                      MEDLINE=2297686; PubMed=12368813;
Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C. Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vorhoexee. Vorhoexee Workler A.;
Golding B., Puehler A.;
Golding B., Puehler A.;
"The complete sequence of the 1,683-kb pSymB megar
fixing endosymbiont Sinorhizobium meliloti.";
fixing endosymbiont Sinorhizobium meliloti.";
Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).
                                                                    EMBL;
TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF03797; Autotransporter; 1.
PROSITE; PS00435; PEROXIDASE 1; 2.
PROSITE; PS00583; PFKB_KINASES 1; 2.
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 2174 AA; 203314 MW; 008EB66297B44182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; E95965; E95965.
GO; GO:0046821; C:extrachromosomal DNA;
GO; GO:0004601; F:peroxidate activity; I
GO; GO:0006979; P:response to oxidative
                                         Hypothetical SEQUENCE 50
                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003
01-MAR-2003
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                                                                                                             Shewanella oneidensis.",
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                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
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Finan T.M., Weidner S., Wong K., Buh
Vorhoelter F.J., Hernandez-Lucas I.,
                                                                                                                         Genome sequence of the dissimilatory metal
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                                                                                                Biotechnol.
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                                                                                 Niotechnol. 20:1118-1123(2002)
AE015532; AAN53941.1; -.
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                                        nl protein; Complete proteome.
502 AA; 52441 MW; D08CA23D6C46B62D CRC64;
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13.7%;
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              Length 502;
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Similarity

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                  "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; APO05954; BAC50565.1; -.
Complete proteome.
SEQUENCE 171 AA; 17448 MW; 995DB08C01498381 CRC64;
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Q89JI3;
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STRAIN-USDA 110;
STRAIN-USDA 110;
MEDLINE=22484998; PubMed=12597275;
MEDLINE=27484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
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CSGA OR BLL5300.
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	Collison SK, Kay WW;		₽.	5.				mal gene replacement; immunogen.	sequence SEQ ID NO:30.			151 AA.	ALIGNMENTS	ABU34624	ABB62708	AAW56163	ABU36440	AB023520	AAY78364	ABB65007	AAB36328	AAB36323	ABR82645	AAB36342	ABR82649	AAB36344	AAB36319	AAB36324	AAB36340
								fimbrin; epitope;							Abb62708 Drosophil	New DNA			Aay78364 H. pylori		Aab36328 Salmonell	Aab36323 Salmonell			April 6497 Argione t		Aab36319 Salmonell	Aab36324 Salmonell	Aab36340 Salmonell

Result No.

Query Match

Length

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Description Aab36355 AgfA::PT3

SUMMARIES

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AAR74625 AAB36352 AAB36355

Aab36352 AgfA::PT3
Aar74625 AgfA sequ
Aab36341 Salmonell
Aaw23570 Salmonell
Aaw23570 Salmonell
Aab36347 AgfA::PT3
Aab36351 AgfA::PT3
Aab363546 AgfA::PT3
Aab36353 AgfA::PT3
Aab36350 AgfA::PT3
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Aab36343 Abr82651 Aar62761

AAB36339 AAB36320 ABR82644

Salmonell Salmonell E. coli c

Aaw23569 Aar52664 Aar52663 Aab36316 Aab36318 Aab36325 Aab36339

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing recombination of a recombinant gene

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 139; 139pp; English.

BESCherich
E. coli C
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Matches
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Best Local Similarity
                       Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant A protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbbial presentation
                                                                                                              WPI; 2000-672631/65.
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                                                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDARKSETTIT OS GYGNGAD V GOGADNSTIELT ON GFRNNATYD OLVTR V V THEMAHAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                          2000WO-CA000356
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                                                                                                                                                                                                           99US-0127888P
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                                                                                                                                            Collison
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Pred. No. 1.7e-66;
; Mismatches 0;
                                                                                                                                           SK,
                                                                                                                                           Kay
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В ş 밁 Ś В Ş

Disclosure;

Page 138; 139pp; English

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RESULT 3
AAR74625
ID AAR7
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Matches
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                                                                                                                 26-APR-1994;
                                                                                                                                                                                                                                     Salmonella
                                                                          26-APR-1993;
                                                                                                                                                         10-NOV-1994
                                                                                                                                                                                              WO9425598-A2
                                                                                                                                                                                                                                                                         Salmonella; AgfA; vaccine
                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
26-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR74625 standard; protein; 151 AA
                (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP. (KING/) KING J.
                                                                                                                                                                                                                                                                                                              AgfA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF1/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNAT------YDQLVTRVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKLLKVAAFAATVVSGSALAGVVÞQWGGGGNHNGGGNSSGÞDSTLSIYQYGSANAALALQ
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(first entry)
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                                                                          93US-00054452
                                                                                                                 94WO-IB000207
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Pred. No. 6.8e-60;
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RESULT 4
AAB36341
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Best Local Simi
Matches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune respons Salmonella in animals (e.g. food producing animals) and humans. (Upo on 25-MAR-2003 to correct PN field.)
                                                                            Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described
                                                                                                                                 WPI; 2000-672631/65.
N-PSDB; AAC64617.
                                                                                                                                                                                                                                                                                                                                    Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB36341 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-358275/44.
N-PSDB; AAQ87467.
                                                      Disclosure;
                                                                                                                                                                                                                              05-APR-1999;
                                                                                                                                                                                                                                                        05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                             WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                             Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2001
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                                                      Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                               response;
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90.7%;
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Pred. No. 4.7e-58;
2; Mismatches 12;
                                                                                                                                                                            SX,
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                                                                                                                                                                          Kay WW
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ns. (Updated
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Matches 137;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella
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29-SEP-1997
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Collinson SK,
                                                                                                                                                     26-APR-1994;
                                                                                                                                                                                                       03-JUN-1997
                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
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                                                                                                   26-APR-1993;
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                                                 (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP
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                                                                                                                                                                                                                                                                                                                                                                                                        enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enteritidis 27655-3b agfA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
Kay WW,
                                                                                                   93US-00054452
                                                                                                                                                     94US-00233788
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                     /note= "Encoded by GCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.7%;
90.7%;
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Pred. No. 4.7e-58;
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RESULT 6
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Best Local Sim:
Matches 136;
    Recombinant agfA gene which encodes foreign
                                            WPI; 2000-672631/65.
N-PSDB; AAC64623.
                                                                                 White AP,
                                                                                                                                                                                                                                                                                                       Salmonella; agfA; chromosomal gene replacement;
                                                                                                                                      05-APR-1999;
                                                                                                                                                            05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                 WO200060102-A2
                                                                                                                                                                                                                                                        Escherichia coli.
                                                                                                                                                                                                                                                                      Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                            (UYVI-) UNIV VICTORIA
                                                                                                                                                                                         12-OCT-2000
                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                vaccine;
                                                                                                                                                                                                                                                                                                                                     AgfA::PT3#2
                                                                                                                                                                                                                                                                                                                                                                                          AAB36347;
                                                                                                                                                                                                                                                                                                                                                                                                                  AAB36347 standard;
                                                                                                                                                                                                                                                                                                                                                                26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated Salmonella gene agfa - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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                                                                                                                                                                                                                                                                                             immune response;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Fig 7; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNPALVNOTASDSSVMVROVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDARKSETTITOSGYGNGADVGOGADNSTIELTONGFRNNATIDOWNAKNSDITVGOYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                Doran JL,
                                                                                                                                                                                                                                                                                                                                   amino acid sequence SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                   99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.0%;
having a segment replaced by a foreign DNA sequence epitope or antigen, expresses recombinant AgfA
                                                                                 Collison
                                                                                                                                                                                                                                                                                               immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 676; DB
Pred. No. 1.4e
2; Mismatches
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                                                                                Kay
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                                                                                                                                                                                                                                                                                                       fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 151;
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC directing recombination of a recombinant gene into the chromosome of the Cromosome species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA CC comprising separating an amino acid polymer comprising a recombinant CC comprising a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC enterobacteriaceae host cell, from the host cell and introducing the CC collifor the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for System the heterologous antigens are presented in high numbers (up to CC sol, 000 copies/cell), the hybrid fimbrin protein possesses both the CC immunogenicity and adhesion properties relevant for an efficient live considered, the carrier fimbrial subunit proteins are usually strong CC immunogens, which may be important for directing an immune response considered the inserted epitope, and hybrid fimbriae are easy and considered the present invention of the present invention considered in the present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
               05-APR-2000; 2000WO-CA000356
                                                                                                                                                           Salmonella enteritidis
                                                                                                                                                                                                            Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                    12-OCT-2000
                                                                                                                        Synthetic
                                                                                                                                                                                                  vaccine;
                                                                                                                                                                                                                                                       AgfA::PT3#6
                                                                                                                                                                                                                                                                                          26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                AAB36351 standard; protein; 151
                                                                                     WO200060102-A2
                                                                                                                                          Escherichia coli
                                                                                                                                                                                                                                                                                                                                 AAB36351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGHHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 81.9
36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVTRVVTHEMAHA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKLLKVAAFAALVVSGSALAGVVFQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151
                                                                                                                                                                                                                                                       amino
                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ĀĀ;
                                                                                                                                                                                              response; immunogen.
                                                                                                                                                                                                                                                   acid sequence
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Pred. No. 6.4e-56;
0; Mismatches 0;
                                                                                                                                                                                                                                                       SEQ ID
                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVMVRQVGFGNNATANOY 151
                                                                                                                                                                                                                                                       NO: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 151;
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RESULT 8
AAB36354
ID AAB3
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AC AAB3
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DT 26-F
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA seguence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SER17/TAR) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                               Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                 AgfA::PT3#9 amino acid sequence SEQ ID NO:28.
                                                                                                                                                                       26-FEB-2001
                                                                                                                                                                                                                                                                                                    AAB36354 standard; protein; 151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 137; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAC64627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CagA and AgfA-homologue fimbrin aubunita, respectively;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLLKVÄAFÄÄIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANÄÄLÄLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDARKSETTITQSGYGNGADVGQGADN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 657; DB 3
Pred. No. le-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kay WW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YDQLVTRVVTHEMAHADQ 105
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                                                                                                                                                                                                                                                                                                                                                                               AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)

CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino caid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the golymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for celiciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the cimmunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong cimmunogens, which may be important for directing an immune response cagainst the inserted epitope, and hybrid fimbriae are easy and cimexpensive to purify in large amount. The present sequence is given in the content of the present invention
                                                                                                                                                                                                                                                        Query Match
Best Local Sin
Matches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                             Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAC64630.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYVI-) UNIV VICTORIA
                                          119 -----
  99
                                                                                  61
                                                                                                                           61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHA--
                                                                                                                                                                                                                _
                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                            MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                            74.6%;
                                                                                                                                                                                                                                                                                                79.8%;
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                                                                                                                                                                                                                                                          ٥,
                                                                                                                                                                                                                                                                            Score 613; DB 3; Length 151; Pred. No. 1.9e-51;
                                        GGNNAALVNOTASDSSVMVROVGFGNNATANOY 151
                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kay WW
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                                                                                                                                                                                                                                                          Indels
                                                                                       TRVVTHEMAHAFR
                                                                                                                                                                                                                                                          44;
                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                   Matches
                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AgfA, CsgA and Agfa-homologue finbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, very comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation are into the animal antivalence are areas are measured in high numbers (up to
                                                                                                                                                                                                                                                                                                                  system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence in given in the present sequence is given in the present sequence is given in the present sequence in given in the present sequence is given in the present sequence in given in the present sequence is given in the present sequence in given in the present sequence is given in the present sequence in given in the present sequence in given in the present sequence in given in the present sequence in given in the present sequence in given in the present sequence in given in the present sequence in given in the present sequence in given in the present sequence in given in the present sequence in given in the present sequence in given in the present sequence in given in the present sequence in given in the present sequence in given in the present sequence in given in the present sequence in given in the present sequence in given in the present sequence in given in the given in the given in the given in the given in the given in the given in the given in the given in the given in the given in the given in the given in the given in the given in the given in the given in the give
                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-2000; 2000WO-CA000356.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AgfA::PT3#1 amino
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                                                                                                                                                                                                                                                                                                      exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-672631/65.
                                                                                                                                                            Similarity
MKILKVAAFAATVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSTYQYGSANAALALQ
                                              MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                  151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Doran JL,
                                                                                                                          78.5%; llarity 80.8%; Conservative
                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coli.
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                                                                                                                                                                                                                                                                                                   present
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                                                                                                                    Score 603; DB 3;
Pred. No. 1.7e-50;
6; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                   invention
                                                                                                                                                                              Length 151;
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                                                                                                                                                                                                                                                                                                                           is given in
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given

in

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The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC Enterobacteriaceae for the production of finbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively, (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species, (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Britan animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for CC suseful for the expression of recombinant AgfA protein which is useful for System the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the carrier fimbrial subunit proteins are usually strong the inserted epitope, and hybrid fimbriae are easy and companies the inserted epitope, and hybrid fimbriae are easy and consensive to nurify in large and hybrid fimbriae are large and given in
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AAB36353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       which encodes foreign epitope or antigen, expresses recorded useful for eliciting immune response in animal.
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epitope, a
y in large
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AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinantion of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or
                                                                                                                  The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SER17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                       White AP,
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DB; AAC64625.
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81.5%;
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Pred. No. 3.4e-50;
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RESULT 12
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Best Local Sim
Matches 123;
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                                                                                                                                  N-PSDB; AAC64626.
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                                                                                                                                                                                                                                                                                                                                                                                             vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                     AgfA::PT3#5 amino acid sequence
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                                                                                                                                             2000-672631/65.
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81.5%;
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    from the host cell and introducing the
conjunction with a carrier or diluent. (I)

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Pred. No. 4.2e-50;
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The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign DI sequence which encodes a foreign epitope or antigen. Also describe

are:

Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal.

DNA sequence AgfĀ

Disclosure; Page 137; 139pp; English

N-PSDB; AAC64624.

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CC assembly system of strains of Salmonella, Escherichia coli and CC Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CegA and AgfA-homologue fimbris subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene CC back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for celiciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to CC immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit protein possesses both the carrier fimbrial subunit proteins are usually strong communogens, which may be important for directing an immune response consists the inserted epitope, and hybrid fimbriae are easy and consists the inserted epitope, and hybrid fimbriae are easy and consists to purify in large amount. The present sequence is given in consists the consists of the exemplification of the present inventor.
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Best Local
WPI; 2000-672631/65
                                                           White AP, Doran JL,
                                                                                                                                                                                           05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine; immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AgfA::PT3#3 amino acid sequence SEQ ID NO:16.
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assembly system of strains of Salmonella, Escherichia coli and
                                                                                                                            (UYVI-) UNIV VICTORIA.
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Pred. No. 6.6e
5; Mismatches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given inexpensive to purify in large amount.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation
                                                                                                    Escherichia
                                                                                                                                                              Salmonella; agfA; chromosomal gene replacement; fimbrin;
                                                                                                                                                                                                                                                   26-FEB-2001
                                                                                                                                                                                                                                                                                          AAB36343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF1/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                           vaccine; immune response; immunogen
                                                                                                                                                                                                        Escherichia coli CsgA amino acid sequence SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                 AAB36343 standard; protein; 151 AA
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Pred. No. 6.7e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising separating an amino acid polymer comprising a recombinant AgfA corotain containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to $500,000 copies/cell), the hybrid fimbria protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and the inserted epitope, and hybrid fimbriae are easy and the exemplification of the present invention
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Best Local S
Matches 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                     E. coli CsgA subunit 15 kDa protein.
                                                             04-DEC-2003
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                                                                                                                                           ABR82651
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                                                                                                                                         standard; protein;
                                                                                                                                                                                                                                              GNGAAVDOTASNSSVNVTOVGFGNNATAHOY 151
                                                                                                                                                                                                                                                                                                                        TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
                                                                                                                                                                                                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
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                                                             (first entry)
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Pred. No. 3.8e-42;
7; Mismatches 29;
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                                                                                                                                                                                                                                                              treatment of a bacterial infection, such as Escherichia coli, Sain or Shigella infection. The peptide that is immobilized on a solid is also useful as a reagent for determining the ability of a plasm protein to bind to bacteria. The present sequence represents an E. 15 kDa protein
                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammalian plasma protein or of generating an immune response in a material from sequences shown in ABR88642, ABR8648-49. The peptide antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic
                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmor or Shigella infections.
                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 41-42; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bjoerck L,
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GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
                      NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                              MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                    SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
                                                          TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
                                                                                                                    MKLLKVEATAATVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQ
                                                                                                                                                                           66.7%;
ilarity 68.9%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olsen A,
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Pred. No. 1.2e
17; Mismatches
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                             151
                                                                                                                                                                                         DB 7;
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Sequence 59, Application US/0823788A

Patent No. 5635617

GENERAL INFORMATION:
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Sequence 3, Application Patent No. 6001592 GENERAL INFORMATION:
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Sequence 57, Appra-
Sequence 57, Appra-
No. 5635617
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APPLICANT: Doran,
APPLICANT: Kay, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:

NAME: King, Joshua

REGISTRATION UNMBER: 35,570

REFERENCE/DOCKET NUMBER: 9200

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                    Sequence 8, Application US/09196387 Patent No. 6277613
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTI
TITLE OF INVENTION: OF USE
                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local (
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FILING DATE: May 28, 1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 8-184459
FILING DATE: 15-July-1996
ATTORNEY,AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
REFERENCE/DOCKET NUMBER: P-5610
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212)953-773
INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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ORIGINAL SOURCE:
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CURRENT APPLICATION DATA:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CELL TYPE: mantle epithelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                               419 LLKSSASASASASASAG-----GGGGGGGNGGGNGGGG
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                                                                                                                                                                                                                                                                                             63 ARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNN 122
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(212)953-7733
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VENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
VENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
VENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
VENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JAPAN
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27.7%;
   A PROTEIN THAT BINDS TO TRF1 AND METHODS OF USE THEREOF
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Pred. No. 0.
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CORRESPONDENCE ADDRESS: ADDRESSEE: Klauber & Jackson

STREET: 411 Hack CITY: Hackensack

411 Hackensack Avenue,

4th Floor

New

Jersey

NUMBER OF SEQUENCES:

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                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09841835 Patent No. 6506587
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                      APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-887-5800
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                            COUNTRY:
ZIP: 076
                                                                                                                                       STREET:
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TELEFAX: 201-343-1684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                            07601
                                                                                                                   Hackensack
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                                                                                                 New Jersey
                                                                                                                                     411 Hackensack Avenue,
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                                                                                                                                         4th Floor
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Patent No. 6277613
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Best Local Similarity
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                                  APPLICATION NUMBER: US
FILLING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09
FILING DATE: June 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                      ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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LENGTH: 673 amino acids
TYPE: amino acid
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APPLICATION NUMBER:
                  FILING DATE: June 10, 19 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
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                                                                                                                                                                                                                                                                                       STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 VNAK--DMAGRKSSPLHFAAGFG 227
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Jackson Esq., David A
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Smith, Susan
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29.4%;
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REGISTRATION NUMBER: 26, REFERENCE/DOCKET NUMBER:

26,742

600-1-230 CIP1

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RESULT 7
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                                      INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tent No.
                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS TITLE OF INVENTION: OF USE THEREOF NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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APPLICANT: Smith, Susan
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TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
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LENGTH: 949 amino acids
                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                        TELEFAX:
                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                        201-343-1684
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29.4%; Pred. No. 0
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6 VAAFAAI-VVSGSALAGVVPOWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64

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US-09-196-387-2
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                  Query Match
Best Local :
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GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 09/095,22:
APPLICATION NUMBER: 01, 1998
ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                            REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELECPHONE: 201-487-5800
                                                                                   HYPOTHETICAL:
                                                                                               TOPOLOGY: 1
                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Smith, Susan
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TELEPHONE: ZVI.
1684
                  Local Similarity
                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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   Conservative
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linear
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11.9%; Score 91.5; DB 3; 29.4%; Pred. No. 1.3; ative 17; Mismatches 65.
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29.4%; Pred. No. 0.8;
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                              Length 1327;
 Indels 19;
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US-09-841-835-2
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US-09-841-835-2
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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APPLICANT: Smith, Sugan
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
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207
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                                                                                        KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
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VNAK--DMAGRKSSPLHFAAGFG 227
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411 Hackensack Avenue,
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Pred. No. 1
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                                                           ---VSRV--KRLVDAAN 206
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US-09-972-115A-8
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TENGTH: 1327
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TYPE: PRT
                                                                                                                                                                  LENGTH: 745
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; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-336-115C-6
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APPLICANT: Weltzin, Richard A.
APPLICANT: Guy, Bruno
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                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/336,115C CURRENT FILING DATE: 1999-06-18 PRIOR APPLICATION NUMBER: US 09/100,258 PRIOR FILING DATE: 1998-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Guy, Bruno
TITLE OF INVENTION: LT and CT in Parenteral Immunization
TITLE OF INVENTION: Methods Against Helicobacter Infection
FILE REFERENCE: 06132/055002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
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APPLICANT: Walter, Funk D.
APPLICANT: Mieczyslaw, Piatyszek A.
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                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-04-10
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CURRENT FILING DATE: 2001-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 080/003C
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                                                                                                                      NAME/KEY: SIGNAL LOCATION: (1)...(20)
                                                                                                                                                                          TYPE: PRT ORGANISM: Helicobacter pylori FEATURE:
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                                                 NAME/KEY: VARIANT LOCATION: 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA
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                SOFTWARE: PatentIn version
SEQ ID NO 5130
LENGTH: 1216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 30227
LENGTH: 2736
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                                                               CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
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                                                                                                                                                                 APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO TITLE OF INVENTION: ENTEROCOCCUS FARCALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
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                                                                                                                                                         FILE REFERENCE: 032796-032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                    VVTHEMAHAGGNNAALVNQTASDSS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSAGTALLVGAAAIGAGVAISNSSGGGG---GGGSSVPPDTTPPKAASGLKIAPDGSSIS 205
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No.
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Pred. No. 1
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US-09-134-000C-5130
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. BRETON et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
                                                                                                                              Sequence 2676, Application US/09540236
Patent No. 6673910
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LENGTH: 589
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TITLE OF INVENTION: NOTITLE OF INVENTION: POTENCE: 2709.
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Best Local
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PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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                                                                                                                                                                                                                                                                                                                                           80 --DVGQ--GADNSTIELTQNG----FRNNATYDQLVTRVVTHEMAHAGGN---NAALVNQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                29 GGNHNGGGNSSGPDSTLSIYQYGS-----ANAALALQSDARKSETTITQSGYGNGA- 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.6%;
Similarity 24.5%;
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                                                                                                                                                                                                                                                                         TASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                          ACPPGOSTGSPVTTVDTAKSGNLVNWKAGALYR--
                                                                                                                                                                                                                                                                                                                                                                               GGLDRNGANANGOTDTFGIYAFDTLTLTERIEINGGLRLDNYHTKYDSATACGGSGRGAI 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLNTQLYSAGRADFEGGNQYSGTIIGDITNVVTAGTNSAGGINDFNGGAGNNVSKFNKS- 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGVQYGNIG-----GKVTNDISGYGRWYTAGORFIGGSSRGDIGTNRATDGITT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---QYGSANAALALQSDARKSETTITQSGYGNGADVGQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gary Breton et. al
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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PNEUMONIAE FOR DIAGNOSTICS A
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Pred. No. 8.2;
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 81.5;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.5;
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TO KLEBSIELLA

31;

Gaps

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; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2676
; LENGTH: 867
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2676
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Search completed: March 11, 2004, 18:44:55 Job time: 13.4 secs
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                                                                              203 VAQ 205
                                                                                                                   148 ANQ 150
                                                                                                                                                          143 RGNQATGAGSFAAGVGNQATGAGSFAAGVGNQANADNAVAVGNKNSITGKDSVAIGSNNT 202
                                                                                                                                                                                   98 R-NNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMV------RQVGFGNNAT 147
                                                                                                                                                                                                                                                                           44 TLSIYQYGSANAALALQSDARKSETTITQSGY----GNGADVGQGADNST--IELTQNGF 97
                                                                                                                                                                                                                                                                                                                  93 TIA----GGRN-----NQATKENSTVGGGKFNQAKGRNSTVAGGYNNEATGIDSTIAGG 142
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Minimum DB :
Maximum DB :
                                                                                                                                                                                                                                                                                                            Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                            Pred. No, is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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768
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       13.4
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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gn2_6/ptcdata/1/pubpaa/USOB_PUBCOMB.pep:*
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gn2_6/ptcdata/1/pubpaa/USIOB_PUBCOMB.pep:*
gn2_6/ptcdata/1/pubpaa/USIOB_PUBCOMB.pep:*
gn2_6/ptcdata/1/pubpaa/USIOC_PUBCOMB.pep:*
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gn2_6/ptcdata/1/pubpaa/USIOC_PUBCOMB.pep:*
gn2_6/ptcdata/1/pubpaa/USIOC_PUBCOMB.pep:*
       354
673
949
1327
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1327
13217
2597
745
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321
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323
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10 US-09-820-843A-21

US-09-841-835-8

US-09-841-835-2

US-09-841-835-2
                                                                                        0 US-09-972-115A-8

105-10-199-937-4

4 US-10-199-937-4

4 US-10-311-406-2

US-09-793-306-146

US-08-834-666A-6
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                                                       US-10-374-780A-590
US-10-021-811-26
                                     US-10-238-075-749
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Sequence 20638, A
Sequence 21, Appl
Sequence 8, Appli
Sequence 10, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 590, App
Sequence 26, Appl
Sequence 749, App
Sequence 27, Appl
Sequence 24, Appl
Sequence 24, Appl
                                                                                                                                                                                                                                                                                         Description
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ALIGNMENTS

US-10-369-493-20638

GENERAL INFORMATION:

Sequence 20638, Application US/10369493 Publication No. US20030233675A1

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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20638
LENGTH: 445
TYPE: PRT
ORGANISM: Rhodopseudomonas palustris
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                                                                                                                                                             Query Match
Best Local Similarity
Matches 44; Conserv
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OTHER INFORMATION: unsure at all Xaa locations
51 GSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNA-----TY 103
                                                                       19
                                                                                                                                                           44;
                                                                     AAFAADSNTVYLNQTGNDQQANITQSGNGNSVGAFNGNSGFLQENGTLSGA-NLLTVKQS 77
                                                                                                                  AAFAA-----IVVSGSALAGVVPQWGGGG-----NHNGG-----GNSSGPDSTLSIYQY 50
                                                                                                                                                               Conservative
                                                                                                                                                             13.4%; Score 103; DB 15; Length 445; 26.3%; Pred. No. 0.046; ive 27; Mismatches 62; Indels 3
                                                                                                                                                           27;
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                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09841835 Patent No. US20020076795A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.0
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Council of Scientific and Industrial Research TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES FILE REFERENCE: Q63915
                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                             MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
OTHER INFORMATION: gi|1781260
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OTHER INFORMATION: PPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 354
TYPE: PRT
ORGANISM: M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                STREET:
APPLICATION NUMBER: FILING DATE:
                                                                                                                                                COUNTRY:
                                                                                                                                                                                CITY: Hackensack
                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 WNGGSTNTGLANAGAGNTGFFDAGNYNFGSLNAGNINSSFGNSGDGNSGFLNAGDVNSGV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 GNGADYGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAG------GNNAALVNQT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 WGGGGNHNGGGNSSGPDS---TLSIYQYGSANAALALQSDARKSETTI-----TQSGY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
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                                                                                                                                  07601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNAGDVNTGLGNSG-NINTGGF-NPGTLNTGFFSAMTQAGPNSGFFNAGTGNSGFGHNDP 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASDSSVMVRQVGFGNNATAN 149
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                                                                                                                                                              New Jersey
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                                                                                                                                                                                            411 Hackensack Avenue, 4th Floor
                                                                                                                                                  USA
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                                                                                                                                                                                                               Klauber & Jackson
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          US/09/841,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.28;
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                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                           0760:
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                       Local Similarity
207 VNAK--DMAGRKSSPLHFAAGFG 227
                                   121 NNAALVNOTASDSSVMVROVGFG 143
                                                                          158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD---
                                                                                                           65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                   99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                          6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                    Score 91.5; DI
Pred. No. 1.1;
                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                     DB 9;
                                                                                                                                                                                                                                  65;
                                                                                                                                                                                                                                                                     Length 673;
                                                                                                                                                                                                                                Indels 19;
                                                                          VSRV--KRLVDAAN 206
                                                                                                                                                                                                                              Gaps
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GENERAL INFORMATION:
APPLICANT: de Lan
APPLICANT: Smith, NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230
TELECOMMUNICATION INFORMATION: FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0 ATTORNEY/AGENT INFORMATION: APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRE1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: APPLICATION NUMBER: CITY: Hackensack New Jersey Application US/09841835 411 Hackensack Avenue, USA de Lange, Titia Klauber & Jackson 201-487-5800 0076795A1 09/196,387 12 US/09/841,835 4th Floor Version #1.30 CIP1

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Sequence 2, Application.

Sequence 10, 1920020076795A1

Patent No. US20020076795A1

GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan

ITITLE OF INVENTION: A PROTEIN THAT BINDS TO

TITLE OF INVENTION: OF USE THEREOF

TITLE OF SEQUENCES: 12
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Best Local S
Matches 42
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                    NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                 TOPOLOGY: 1: MOLECULE TYPE:
                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
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 HYPOTHETICAL:
                                                                                                                                      TELEFAX: 25
TELEFAX: 133521
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                                                       TYPE: amino acid
STRANDEDNESS: sir
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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protein
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RESULT 7
US-10-199-937-4
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APPLICANT: Christenson, Erik
APPLICANT: Christenson, Erik
APPLICANT: DeMaggio, Anthony J.
APPLICANT: Goldman, Phyllis S.
APPLICANT: McElligott, David L.
TITLE OF INVENTION: TANKYRASE2 MATERIALS ANI
FILE REFERENCE: 27866/36559
CURRENT APPLICATION NUMBER: US/10/199,937
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/606,035
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Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                             Sequence 4, Application US/10199937
Publication No. US20030190739A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 080/003C
CURRENT APPLICATION UMBER: US/09/972,115A
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/128,577
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 1999-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Geron Corporation APPLICANT: Gregg, Morin B. APPLICANT: Walter, Funk D.
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TITLE OF INVENTION: A Second Mammalian Telomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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ilarity 29.4%;
Conservative 17
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Pred. No. 2.6;
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Pred. No. 2.6;
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                                                                                   RESULT 9
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US-10-311-406-2
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Sequence 146, Application US/09793306 Patent No. US20020098200A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LENGTH: 1327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-937-4
                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10311406
Publication No. US20030134388A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sasaki, Masahiro
APPLICANT: Yamada, Hideyuki
APPLICANT: Yamada, Hideyuki
APPLICANT: Osada, Katsue
APPLICANT: Osada, Katsue
TITLE OF INVENTION: MEDIUM SUPPLEMENT AND ANIMAL CELL CULTURE MEDIUM
FILE REFERENCE: U 014351-5
CURRENT APPLICATION NUMBER: US/10/311,406
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: PCT/JP02/03836
PRIOR FILING DATE: 2002-04-17
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PRIOR APPLICATION NUMBER: 60/141,582
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 178
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                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                            101 ATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                               715 AGSSTSGGTSTYGYSSRHRGGSVSSTGSSSNTDSSTKNAGSRTSGGTSTYGYSSSHRGGS
                                                                                                                                                                                                                                                       59 LQSDARKSET------TIT---QSGYGNGADVGQGADNSTIELTQN-GFRNN 100
                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NNAALVNQTASDSSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 VNAK--DMAGRKSSPLHFAAGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD---
                                                                                                                                                                                                                                                                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIVQYGSANAALALQSDAR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 11.9%;
Similarity 29.4%;
                                                                                                                                      GG----TSTYGYSSSHRGGSVSSTGSSSNTDSS--TKNAGSSTSGGSSTY 878
                                                                                                                                                                                                                                                                                                                                     SGSALAGVVPQWGGGGNHNGG-----GNSSGPDST-----LSIYQYGSANAALA 58
                                                                                                                                                                                                                   VSSTGSSSNTDSSTKNAGSRTSGGTSTYGYSSSHRGGSVSSTGSSSNTDSSTKNAGSRTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSETŢIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                               11.5%; Score 88.5; DB 14; ilarity 22.2%; Pred. No. 4.6; Conservative 29; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 91.5;
Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                             Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1327;
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US-08-834-666A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 014058-008740US
CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR FILING DATE: 2000-08-08
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 1164
SOFTWARE: Patentin Ver. 2.1
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Best Local S
Matches 30
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Publication No. US20020044949A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
APPLICANT: Lissolo, Ling
APPLICANT: Tomb, Jean-Francois
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APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
TITLE OF INVENTION: of Tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Campos-Neto, Anton
APPLICANT: Skeiky, Yasir
APPLICANT: Ovendale, Pamela
                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,666A
FILLING DATE: 01-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T
                                                                                                                                                                                       ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Clark & E
                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: 76 kDa Helicobacter Polypeptides and TITLE OF INVENTION: Corresponding Polynucleotide Molecules
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Miller, Charles
APPLICANT: Al-Garawi, Amal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 597
                                          CLASSIFICATION: 424
                                                                                                                                                                                                                                                                              CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 FGNSGNNNIGFFNSG-NNNVGFFNSGNNN------FGFGNAGDINTGF 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452 GTLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399 GNAGD--TNTGFGNAGFFNMGIGNAGNEDMGVGNGGSFNVGVGNAGNQS-----VGFGNA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 DNSTIELTONGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
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                                                                                                                                                                                                                                                                                                                     176 Federal Street
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                                                                                                                                                                                            Diskette
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                                                                                                                                                                                                                                                                                                                                                                                      64
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Best Local S
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                                                              TITLE OF INVENTION: POLYPEDTIDES AND POLYPEDTIDES IN PLANTS
FILE REPERENCE: MBI-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR PILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR PILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR APPLICATION NUMBER: 60/336,049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-428-7045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                  APPLICATION NUMBER: 60/338,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 AYQAVFLAINAAVGL---WNTIGYAVMCGNGNGTESGPGSVIFNDQPGQDSTQITCNRFE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 RNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNAT 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34;
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Jiang, Cai-Zhong
Heard, Jacqueline E
Haake, Volker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STGPGKSMSIDEFKKLNEAYQIIQQALKNQSGFPELG-GNGTKV---SVNYNYECRQTAD 214
                                                                                                                                                                                                                                                                           Yu, Guo-Liang
                                                                                                                                                                                                                                                                                        Pineda, Omaira
                                                                                                                                                                                                                                                                                                         Pilgrim, Marsha L
Dubell III, Arnold T
                                                                                                                                                                                                                                                                                                                                                 Broun,
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Keddie, James
                                                                                                                                                                                                                                                                                                                                                                                                     Adam, Luc J
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NUMBER: 10/171,468
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                    2001-12-11
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20.0%; Pred. No. 4
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ER: 06
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US-10-021-811-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: G3384 Orthologous to G256
US-10-374-780A-590
RESULT 13
                                                                                                                                                                                                                                                               ; ORGANISM: Oryza sativa
US-10-021-811-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.2
SEQ ID NO 590
LENGTH: 321
                                                                                                                                                                                                                                                                                                                  SEQ ID NO 26
LENGTH: 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26, Appropriate Publication No.
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cahoon, Rebecca E.
APPLICANT: Fang, Yiwen
APPLICANT: Fang, Yiwen
APPLICANT: Odell, Joan
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
FILE REFERENCE: BB1294 US NA
CURRENT APPLICATION NUMBER: US/10/021,811
CURRENT FILING DATE: 2001-12-14
                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 10/225,067
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 10/225,066 PRIOR FILING DATE: 2002-08-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                            Local
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                                                   249 -----
                                                                                                                      199 AAYASSADNIARLLQGWMRPGGG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 AAIVVSGSALAGVVPQW---GGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKS
                                                                                   67 ETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                         10 AAIVVSGSALAGVVPQW---GGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKS
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                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/10021811
                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                          11.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.1%; Score 85; 26.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GEGAASASASASQSGAAAAATAQTPECSTETSKWATGGG 287
                                                   - GEGAASASASASQSGAAAAATAQTPECSTETSKMATGGG
                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                          Score 85;
Pred. No.
                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GGGNGKGPEAS-----GSTSTTATTQQQPQCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 15; Length 321;
                                                                                                                                                                                                                          DB 14; Length 323;
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                                                                                                                      -GSTSTTATTQQQPQCS
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                                                                                                                                                                                           Gaps
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; Sequence 749, Application publication No. US20030148; GENERAL INFORMATION: APPLICANT: I.N.S.E.R.M.; TITLE OF INVENTION: Polyr; TITLE OF INVENTION: E.cc.

Polynucleotides which are of nature B2/D+ A-E.coli, and biological uses of these polynuc

polynucleotides

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US-10-238-075-749

Application US/10238075

US20030148324A1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-09-905-176-24
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                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/218,016
PRIOR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 322
                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24, Application US/09905176 Patent No. US20020150906A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/905,176
CURRENT FILING DATE: 2002-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHOD FOR DETERMINING THREE-DIMENSIONAL PROTEIN STRUCTURE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 0003145
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 1576
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CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT FILING DATE: 2002-09-10
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TYPE: PRT
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                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1025 DYIADALGGNAVVNTDGSITTPTYAIAGGSYNNVGDALEAIDTTLDDALLWDTTANGGNG 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1085 A 1085
                              186 ANSKRIDDONOLLLGEGDHAETYTGGLKYDANNIYLATQYTQTYNATRAGSLGFANKAON 245
                                                                             105
                                                                                                         126 SDFFGLVGLNFALQYQGKNGSVSGEGATNNGRGALKQNGDGFGTSVTYDIFDGISAGFAY 185
147 -- TANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 DQLVT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              906 KISSNSTDAINGSQLYGVADSFTSYLGGGADISDTGVLSGPTYTIGGTDYTNVGDALAAI 965
                                                                                                                                                  72 QSGYG-----NGADVGQGADNS---TIELTQNGFRNNATYD-----
                                                                                                                                                                                                                           12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT
                                                                                                                                                                                            88 VVYDVTSWTDVLPEFGGD----
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                                                                       QLVTRVVTHEMAHAGG-----NNAALVNQ-TASDSSVMVRQVGFGNNA-- 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALQSDARKSETTITQSGYGNG----ADVGQGADNSTIELTQNGFRNNATY 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----RVVTHEMAHAGG--NNAA----LVNQTASDSSVMVRQVGFGNN 145
                                                                                                                                                                                                                                                                                      11.0%; Score 84.5; Di
23.0%; Pred. No. 2.2;
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                                                                                                                                                                                                                                                                     20;
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                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                 ; OTHER INFORMATION: Pfam consensus sequence US-09-996-194-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-996-194-16
                                                                                                                                                                                 SEQ ID NO 16
LENGTH: 65
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                           Matches
                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. US20020151
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16,
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/250,073
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/253,878
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/250,338
PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/250,348
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/996,194
CURRENT FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 35800/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: 84242, 8035, 55304, 52999, and 21999, TITLE OF INVENTION: No. US20020151696A1el Human Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bandaru, Rajasehkar
                                                                                          Local
34 RNH--YDQLVTRVVTHEIAHALGFSVGL 59
                                   98 RNNATYDQLVTRVVTHEMAHAGGNNAAL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 FEVAAQY 252
                                                                         l Similarity
19; Conserv
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                                                                                                                                                                                                                                                                        FastSEQ for Windows Version 4.0
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                                                                       Conservative
                                                                                      10.9%;
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                                                                     Score 84; DB
Pred. No. 0.33
3; Mismatches
                                                                                        0.33;
                                                                                                         DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Proteins and Methods of Use Thereof
                                                                                                         Length 65;
                                                                       Indels
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                                                                   Gaps
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Search completed: March 11, Job time: 25.6 secs 2004, 19:18:41

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Database Post-processing: Minimum Match 0% Maximum Match 10 Minimum DB Maximum DB Total number of hits satisfying chosen parameters: Searched Scoring table: Sequence: Perfect score: OM protein seq length: 0 seq length: 2000000000 protein search, using sw model March 11, 2004, 18:24:14; Search time 10.3 Seconds (without alignments) 1410.186 Million cell updates/sec BLOSUM62 PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 283366 ведв, Gapop 10.0 , Gapext 0.5 1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151 US-09-543-407-30 Listing first 45 summaries GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. 96191526 residues 100% 283366

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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681 681 517 502.5 502.5 104.5		Length D 151 151 151 152 152 153	2222222 E	ID JC6039 A10635 870788 D90806 D90806 H85655 S70787 C90806
	10 01 01 01		0000	\$70787 C90806 G85665 \$42136
		151 151 2174	000	JC6040 AH0635 E95965
12.8 12.8 12.7	7 8 8	145 645	NNN	AD3143 H98144 F70825
12 12	່ວ່ວ	313 354	NN	T04776 B70663
12	່. ່ ເ	256 256	NN	D96831 T03371
12 12	 o N	2204 1028	NN	A70524 A56038
12	0.0	1213 575	NN	S16356 S35327
==		409 573	N N	T20847 C86266
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86 86	86.5 86.5	88 87.5 87	88 88 5.88	88.5	89.5 89
11.2	11.3	11.5 11.4 11.3	11.5	11.6	11.7 11.6
582 639	3624 262 590	1778 1053 590	1217 407 586	959 967	1238 343
NNN	100	N N N	N N N	NN	8 8
F70675 C42049	AD0835 S00275 A45621	T50074 B70987 E70946	S52714 T21956 T26667	B44402 S66852	AH0038 T05221
probable PPE prote leishmanolysin (EC	large repetitive p tail fiber protein leishmanolysin (EC	probable PPE prote probable PPE prote	sericiniB - silkwo hypothetical prote hypothetical prote	nuclear pore compl hypothetical prote	probable exported hypothetical prote

ALIGNMENTS

A;Description: major component of thin aggregative fimbriae A;Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator C;Keywords: fimbria C;Keywords: fimbria F;1-20/Domain: signal sequence #status predicted <SIG> F;21-151/Product: fimbrin protein agfA #status experimental <MAT> A;Molecule type: protein
A;Residues: 21-52 <CO2>
A;Residues: 21-52 <CO2>
A;Experimental source: strain 27655-3b
A;Note: the authors translated the codon ACG for residue 44 as
A;Note: the authors translated the codon ACG for residue 44 as
A;Collinson, S.K.; Emody, L.; Muller, K.H.; Trust, T.J.; Kay, W
J. Bacteriol. 173, 4773-4781, 1991 fimbrin protein agfA precursor - Salmonella enteritidis C;Species: Salmonella enteritidis C;Species: Salmonella enteritidis C;Species: Salmonella enteritidis C;Species: John St. C;Specie Ś 8 A;Title: Purification and characterization of thin, aggregative fimbriae from Salmonella A;Reference number: A44898; MUID:91310586; PMID:1677357 ş 밁 В A;Gene: agfA C;Function: A;Molecule type: protein A;Residues: 21-33 <CO3> A; Accession: PC6015 A;Molecule type: DNA A;Residues: 1-151 <COL> A; Accession: JC6039 C; Genetics: A; Note: sequence extracted from NCBI backbone (NCBIP:45936) A;Accession: A44898 A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43599.1; PID:g1184714 Matches Query Match Best Local Similarity Status: preliminary 121 61 1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ NNAALVNQTASDSSVMVRQVGFGNNATANQY SDARKSETTITOSGYGNGADVGOGADNSTIELTONGFRNNATIDOWNAKNSDITVGQYGG SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG MKLLKVAAFAAIVVSGSALAGVVPQWGGGGHNGGGNSSGFDSTLSIYQYGSANAALALQ Conservative 88.7%; Score 681; DB 2; Length 151; 90.7%; Pred. No. 3.3e-49; Live 2; Mismatches 12; Indels aggregative fimbriae. W.W. 0, Gaps 60 60 0

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121

NNAALVNQTASDSSVMVRQVGFGNNATANQY

151

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A;Experimental source: strain Ki2, substrain W3110

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G64846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: csgA protein; major curlin plucel...
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change
C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change
C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change
C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change
C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change
C;Date: 12-Feb-1998 #text_chan
                                       A;Cross-references: GB:AE000205; GB:U00
A;Experimental source: strain K-12, sub
R;Olsen, A.; Arngvist, A.; Hammar, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Expression of two csg operons is required for production A;Reference number: S70783; MUID:96414468; PMID:8817489 A;Accession: S70788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Notice 413, 848-852, 2001

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;

A;Title: Complete genome sequence of a multiple drug resistant

A;Title: Complete genome sequence of a multiple drug resistant

A;Title: Complete genome sequence of a multiple drug resistant

A;Title: Complete genome sequence of a multiple drug resistant

A;Title: Complete genome sequence of a multiple drug resistant

A;Title: Complete genome sequence of a multiple drug resistant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-151 < HAM>
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A;Molecule type: DNA
A;Residues: 1-151 <PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Parkhill, J.; Dougan, G.; Jar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               major curlin
                                                                                                                                                            ;Molecule type: DNA
;Residues: 1-151 <BLAT>
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Best Local S
Matches 137
                                                                                                                                                                                                                                  Status: nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62282.1; PID:g1147564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ajor curlin chain precursor [imported]
Species: Salmonella enterica subsp. e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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species has also been called Salmonella typhi
ov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
AI0635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                          acid sequence not shown; translation not
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90.7%;
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in, A.;
                                                                                                             GB:U00096; NID:g1787265; PIDN:AAC74126.1;
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Pred. No. 3.3e-49;
2; Mismatches 12
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Davis, P.; Davies,
                                          substrain MG1655
M.; Sukupolvi, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151
                                          S.; Normark,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.R.; Pickard, D.;
ies, R.M.; Dowd, L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-Mar-2002
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Matches Query Match Best Local :

104;

Conservative

18;

Score 502.5; DB 2 Pred. No. 1.6e-34; 8; Mismatches 29

Indels Length

1;

Gaps

DB 2;

152;

Similarity

65.4%;

60

QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAG MKILKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAL MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL

119 60

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C;Genetics:
A;Gene: ECs1420
              R;Hayashi, T.; Makino, gasawara, N.; Yasunaga, DNA Res. 8, 11-22, 2001
                                                                                                                       A;Title: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: D90806
                                                                                                                                                                                                                             curlin major subunit CsgA [imported] -
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision
C;Accession: D90806
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                                                                                                      A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Olsen, A.N.; Arnqvist, A.M.
submitted to the EMBL Data Library,
A;Reference number: S34559
A;Accession: S34559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-133,'RQRDSGWLW' <OLS3>
A;Cross_references: EMBL:L04979; NID:g290424;
A;Experimental source: strain K-12, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-133, 'RQRDSGWLW'
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                                                                                                                                                                                          Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii
Kasunaga, T.; Kuhara, S.; Shiba, T.; Hattori,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.15
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Pred. No. le-35;
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W3110
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                                                                                                                                                                                          Shinagawa,
                                                  GSPDB:GN00154
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N;Alternate names: C
C;Species: Escherich
C;Date: 12-Feb-1998
C;Accession: S70787;
R;Hammar, M.; Arnqvi
                                                                                                                                                                                                                                                                                                               A.Title: Expression of two csg operons is required for production A.Reference number: S70783; MUID:96414468; PMID:8817489
A.Accession: S70787
A.Recession: S70787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; R
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamou
Nature 409, 529-531, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85665
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-152 <STO>
A;Cross-references: GB:AE005174; NID:g12514574; PIDN:AAG55788.1; GSPDB:
A;Genetics:
A;Genetics:
                                                          Science 277, 1453-1462, 1997
A,Title: The complete genome sequence of Escherichia coli A,Reference number: A64720; MUID:97426617; PMID:9278503 A,Accession: P64846
A,Status: nucleic acid sequence not shown; translation not
                                                                                                                                                               A;Cross-references: EMBL:X90754; NID:gl147558; PIDN:CAA62281.1; PID:gl147563 A;Experimental source: strain K12, substrain W3110 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Augum R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; R.A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 curlin nucleator protein csgB precursor - Escherichia coli (strain K-12) N;Alternate names: csgB protein; curlin nucleation component; minor curl C;Species: Escherichia coli
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                     A; Molecule type: DNA
A; Residues: 1-151 < Bi
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A; Residues: 1-151 <H
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Best Local S
Matches 104
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Accession: H85665
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  GB: AE000205;
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  GB:U00096;
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Pred. No. 1.6e-34;
B; Mismatches 29;
                                                                 shown; translation not
  NID: g1787265;
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  PIDN: AAC74125
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V.; Riley,
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PID:g1787278
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K.; Aj
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A;Accession: G85665
A;Status: preliminary
A;Molecule type: DNA
A;Residues: I-151 <STV
A;Cross-references: G

1-151 <STO>

GB:AE005174;

NID:g12514573;

PIDN: AAG55787

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GSPDB:GN00145;

UWGP: 216

preliminary

curlin minor chain precursor, CsgA homolog [importe C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 C;Accession: G8565 R.Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Di Nature 409, 529-533, 2001 Nature 409, 529-533, 2001 A;Title: Genome sequence of enterohemorrhagic Esche A;Reference number: A85480; MUID:21074935; PMID:112

Mau, B.; Glasner, A.; Dimalanta, E.;

J.D.; Rose, Potamousis,

D.J.; Mayhew K.; Apodaca,

#text_change 14-Sep-2001

of enterohemorrhagic Escherichia 80; MUID:21074935; PMID:11206551

0157:H7

G85665

[imported]

Escherichia coli (strain

0157:H

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A; Gene: csgB
A; Map position:
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                minor curlin subunit precursor CsgB [imported] - EsC;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001
C;Accession: C90806
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A;Reference number: A99629; MUID:21156231; PMID:11258796
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DNA Res. 8, 11-22, 2001
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A; Residues: 1-151 <HAY>
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                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                       Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:g13360879; GSPDB:GN00154
Experimental source: strain O157:H7, substrain RIMD 0509952
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Best Local
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Hayashi, T.; Makino,
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Best Local
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                                    RNNATYDQLVTRVVTHEMAH---AGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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SNRAKIDQ----TGDYNLAYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY 129
                                                                        AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
                                                                                                           SSGPDSTLSIYOYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF
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T.; Kuhara,
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Pred. No. 0.0
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Shiba, T.; Hat
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C;Keywords: zinc finger
F;1164-1450/Region: zinc finger CCHC motif
F;1451-1464/Region: zinc finger CCHC motif
F;1478-1491/Region: zinc finger CCHC motif
F;1530-1514/Region: zinc finger CCHC motif
F;1530-1543/Region: zinc finger CCHC motif
F;1530-1543/Region: zinc finger CCHC motif
F;1579-1592/Region: zinc finger CCHC motif
F;1579-1592/Region: zinc finger CCHC motif
F;1679-1592/Region: zinc finger CCHC motif
F;1679-1592/Region: zinc finger CCHC motif
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A;Residues: 1164-1174,1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-.
A;Cross-references: EMBL:L03710
R;Martindale, D.W.; Taylor, F.M.
Nucleic Acids Res. 16, 2189-2201, 1988
A;Title: Multiple introns in a conjugation-specific gene from Tetrahymena thermophila.
A;Reference number: 803650; MUID:88189811; PMID:3357771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 236-250,'I',252-255,'N',257-773
A;Cross-references: EMBL:X06462
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submitted to the EMBL Data Library, October 1992
A:Reference number: S42136
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Nucleic Acids Res. 21, 4610-4614, 1993
A;Title: Retroviral-type zinc fingers and glycine-rich repeats
A;Reference number: S42135; MUID:94051569; PMID:8233798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-1748 <TAY>
A;Cross-references: EMBL:L03710; NID:g161751; PID:g161752
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
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Best Local
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                                                                                                         1640
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                                                                                                                                                                                                        Similarity
                                                         GQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVG
                                                                                                                                        QWGGGGNHNGG----GNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNNATYDQLVTRVVTHEMAH---AGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNRAKIDO----TGDYNLAYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source:
                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strain O157:H7, substrain
                                                                                                                                                                                                      13.2%;
29.7%;
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                                                                                                                                                                                                  Score 101;
Pred. No. 2.
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                                                                                                                                                                                 Mismatches
                    ---QNENTGGGGWGSSNSNQTNNESS-----
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6
                                                                                                                                                                                                                         BB
                                                                                                   ---CQSNVQES-TTTSSGGWGS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #text_change 07-Dec-1999
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                                                                                                                                                                                                                      Length 1748;
                                                                                                                                                                                 Indels
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                                                                                                                                                                               40;
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A; Residues: 1-151 < P.
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                                                                                                                                                                                                                                 A;Gene: STY1180
                                                                                                                                                                                                                                                                            A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                              A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AH0635
                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 413,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Parkhill, J.; Dougan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser J. Bacteriol. 178, 662-667, 1996
A;Title: Salmonella enteritidis agfBAC operon encoding A;Reference number: JC6039; MUID:96146512; PMID:8550497 A;Accession: JC6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AH0635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: minor component of thin aggregative fimbriae A; Note: fimbriae bind to fibronectin, plasminogen, tissue \mathbf{p}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fimbrin protein agfB precursor - Salmonella enteritidis
C;Species: Salmonella enteritidis
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: I-151 <COL>
A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43598.1;
A;Experimental source: strain 276755-3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: JC6040
R;Collinson, S.K.; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h, T.; Connerton, P.; Crc
S.; Moule, S.; O'Gaora,
                                                                                                                                             Matches
                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;1-21/Domain: signal sequence #status
;22-151/Product: fimbrin protein agfB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     848-852, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST-----IELTQ
                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                      .-151 <PAR>
:ences: GB:AL513382; PIDN:CAD08267:1; PID:g16502314; GSPDB:GN00176
NGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                          GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ 73
                                                                                         GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST----IBLTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGFRNNATYDOLVTRVVTHEMAHAGGNNAALVNOTASDSSVMVROVGFGNNATANOV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ
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                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Igan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
                                                                                                                                                           13.0%;
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28.2%; Pred. No. 0.
                                                                                                                                        16;
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                                                                                                                                                      Score 99.5; DB 
Pred. No. 0.22;
                                                                                                                                   Mismatches
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#status predicted <MAT>
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                                                                                                                                                                             Length
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A;Cross-references: GB:AL591985; PIDN:CAC49389.1; PID:g15140875; GS
A;Experimental source: strain 1021, megaplasmid pSymB
A;Experimental source: strain 1021, megaplasmid pSymB
A;Experimental source: strain 1021, megaplasmid pSymB
A;Chain, P; Cowie, T.
Davis, R.W.; Dreano, S.; Federspiel
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.
A;Title: The composite genome of the legume symbiont Sinorhizobium
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                               C;Accession: AD3143
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks
erage, G.; Gillet, W.; Grant, C.; Guenthner,
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
AD3143
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                                                                                                                                                  A;Title: The Genome of the Natural Genetic A;Reference number: AB2577; MUID:21608550; A;Accession: AD3143
                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein Atu4768 [imported] C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2003
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A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Finan,
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                                                                                                                                                                                                                               A; Authors: Yoo,
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Best Local S
Matches 32
                          | Polecule type: DNA
| Molecule type: DNA
| Residues: 1-145 <KUR>
| Cross-references: GB:AE008689; PIDN:AAL45562.1; PID:g17743277; GSPDB:GN00187
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Gene: SMb21548
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Residues: 1-2174 <KUR>
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/Species: Sinorhizobium meliloti
/pate: 24-Aug-2001 #sequence_revision
                                                                                                                               Status: preliminary
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                    Atu4768
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Kutyavin, T
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Apecies: Nycobacterium tuberculosis
C;Apecies: Nycobacterium tuberculosis
C;Apecies: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003
C;Accession: F70825
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; F.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
N.;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Deciphering the biology of Mycobacterium tuberculosis from the comple
A;Heference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70825
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule true: NA

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RESULT

A; Molecule type: DNA A; Residues: 1-645 < C

<C0L> B

AL021958;

GB:AL123456;

NID:g3261536; PIDN:CAA17522.1; PID:e125329

from the complete

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Holroyd,

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hypothetical protein AGR_L_228 [imported] - C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oc;Accession: H98144
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Science 294, 2323-2328, 2001
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A; Residues: 1-145 < KUR>
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Q-VGRGCSANVSQGGNDNVA 138
                                QLVTRVVTHEMAHAGGNNAA
                                                            IVGHQYGRHNLS-AVGQEGHDNYGSTTQNGNRNVAGIGQFGSNHTTILTQDGNGNIAAGV 119
                                                                                         LSIYOYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIBLTQNGFRNNATYD
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Pred.
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kelz, B.
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A;Experimental source: strain H37RV
C;Genetics:
A;Genetics:
A;Gene

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

March 11, 2004, 18:14:48; Search time 6.3 Seconds (without alignments) 1248.031 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-543-407-30
768
1 MKLLKVAAPAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

141681

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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SEQUENCE FROM N.A. SERCIES-S.typhi; STRAIN-Ty2 / ATCC 700931; SPECIES-S.typhi; STRAIN-Ty2 / ATCC 700931; MEDLINE-22531367; PubMed-12644504; Deng W., Liou SR., Plunkett G. III, Mayhew G.F., Rose D.J., Deng W., Liou SR., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;	., Haque A., Hien T.T., Holroyd, Leather S., Woule S., O'Gaora d K., Simmonds M., Skelton J., B.G., B.G.; ence of a multiple drug resistant CT18.";	413:852-856(2001). CE FROM N.A. S=S.typhi; STRAIN=CT18; E=21534947; PubMed=11677608; I J., Dougan G., James K.D., Thomson N.R., Pickard D., Will J., Dougan G., Bentley S.D., Holden M.T.G., Sebaihiu er C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihiu S., Basham D., Brooks K., Chillingworth T., Connerton P., S., Basham D., Brooks K., Dowd L., White N., Farrar J., A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,	SEQUENCE FROM N.A. SERCIES-S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; SERCIES-S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE-21534948; PubMed=11677609; MCCLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";	Salmonella typh; and Salmonella typh; and Salmonella enteritidis. Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella. NCBI_TaxID=602, 601, 592; [1] SEQUENCE FROM N.A. SPECIES=5. typhimurium; STRAIN=SR-11; SPECIES=5. typhimurium; STRAIN=SR-11; SPECIES=5. typhimurium; STRAIN=SR-11; SPECIES=5. typhimurium; STRAIN=SR-11; SPECIES=5. typhimurium; STRAIN=SR-11; SPECIES=5. typhimurium; STRAIN=SR-11; SPECIES=5. typhimurium; STRAIN=SR-11; SPECIES=6	

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Query Match
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Matches 137
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EMBL; AL627269; CAD08268.1; --
EMBL; AE016840; AA069399.1; --
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SPECIES-S.enteritidis; STRAIN=27655-3B;

MEDLINE=91310586; PubMed=1677357;

Collinson S.K., Emoedy L., Mueller K.-M., T;

Collinson S.K., Emoedy L., Mueller K.-M., T;
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-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.
COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., K
"DNA-based diagnostic tests for Salmonella species
the structural gene for thin, aggregative fimbriae.
T. Clin. Microbiol. 31:2263-2273(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=S.enteritidis; STRAIN=27655-3B; MEDLINE=94013373; PubMed=8104955; Doran J.L., Collinson S.K., Burian J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96146512; PubMed=8550497; Collinson S.K., Clouthier S.C., E Collinson E.K., Clouthier S.C., E Collinson Ela enteritidis agfBAC op
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SIMILARITY: BELONGS
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                                                                                                   MKLLKVAAFAATVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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REF. 6).
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aggregative fimbriae
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MEDLINE=970612...
Oshima T., Aiba H., b...
Oshima T., Aiba H., b...
Nemoto K., Inada T., Itoh I.,
Ikemoto K., Inada T., Itoh I.,
Motomura K., Nakamura Y.,
Motomura K., Nakamura Y.,
Tagami H., Ta
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"The complete genome sequence o Science 277:1453-1474(1997).
                                  J. Bacteriol. 173:4773-4781(1991).
-i- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.
COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A
                                                                                                                                                                                                                                     MEDLINE=93023873; PubMed=1357528;
Arnqvist A., Olsen A., Pfeifer J.,
"The Crl protein activates cryptic
fibronectin binding in Bscherichia
Mol. Microbiol. 6:2443-2452(1992).
                                                                                                         MEDLINE-91310586; PubMed=1677357; Collinson S.K., Emcedy L., Trust T. "Purification and characterization Salmonella enteritidis.";
                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 21-40.
STRAIN=K12 / YMEL;
MEDLINE=93023873;
                                                                                                                                                                                                                                                                                                                                                                                                              "A 718-kb DNA sequence of the E corresponding to the 12.7-28.0 DNA Res. 3:137-155(1996).
                                                                                                                                                                                                  SEQUENCE
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Blattner F.R., Plunkett G. III, Bloch
Riley M., Collado-Vides J., Glasner J.
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P28307;
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MEDLINE=96414468; PubMed=8817489;
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MEDLINE=93211294; P
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                      BELOW
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                      DEGREES
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A., Goeden M.A., Ro
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RESULT 3
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                                             Appl. Environ. Microbiol. 67:2367-2370(2001).

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STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=2107495; PubMed=11206551;

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28-FEB-2003
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or send a
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STRAIN=0157:H7 / ATCC 43895;

MEDLINE=21218556; PubMed=11319125;

Whlich G.A., Keen J.E., Elder R.O.;

Whatations in the csgD promoter associated with variations expression in certain strains of Escherichia coli 0157:H7."

Appl. Environ. Microbiol. 67:2367-2370(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Major curlin subunit precursor. CSGA OR Z1676 OR ECS1420. Escherichia coli O157:H7.
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BL; X90754; CRA62282.1; -.
BL; AE000205; AAC74126.1; -.
BL; D90741; BAA35832.1; -.
BL; D90742; BAA35840.1; -.
R; S70788; S70788.
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an email to license@isb-sib.ch).
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sequence of enterohaemorrhagic
109:529-533(2001).
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X MEDLINE=21156231; PubMed=11258796;

A Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yoko A Hayashi T., Makino K., Ohnishi M., Murata T., Tanaka M., Tobe A Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Yasun R., Ida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasun R., Complete genome sequence of enterohemorrhagic Escherichia col T. (Complete genome sequence of enterohemorrhagic Escherichia col T.) DNA Res. 8:11-22(2001).

DNA Res. 8:11-22(2001).

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28-FEB-2003 (Rel. 41, Last annotation
Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
SEQUENCE FROM N.A.
STRAIN=K12 / MC4100;
STRAIN=96414468; PubMed=8817489;
MEDLINE=96414468; PubMed=8817489;
Hammar M., Arnqvist A., Bian Z., Olsen A., Normark S.;
"Expression of two csg operons is required for production fibronectin- and congo red-binding curli polymers in Esche
                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 83334;
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STRAIN=0157:H7 / R
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SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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"Sigma S-dependent growth-phase induction of the csgBA promoter in Escherichia coli can be achieved in vivo by sigma 70 in the absence of the nucleoid-associated protein H-NS.";
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-i- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AF COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF CIPIL IN MONAGED.
                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino E., Ohnishi M., Kurokawa K., Tanaka M., Tobe T ida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;
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Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhaw G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
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Posfai G., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
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                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95157246; PubMed=7854117;
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SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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nce 277:1453-1474(1997).
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EMBL; D90741; BAA35831.1; -
EMBL; AR005315; AAG55787.1; -
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0827M3;
28-FEB-2003 (Rel. 41, Createa)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
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-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNCIONES SURFACE STRUCTURES THAT ASSEMBLE TEMPERATURES BELOW 37 DEGREES CELSIUS. CELSIUS. THE MINOR SUBUNIT IS THE NU
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367, PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi st
and CT18.";
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                                                                                                     TO THE CSGA/CSGB FAMILY.
                         copyright. It is produced through a collaboration -
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Pred. No. 0.
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Matches 33
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01-OCT-1996
01-OCT-1996
28-FEB-2003
                                                                                                                                                                                                                              SPECIES-S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609; MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Lat. Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulv. Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SPECIES-S.typhimurium; STRAIN-SR-
MEDLINE-98117058; PubMed-9457880;
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                                                                                                     SPECIES=S.enteritidis; STRAIN=27655-3B;
MEDLINE=96146512; PubMed=8550497;
COllinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W. "Salmonella enteritidis agfBAC operon encoding thin, aggregativ
                                                                                                                                                                                                                                                                                                                                                          Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.; "Curli fibers are highly conserved between Salmonella typhimurium a Bscherichia coli with respect to operon structure and regulation."; J. Bacteriol. 180:722-731
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CSGB OR AGFB OR STM1143.
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Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                         Nature 413:852-856(2001).
                                                                                                                                                                                                                   "Complete genome
                                                                Bacteriol. 178:662-667(1996). - FUNCTION: CURLIN IS THE STRU
                                     FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
                         FIBRONECTIN. THE MINOR SUBUNIT IS
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1 21 POTENTIAL.
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(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
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S., Layman D.,
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                                                                                                                                        STRAIN-Oregon-R;
MEDLINE=91293102; PubMed=1712294;
Mevel-Ninio M.T.M., Terracol R., Kaf
Mevel-Ninio M.T.M., Terracol R., Kaf
"The ovo gene of Drosophila encodes
for female germ line development.";
EMBO J. 10:2259-2266(1991)
                                                                                                                                                                                                                                               Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.; "Multiple products from the shavenbaby-ovo gene r melanogaster: relationship to genetic complexity. Mol. Cell. Biol. 14:6809-6818(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                        Ovo protein (Shaven OVO OR SVB.
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                                                                                                                                                                                                                                                                                         MEDLINE=95021209; PubMed=7935398;
Garfinkel M.D., Wang J., Liang Y.,
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                                FUNCTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF I LINE CELLS: PLAYS A ROLE IN GERM LINE SEX DETERMINATION.

SUBCELLULAR LOCATION: Nuclear (potential).

DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND ACCUMULATES IN NURSE CELLS DURING OGGENESIS. STORED IN THE BUT IS RAPIDLY LOST IN THE EMBRYOS EXCEPT FOR ITS CONTIL PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS.

SIMILARITY: Contains 4 C2H2-type zinc fingers.
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             SWISS-PROT entry is copyright.
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PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Zinc_finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0003028; ovo.
InterPro; IPR007087; Znf C2H
Pfam; PF00096; zf-C2H2; 3.
SMART; SM00355; Znf C2H2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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entities requires a license agreement (some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nicotinamide + {ADP-D-ribosyl}(N+1)-acceptor.

-i- SUBUNIT: Oligomerizes and associates with TNKS2. Interacts with the cytoplasmic domain of LNEP/Otase in SLC2A4/GLUT4-vesicles. Binds to the N-terminus of telomeric TRF1 via the ANK repeats.

-i- SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and the County of the N-terminus of telomeric TRF1 via the ANK repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE 2055628; PubMed=10988299;
Chi N.-W., Lodish H.F.;
"Tankyrase is a Golgi-associated mitogen-activated protein kinase substrate that interacts with IRAP in GLUT4 vesicles.";
J. Biol. Chem. 275:38437-38444 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity and can modify TRF1, and thereby regulation of telomere length.
-1- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION, AND MUTAGENESIS OF HIS-1184 AND GLU-1291 MEDLINE=21602874; PubMed=11739745; Cook B.D., Dynek J.N., Chang W., Shostak G., Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cook B.D., Dynek J.N., Chang W., Shost "Role for the related poly(ADP-Ribose)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION,
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J. Cell Sci. 112:3649-3656(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith S., de Lange T.;
"Cell cycle dependent localization of the telomeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99454782; PubMed=10523501;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith S., Giriat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tankyrase 1 (EC 2.4.2.30) (TANK1) (Tankyrase interacting ankyrin-related ADP-ribose polymeTNKS OR TINSI OR TINI OR TINFI OR PARPL. Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99040105; PubMed=9822378;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human telomeres.";
                                                                                                                                                                                                          SIMILARITY: Belongs to the PARP family.
SIMILARITY: Contains 15 ANK repeats.
SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
                                                                                                                                                                                                                                                                                                                                                                       PTM:
                                                                                                                                                                                                                                                                                                                                                                                         IsoId=095271-2; Sequence=VSP_004538, VSP_004539;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Ubiquitous; highest levels in testis.
                                                                                                                                                                                                                                                                                                                                          PTM: Upon insulin-stimulation, phosphorylated on serine residues by MAPK kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with juxtanuclear SLC2AA/GLUT4-vesicles. A minor proportion is also found at nuclear pore complexes and around the pericentriolar matrix of mitotic centromeres. During interphase, a small fraction of TNKS is found in the nucleus, associated with TRF1.

ALTERNATIVE PRODUCTS:

Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=1
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                                                                                                                                                                                                                                                                                                            ADP-ribosylated (-auto)
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                                                                                                                                                                It is produced through
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tankyrase
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Phosphorylation; Alternative splicing.

215 247 ANK 1
REPEAT 216 247 ANK 1
REPEAT 281 313 ANK 2
REPEAT 368 400 ANK 4.
REPEAT 368 400 ANK 5.
REPEAT 401 433 ANK 5.
REPEAT 434 466 ANK 7.
REPEAT 521 556 ANK 7.
REPEAT 521 556 ANK 7.
REPEAT 520 622 ANK 9.
REPEAT 683 715 ANK 10.
REPEAT 716 748 ANK 11.
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REPEAT 902 934 ANK 15.
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MIM; 6
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PROSITE; PS50197; ANK_REP REGION; 1.
PROSITE; PS50105; SAM_DOMAING: 1.
Transferase; GlycosylTransferase; NAD; Golgi stack; Telomere;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR01415; ANKYRIN.
SMART; SM00248; ANK; 17.
SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0000781; C:chromosome, telomeric region; IDA. GO; GO:000350; F:NAD ADP-ribosyltransferase activity; IDA. GO; GO:0005515; F:protein binding; IPI. GO; GO:0007004; P:telomerase-dependent telomere maintenance;
                                                                                                                                                                                                                                                 MUTAGEN
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AF082558;
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                                                                                                                                                              Similarity
VNAK - - DMAGRKSSPLHFAAGFG
                      NNAALVNOTASDSSVMVROVGFG
                                              GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD----
                                                                      KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
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AAC79843.1;
AAC79844.1;
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29.4%;
                                                                                                                                                                                                 142010
                                                                                                                                               17;
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                                                                                                                                                         Score 91.5;
Pred. No. 4.
                                                                                                                                                                                                                                  /FTId=VSP 004538.
Missing (In isoform 2).
/FTId=VSP 004539.
H->A: LOSS OF ACTIVITY; WHEN ASSOCIATED WITH A-1291.
                                                                                                                                                                                                                                                                                                                         PARP.
POLY-HIS.
POLY-PRO.
POLY-SER.
                                                                                                                                                                                                                                                                                                   POLY-SER.
EST -> GH
                                                                                                                                                                                                            E->A: LOSS OF ACTIVITY; WHEN WITH A-1184.
                                                                                                                                                                                                                                                                                                                                                                             SAM
                                                                                                                                                Mismatches
                       143
                                                                                                                                                                                                 E14DE985C710B957
                                                                                                                                                                                                                                                                                                -> GHS (in isoform
                                                                                                                                                                         띪
                                                                                                                                                                       1;
                                                                                                                                               65;
                                                                                                                                                                      Length 1327;
                                                                                                                                                                                                 CRC64;
                                                                                              -ŚSSSPSŚPGSSĹĀESPEĀA
                                                                                                                                                Indels
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                                              -VSRV--KRLVDAAN
                                                                                                                                                                                                                         ASSOCIATED
                                                                                                                                               19;
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                                                                                                                                               Gaps
                                                                       120
                                                                                              157
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RESULT 9
OMPB_RICJA

(Rel.

26, Created) 26, Last seq

sequence

update)

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RESULT 10

N100 YEAST

ID N100 YEAST

AC Q02629;

DT 01-JUL-1993

DT 01-JUL-1993
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Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                            CHAIN .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (By similarity).
-!- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered layer with hexagonal symmetry.
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsia japonica.
Rickettsia, Proteobacteria, Alphaproteobacteria,
Bacteria, Proteobacteria, Alphaproteobacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Outer membrane protein B precursor (168 kDa surface-layer protein) (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB) (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OMPB_RICJA STANDARD; PRT; 1656 AA.
006653;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS AMAJOR-
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By
                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMs; TIGR01414; autotrans_barl; 2.
Antigen; S-layer; Cell wall.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB003681; BAA20138.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-YH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Uchiyama T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=35790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OMPB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequencing of japonica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity)
                                                                                                                                                   105
                                                                                                                                                                               548
                                                                                                                                                                                                                                          509
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF03797; Autotransporter;
                                                                                                                                                                                                            66
                                                                                                                                                                                                                                                                                                   40;
                                                                                                                                                                                                                                                                      6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARK
                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                     NAQTLTISGTIGIIGANNTTLGQFNIGSSKTTLNGGNVAINELVIGNNGS
                                                                                                                                                 QLVTRVVTHEMAHAGGNNAAL-----VNQTASDSSVMVRQVGFGNNAT 147
                                                                                                                                                                                                            SETTITQSG----YGNGADVGQGADNSTIELT----
                                                                                                                                                                                                                                          VLAAGAITLDGSATI----TGDIGNGGG
                                                                                                                                                                               ---TLTLGGANIISANGGTINFQANGGTIKLTSTQNNIVVDCDLAIATDQTGVVDASSLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR006315; Autotransport. IPR005546; Autotransporter.
                                                                                                                                                                                                                                                                                                                                                            528 5
1656 AA;
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                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the gene encoding the protein rOmp
                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                         1338
                                                                                                                                                                                                                                                                                                                                                                                           1656
                                                                                                                                                                                                                                                                                                                                                                            533
                                                                                                                                                                                                                                                                                                                 11.7%;
23.5%;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                             120 kDa SURFACE-EXPOSED PROTEIN 32 kDa BETA PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                            POLY-GLY
                                              PRT;
                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                            3132A69C9DD5999F CRC64;
                                                                                                                                                                                                                                                                                                                 No.
                                              959
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                                                                                                                                                                                                                                                                                                                                Length 1656;
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L outstation -
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RESULT
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Best Local
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GO; GO:0005643; C:nuclear pore; IDA.
InterPro; IPR007230; Nucleoporin.2:
InterPro; IPR004325; Nucleoporin.FG.
Pfam; PF04096; Nucleoporin.FG; 25.
Nucleoporin.FG; 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A new family J. Cell Biol. [2]
                                                                                                                                                                                                                                                                                                         Nuclear protein; Transport; Repeat.

DOMAIN 33 571 29 X 6 AA APPROXIMATE REPEATS

G-L-F-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z15035; CAA78753.1; --
EMBL; X75780; CAA53406.1; --
EMBL; Z28068; CAA61905.1; --
EMBL; Z28068; CAA61905.1; --
PIR; B44402; B44402.
                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence of a 20.7 kb region of yeast chromosome XI includes the NUP100 gene, an open reading frame (ORF) possibly representing a nucleoside diphosphate kinase gene, tRNAs for His, Val and Trp in addition to seven ORFs with weak or no significant similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93054906; PubMed=1385442; Wente S.R., Rout M.P., Blobel G.; "A new family of yeast nuclear pore J. Cell Biol. 119:705-723(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-2004 (Rel. 43, Last annotation Nucleoporin NUP100/NSP100 (Nuclear por NUP100 OR NSP100 OR YKL068W OR YKL336.
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Essential component of nuclear pore complex. Nucleoporins may be involved in both binding and transl the proteins during nucleocytoplasmic transport.

SUBCELLULAR LOCATION: Nuclear pore complex.

DOMAIN: Contains G-L-F-G repeats.

SIMILARITY: Belongs to the GLFG family of nucleoporins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                          131
                                            294 MNSST--
                                                                                                          243
                                                                                                                                        90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins.";
10:S69-S74(1994).
                                                                                                                                                                                                                                     35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         .ine; 139824; -.
                                                                                                                                                                                                                                                    Similarity
                                                                         SDSSVMVRQVGFGNN 145
                                                                                                     SFGSKPVGSGSLFGQSNNTLGNTTN--NRNGLFGQM-
                                                                                                                                                                                             GGGGNHNGGGNSSGPDSTLSIY--QYGSANAALALQSDARKSETTITQSGYGN-----GA
                                                                                                                                          DVGQ.
                                                                                                                                                               GNGSNIFGAGNNSQSNTTGSLFGNQQSSAFGTNNQQGSLFGQQSQNTNNAFGNQNQLGGS
                                                                                                                                                                                                                                                                                                 959 AA;
                                                                                                                                                                                                                                  11.6%;
ilarity 25.9%;
Conservative 2
                                           -QGVFGQN 305
                                                                                                                                                                                                                                                                                                 99988 MW;
                                                                                                                                -GADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTA
                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                               Score 89; DB 1
Pred. No. 5.3;
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        annotation update)
                                                                                                                                                                                                                                                                                              D3985F9901BBAA51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pore protein NUP100/NSP100)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complex proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no restrictions ong as its content is in
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                                                                                                                                                                                                                                52;
                                                                                                                                                                                                                                                              Length 959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e complex.
and translocation
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no
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RA Wood V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Cliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Weller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Weller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moest D., Hilbert H.,
RA Borzym K., Langer I., Beritach H., Reinhardt R., Pohl T.M.,
RA Bger P., Zimmermann W., Wedler H., Reinhardt R., Pohl T.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Spakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RT The genome sequence of Schizosaccharomyces pombe.",
RI Nature 415:871-880(2002).
                                                between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                               Tange Y., Hirata A., Niwa O.;
"An evolutionarily conserved fission yeast protein, in normal nuclear morphology and chromosome stabilit Dis3, Pimi/RCC1 and an essential nucleoporin.";
J. Cell Sci. 115:4375-4388(2002).
-!- SUBUNIT: Monomer. Interacts with ned1.
-!- SUBCELLULAR LOCATION: Nuclear pore complex (By second complex).
                                   entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                            This
                                                                                                                                                                                         -!- DOMAIN: Contains G-L-F-G repeats.
-!- SIMILARITY: Belongs to the GLFG family of nucleoporins.
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22263608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98162722;
Yoshioka S., Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1428-1778 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification
                                                                                                                                                                                                                                                                                                                                                                                                DENTIFICATION, AND SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21848401; PubMed=11859360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Last sequer
28-FEB-2003 (Rel. 41, Last annotz
Nucleoporin nup189 (Nuclear pore
NUP189 OR SPAC1486.05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N189
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                                                                                                                                                      SWISS-PROT entry is copyright.
  AL133357;
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                                                                                                                                                                                                                                                                                                                                                                             PubMed=12376568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K., Nakai K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=9501991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K., Nakai K., Okayama H., Nojima H.;
open reading frames in Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last annotation
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                                                                                                                                                                                                                                                                                                              stability,
                                                                                                                                                                                                                                   similarity).
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RESULT
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Best Local :
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                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=87283911; PubMed=3302276;

MEDLINE=87283911; PubMed=3302276;

Riede I. Drextler K., Eschbach M.L., Henning U.;

PUAR sequence of genes 38 encoding a receptor-recognizing pacteriophages T2, K3 and of K3 host range mutants.";

J. Mol. Biol. 194:31-39(1987).

-i- FUNCTION: V938 is at the tip of the long tail fibers of the only tail fibers of the cellular receptor.

-i- nhade recognition site for the cellular receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P07875;
01-AUG-1988
01-AUG-1988
01-AUG-1990
Pfam; PF05268;
Fiber protein;
SEQUENCE 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenebB Spombe; SPAC1486.05; -...
GO; GO:0016020; C:membrane; ISS.
GO; GO:0005643; C:nuclear pore; ISS.
GO; GO:0006606; P:protein-nucleus import;
InterPro; IPR007230; Nucleoporin.
InterPro; IPR004325; Nucleoporin.FG.
                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use as long as its content use as long as long as its content use as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long as long
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DOMAIN 9
                                                                                    EMBL; X05312; CAA28935.1; PIR; S00275; S00275.
                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, T4-like viruses.
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                                     InterPro; IPR007932; Tail_fibre_GP38.
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770074; T50074.
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PF03093; Nucleoporin_FG; 24.
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(Rel.
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protein (Protein Gp38).
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Pred. No. 13;
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  0567366918F6C745 CRC64;
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                  DISULFID
                                                                                                                                                                                                                                                  Zymogen;
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -|- CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 and basic residues at P2 and P3'. A model nonapeptide cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.
-|- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-|- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-an-
-|- SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Leishmania donovani.";

Mol. Biochem. Parasitol. 48:173-184(1991).
-i- FUNCTION: Has an integral role during in the mammalian host.
-i- CATALYTIC ACTIVITY: Preference for hyd.
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P23223;
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NCBI_TaxID=5661;
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10-OCT-2003
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  DISULFID
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InterPro; IPR001577; Peptidase M8.
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Eukaryota;
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(Rel. 20, Last sequence update)
(Rel. 42, Last annotation update)
sin precursor (EC 3.4.24.36) (Cell
ace glycoprotein) (GP63 protein) (J
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    11.3%;
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adhesion; GPI-anchor; Lipoprotein.
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Best Local
                                        Zymogen;
SIGNAL
                                                                                              GlycoSuiteDB; P43150; ... InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001577; Peptidase M8.
Pfam; PF01457; Peptidase M8; 1.
                                                                                                                                                                                                     use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                   MEDIINE-33149206; PubMed-8426614;
Medina-Acosta E., Karess R.E., Russell D.G.;
Medina-Acosta E., Karess R.E., Russell D.G.;
"Structurally distinct genes for the service protease of Leishmania mexicana are developmentally regulated.";
Mol. Biochem. Parasitol. 57:31-46(1993).

-I- FUNCTION: Has an integral role during the infection of macrophagin the mammalian host.

-I- CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 are considered and p3'. A model nonapeptide is p1 are considered and p3'.
                                                                        PRINTS; PR00782; LSHMANOLYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                             EMBL; X64394; CAA45733.1;
PIR; S19916; S19916.
HSSP; P08148; 1LML.
                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and
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                                                               Hydrolase;
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Eukaryota; Euglenozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-CCT-2003 (Rel. 42, Last amoutation update)
Leishmanolysin C1 precursor (EC 3.4.24.36) (C)
(Major surface glycoprotein) (GP63 protein)
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COFACTOR: Binds I zinc ion per subunit (By simil DEVELOPMENTAL STAGE: Expressed in both the promasumilarity. Pro-
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ion; Multigene
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GPI-anchor amidated a similarity).
POTENTIAL.

ACTIVATION PEPTIDE (POTENTIAL).
LEISHMANOLYSIN C1.
ZINC (CATALYTIC) (BY SIMILARITY
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Pred. No. 4.9;
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There are no restrictions
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P18127;
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01-NOV-1990
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-!- FUNCTION: Ice nucleation proteins enable
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SUBCELLULAR LOCATION: Outer membrane (By similarity).
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OCTAPEFTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
MISCELLAMBOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
SIMILARITY: Belongs to the bacterial ice nucleation protein
family.
                                                                                                               European
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Best Local Similarity 26.4%; Pred. No. 18;
Matches 39; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 81.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE NUCLEATION; 57.
Ice nucleation; Repeat; Outer membrane.
SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;
                                                                                            1165 GYGSTQTAGYNSILT--TGYGSTQTAQE 1190
                                                                                                                                                                                           1105 TGTAGADSSLIAGYGSTQTAGYDSNLTAGYGSTQTAREDSSLTAGYGSTSTAGHDSSLIA 1164
                                                                                                                                                                                                                                                                                     1055 GSTGTAGADSTL-IAGYGSTQTA------GSDSSLT-AGYGSTQTARQGSDITAGYGS 1104
                                                                                                                          127 ----NQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                        82 -- GQGADNSTIE---LTQN-GFRNNATYDQLVTRVVTHEMA------HAGGNNAALV- 126
                                                                                                                                                                                                                                                                                                                           34 GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGN------GADV-----
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Result
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Maximum DB seq length: 200000000
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Copyright (c) 1993 - 2004 Compugen Ltd.
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O33802 salmonella
C7x243 citrobacter
C7x240 citrobacter
C8cw63 escherichia
C7x237 enterobacte
C954069 salmonella
C98ih3 shewanella
C98ij5 escherichia
C98ij3 bredyrhizob
C89ji4 bradyrhizob
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C7ucz1 shigella fl
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12.3	12.3	12.3	12.3	12.4	12.4	12.4	12.4	12.4	12.4	12.6	12.6	12.6	12.7	12.7	12.7	12.7	12.7	12.8	12.8	12.8	12.9	12.9	13.0	13.0	13.2	13.2	13.2	13.3
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Q8tgel saccharomyc	Q8t4e0 drosophila	ш		O22638 zea mays (m	Q7x238 enterobacte	Q9vm71 drosophila		Q89ji5 bradyrhizob		Q9syz5 arabidopsis		Q8cmj0 shewanella				Q7x4s5 pseudomonas	Q9s3j8 escherichia		Q8niv1 neurospora	O93397 cyprinus ca	O87327 pseudomonas	Q89d03 bradyrhizob	Q92uu8 rhizobium m		Q7uwz8 rhodopirell	Q94821 tetrahymena	Q8awa8 lampetra fl	Q8efu3 shewanella

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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151	61 SDARKSETTITOSGYGNGADVGOGADNSTIBLTONGFRNNATYDOLVTRVVTHEMAHAGG 120	1 MKLLKVAAFAAIVVSGSAVAGVVPQWGGGGHHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	Query Match 87.5%; Score 672; DB 2; Length 152; Best Local Similarity 89.4%; Pred. No. 3e-46; Matches 135; Conservative 3; Mismatches 13; Indels 0; Gaps 0;	SEQUENCE 152 AA; 15401 MW; 9DA7DADC2364B006 CRC64;	NON_TER 152	EMBL; AJ000514;		odimonetia cyphimulium Sx-ii with modse small litestimat epitheliai Cells.":	"Expression of chin, aggregative rimbride prom	Normark S.J., Rhen M.;		MEDLINE=98053981; PubMed=9393832;	SEQUENCE FROM N.A.	[1]	NCBI TaxID=602;	Enterobacteriaceae; Salmon	Bacteria;	Salmonella typhimurium.		AqfA protein (Fragment).	01-DEC-2001 (TrEMBLrel. 19, Last	01-JAN-1998 (TrEMBLrel. 05,		033802;	033802 PRELIMINARY: PRT: 152 AA	RESULT 1

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01-OCT-2003
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                                                                                                                                             Zogaj X., Bokranz W., Nimtz M., Romling U.; Production of Cellulose and Curli Fimbriae Enterobacteriaceae Isolated from the Human G Infect. Immun. 72:4151-4158 (2003).

EMBL; AJ515701; CAD56675.1; -. SEQUENCE 149 AA; 15260 MW; 946DD52017F64
                                                                                                                                                                                                                                                                                                                                   Citrobacter freundii.
Citrobacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
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Q7X243;
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NCBI_TaxID=213763;
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Bacteria; Proteobacteria;
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Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete ge
of uropathogenic ascherichia coli.",
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Enterobacter.
                                                                                                                                                                                                                     Enterobacter sakazakii.
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                                                                                                                  NCBI_TaxID=28141;
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MEDLINE=22388234; PubMed=12471157;
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EMBL; AJ515702; CAD56678 1; -.
                   Shewanella oneidensis.
Bacteria; Proteobacteria;
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Enterobacteriaceae; Salmonella.
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RESULT 8
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Q9S3J5;
01-MAY-2000
01-MAY-2000
01-MAR-2001
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Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C. Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Seshat J., Beanan M., Brinkac L., Daugherty S., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vanathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Meller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Wigenome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis.";
Nat. Biotechnol. 20:1118-1123(2002).
                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2001 (TrEMBLrel. 16,
Curlin subunit monomer (Frag
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"Non-curliation of Escherichia coli 078:K80 isolates associated IS1 inserti on in csgB and reduced persistence in poultry infect FEMS Microbiol. Lett. 175:247-253(1999).

EMBL; AJ131756; CAB45380.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Complete proteome. SEQUENCE 502 AA; 52441 MW; D08CA23D6C46B62D CRC64;
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TIGR;
                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                     Escherichia coli
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EMBL; AE015532; AAN53941.1;
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                                                                                                                                                                                                                                                                           Enterobacteriaceae;
                                                                                                                                                                                                                                                                                          Bacteria;
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                                                     26;
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                                                                                                                                                                                                                                                                                          Proteobacteria;
                                                                                                         29 AA; 2789 MW;
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27.0%;
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RESULT 10
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O89JI3;
01-JUN-2003 (TrEMBLrel. 2:
01-JUN-2003 (TrEMBLrel. 2:
01-JUN-2003 (TrEMBLrel. 2:
  Complete
SEQUENCE
                                       Bradyrhizobium japonicum USDA1
DNA Res. 9:189-197(2002).
EMBL; AP005954; BAC50565.1; -
                                                                                                                                                                      Kaneko T., Nakamura Y., Sasamoto S., Watanabe A.,
                                                                                                                                                        Kohara
                                                                                                                                                                                                                      MEDLINE=22484998; PubMed=12597275;
                                                                                                                                                                                                                                                  STRAIN=USDA 110;
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                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
Bradyrhizobiaceae; Bradyrh
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Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Mard N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., "Genome sequence of the dissimilatory metal ion-reducing bacterium characterium and the sequence of the dissimilatory metal ion-reducing bacterium
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Alteromonadaceae; Shewanel
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  Shigella f
Bacteria;
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         Minor curlin subu
CSGB OR S1108.
Shigella flexneri
                                                                                                                                                                                                                                                                                                                                 "Complete genomic sequence of nitrogen-fixing Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bradyrhizobiaceae; Bradyrhizobium.

MCBI __TaxID=375;
                                                                                                                                                                                                                                                                                                      SEQUENCE
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., I
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M.
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H.,
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  Proteobacteria;
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4; Mismatches
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., Wada T., Yar
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STRAIN-66:H1 / CFT073 / ATCC 700928;

WBDLINE=22388234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mossic structure revealed by the complete genome sequen

of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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MEDLINE=22590274; PubMed=12704152;
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darl
Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou
Schwartz D.C., Blattner F.R.;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
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NCBI_TaxID=217992;
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01-JUN-2003
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                                                                                                                                                                                                                              Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes I Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J., Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I., Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A., Utterback T., Rizzo M., Lee K., Kosack D., Moestel D., Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S., Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
InterPro; IPR000437; Prok_lipoprot_S. PROSITE; PS00013; PROKAR_LIPOPROTEIN; Complete proteome.
SEQUENCE 157 AA; 16175 MW: C385R48
                                                                                                                                        "Complete genome sequence and comparative metabolically versatile Pseudomonas putida Environ. Microbiol. 4:799-808(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang Yang J., Yang G., Wu H., Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wer
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Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22423060; PubMed=12534463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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STRAIN=301 / Serotype 2a;
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                                                                                                                  EMBL; AE016786; AAN69002.1;
                                                                                                                                                                                                               Fraser C.M.;
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                                                                                               TIGR; PP3398;
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through comparison with genomes of Escherichia coli K12
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Ding K., Chen S.,
Wen Y., Hou Y.,
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                March 11, 2004, 18:33:51; Search time 171.3 Seconds (without alignments) 860.386 Million cell updates/sec
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1: /cgn2_6/ptodata/2/paa/PCTU:
2: /cgn2_6/ptodata/2/paa/US06
3: /cgn2_6/ptodata/2/paa/US07
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ALIGNMENTS

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US-09-543-407-12

US-09-543-407-12

; Sequence 12, Application US/09543407
; GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
; CURRENT FILING DATE: 2000-04-05
; CURRENT FILING DATE: 2000-04-05
; CURRENT FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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Regult No.

Score

Query Match Length

DB ID

Description

SUMMARIES

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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
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US-09-543-407-14
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                                                                                                                   Sequence 5, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
                APPLICANT: Collinson, S. Karen APPLICANT: Kay, William W. APPLICANT: Kay, William W. TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS FILE REFERENCE: 920043.406
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CURRENT APPLICATION NUMBER: US/09/543,407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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TYPE: PRT
ORGANISM: Artificial Sequence
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Local Similarity 87.6%;
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Pred. No. 2e-65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 57, Application
Query Match
Best Local Similarity
Matches 135; Conserv
                                                                                                                          TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
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SOFTWARE: FastSEQ for
SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
COUNTRY: U.S.A.
ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
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                                                                                                  TYPE: amin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
                                                                                                                                                                                                                                                                  NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 92
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                88.6%;
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Windows Version 4.0
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                                                                                                                                                                                                                                                                  920043.403C3
                Score 690; DB 6; Length 151; Pred. No. 8.6e-65;
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Pred. No. 2.5e-65;
4; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                         Version
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Conservative

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Mismatches

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Gaps

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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 151
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US-09-543-407-24
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
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Best Local :
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APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
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APPLICANT: Doran, James 1
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ORGANISM: Artificial Sequence
FEATURE:
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Collinson, S. Karen
Kay, William W.
                                                                                                                                                                                                                                                                      Application US/09543407
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Pred. No. 4.6e-61;
0; Mismatches (
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RESULT 8 US-09-543-407-20

Sequence 20, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Asron P.
APPLICANT: Doran, James L.

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SEQ ID NO 18
LENCTH: 151
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local :
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Best Local Similarity
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OTHER INFORMATION: FOTHER INFORMATION
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APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                               SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                  NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
NNAALVNOTASDSSVMVRQVGFGNNATANQY
                                                                                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                        MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragmen encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 613; DB 19;
Pred. No. 1.4e-56;
7; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 614;
Pred. No. 1
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.1e-56;
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CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 31
                                                                                                                                                                                                                 Best Local Similarity Matches 116; Conserv
                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 122; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: White, Aaron P. APPLICANT: Doran, James L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
OTHER INFORMATION:
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ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT: Collinson, S. Karen
PPLICANT: Kay, William W.
TILE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
ITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                ENGTH: 131
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                                    141
121 GEGNNATANOY 131
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                                                                                                                                                             GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                                AHANNATANOY 151
                                                                                        VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNYDQLVTRVVTHEM 140
                                                                                                                                        GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNAALVNOTASDSSVMVROVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNAALVNYDOLVTRVVTHEMAHANNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09543407
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                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence containing the replacement fragmer encoding PT3 from GP63 of Leishmania major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant Salmonella enteritidis 3b afgA
                                                                                                                                                                                                                                 78.0%;
88.5%;
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80.8%;
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                                                                                                                                                                                                               Score 608; DB 19;
Pred. No. 3.9e-56;
4; Mismatches 11;
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Pred. No. 2.2e-56;
7; Mismatches 22;
                                                                 TVGQYGGNNAALVNQTASDSSVMVRQV
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                                                                                                                                                                                                                                                  Length 131;
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                                                                 120
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APPLICANT: DOTAI, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILTE REFERENCE: 92004.406
FILE REFERENCE: 92004.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 151
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                        ; FEATURE:
; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA;
; OTHER INFORMATION: sequence containing the replacement fragment;
; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
US-09-543-407-22
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                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 22 LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
                         Query Match
Best Local Similarity
           Matches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L
                                                                                                                                                                                                                                                                                                     APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT FILING DATE: 2000-04-05
CURRENT FILING DATE: 2000-04-05
RUMBER OF SEQ ID NOS: 59
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Best Local Similarity
                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
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                           77.5%;
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  Score 604; DB
Pred. No. 1.2e
6; Mismatches
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Pred. No. 9.8e-56;
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    DB 19;
L.2e-55;
les 23;
                                           Length 151;
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      Indels
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Gaps
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60

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CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 30
                                          SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 16 LENGTH: 151
                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/09543407 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 122;
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Best Local :
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                                                                                                                   APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043-406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: KAY, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
                                                                                                  NUMBER OF SEQ ID NOS: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGHNNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 603; DB 19;
Pred. No. 1.6e-55;
6; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                              151
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                                                                                           ; MOLECULE TYPE: protein US-08-233-642A-55
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Query Match
Best Local Similarity 100.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 55, Application US/08233642A
GENERAL INFORMATION:
APPLICANT: Kay, William W.
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 121; Conservative
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Best Local Similarity
                                                                                                                                                                                                                TELEX: 3723836 SEEDANBERRY INFORMATION FOR SEQ ID NO: 55:
                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION UNMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642A
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
NUMBER OF SEQUENCES: -
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONBILLATITLE OF INVENTION: BASED VACCINES
                                                                                                                              LENGTH: 120 amino acida
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6300 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Washington COUNTRY: U.S.A. ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay, William W.
Collinson, S. Karen
Clouthier, Sharon C.
Doran, James L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6300 Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seed and Berry
          71.9%; Score 560; DB 6; Length 120 100.0%; Pred. No. 4.5e-51; vative 0; Mismatches 0; Indels
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80.1%;
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Pred. No. 4.5e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
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            Gaps
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22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV

81

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GEQUENCE 7, Application US/09543407

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION UNMERSE: US/09/543,407
UNMBER OF SEQ ID NOS: 59
SOFTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 151
TYPE: PRT
ORGANISM: Escherichia coli
US-09-543-407-7
Search completed: March 11, 2004, 19:13:09 Job time : 172.3 secs
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US-09-543-407-7
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                                                                                                                                                                                                                                                              Query Match 66.8%; Score 520; DB 19; Length 151; Best Local Similarity 66.9%; Pred. No. 1.1e-46; Matches 101; Conservative 21; Mismatches 29; Indels
                                                                                       121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                121
                                                                                                                          82 GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 127
                                                                                                                                                                                          1 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 60
                                                            GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                                                                                                                                        0;
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Fri Mar 12 09:41:49 2004

GenCore
Copyright (c) 1993

OM protein - protein search, using st
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2004, 18:35:05; Search time 5.3 Seconds (without alignments) 376.014 Million cell updates/sec

Title: US-09-543-407-12
Perfect score: 779
Sequence: 1 MKLLKVAAFAAIVVSGSALA......VTRVVTHEMAHANNATANQY 151
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 125546 seqs, 13197846 residues
Total number of hits satisfying chosen parameters: 125546
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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Pending_Patents_AA_New:*

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4: /cgn2_6/ptodata/1/paa//US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa//US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa//US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa//US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	Çī	4	ω	2	_	Regult No.
71.5	71.5	72	72.5	73	73	74	74	74.5	75	75	75	76	76	76	77	78.5	81.5	82	82	85	90.5	91.5	92	439	517	Score
9.2	9.2	9.2	9.3	9.4	9.4	9.5	9.5	9.6	9.6	9.6	•	9.8	9.8	9.8	9.9	10.1	10.5	10.5	10.5	10.9	11.6	11.7	11.8	56.4	66.4	Query
251	179	434	318	246	205	250	191	1160	533	424	399	382	321	250	351	430	1871	386	386	956	234	443	1327	131	151	Length
9	σ	თ	σ	σ	σ	0	σ	σ	6	0	_	σ	_	σ	۲	σ	۲	σ	9	σ	σ	σ	۲	v	G	B
US-10-767-701-32417	US-10-767-701-42696	US-10-045-674A-594	US-10-417-884A-5818	US-10-779-461-41	US-10-767-701-40104	US-10-779-461-6	US-10-767-701-47075	US-10-603-150-2	US-10-045-674A-527	US-10-045-674A-591	PCT-US04-05654-2748	US-10-771-241-299	PCT-US04-05654-590	US-10-779-461-40	PCT-US04-05654-1755	US-10-451-467A-314	PCT-US03-02038-26	US-10-100-683-10327	US-10-100-683-10326	US-10-093-037A-63	US-10-767-701-45603	US-10-100-683-7608	PCT-US04-02338-49	US-09-741-873C-2	US-09-741-873C-4	ID
Sequence 32417, A	Sequence 42696, A	Sequence 594, App	Sequence 5818, Ap	Sequence 41, Appl	4	Sequence 6, Appli	47	Sequence 2, Appli	52	Sequence 591, App		Sequence 299, App	590,	Sequence 40, Appl	1755	314,	Sequence 26, Appl	Sequence 10327, A		Sequence 63, Appl	45603,	760	Sequence 49, Appl	e 2,	Sequence 4, Appli	Description

71.5 9.2 471 6 US-10-746-795A-22 71 9.1 125 6 US-10-767-701-58970 71 9.1 310 6 US-10-695-499-192 71 9.1 310 6 US-10-695-499-192 71 9.1 310 6 US-10-695-499-192 71 9.1 319 6 US-10-695-499-70 71 9.1 364 1 PCT-US04-05554-7756 70.5 9.1 273 6 US-10-627-556-392 70.5 9.1 273 6 US-10-627-556-392 70.5 9.1 353 6 US-10-627-556-396 70.5 9.1 505 6 US-10-627-556-402 70.5 9.1 505 6 US-10-627-556-398 70.5 9.1 505 6 US-10-627-556-398 70.5 9.1 505 6 US-10-627-556-398 70.5 9.1 505 6 US-10-627-556-398 70.5 9.1 505 6 US-10-627-556-398 70.5 9.1 1048 1 PCT-US04-05654-2086 70 9.0 179 6 US-10-767-701-35046 70 9.0 179 6 US-10-767-701-5183 70 9.0 199 6 US-10-767-701-5183	1	44	43	42	41	_		_		36 7			33	32	31	30	29	28	27 7
1471 3125 3125 3126 3126 3126 3126 3126 3126 3126 3126	70	70	70	70	70	0.5	0.5	0.5	0.5	0.5	0.5	0.5	71	71	71	71	71	71	1.5
H	9.0	9.0	9.0	9.0	9.0	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.2
6 US-10-746-795A-22 6 US-10-786-850-4 6 US-10-695-499-192 6 US-10-695-499-192 6 US-10-695-499-68 1 PCT-US04-05654-1756 6 US-10-695-499-70 6 US-10-695-499-70 6 US-10-627-556-396 6 US-10-627-556-396 6 US-10-627-556-396 6 US-10-627-556-398 1 PCT-US04-05654-2086 6 US-10-767-701-35342 6 US-10-767-701-35343 6 US-10-767-701-35343 6 US-10-779-461-59	574	245	199	179	175	1048	521	505	505	353	273	273	619	364	319	310	310	125	471
US-10-746-795A-22 US-10-766-701-58970 US-10-695-499-192 US-10-695-499-192 US-10-695-499-68 PCT-US04-05654-1756 US-10-627-556-392 US-10-627-556-396 US-10-627-556-400 US-10-627-556-400 US-10-627-556-400 US-10-627-556-400 US-10-627-556-400 US-10-627-556-400 US-10-627-556-400 US-10-627-556-400 US-10-627-556-398 PCT-US04-05654-2086 US-10-767-701-35342 US-10-767-701-51583 US-10-767-701-51583	_	6	σ	0	σ	_	ð	9	σ	σ	9	σ	σ	1	σ	σ	σ	σ	σ
	PCT-US04-05654-334	JS-10-779-461-59	JS-10-767-701-51583	JS-10-767-701-35342	JS-10-767-701-35046	PCT-US04-05654-2086	JS-10-627-556-398	JS-10-627-556-402	JS-10-627-556-400	JS-10-767-701-45455	JS-10-627-556-396	JS-10-627-556-392	JS-10-695-499-70	PCT-US04-05654-1756	JS-10-695-499-68	JS-10-695-499-192	JS-10-786-850-4	JS-10-767-701-58970	JS-10-746-795A-22
	334, App	59, Appl	51583, A	35342, A	35046, A	2086, Ap		402, App	400, App	45455, A	396, App	392, App	70, Appl	1756, Ap	68, Appl	192, App	4, Appli	58970, A	22, Appl

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR FILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR PILING DATE: 1994-10-05
PRIOR PILING DATE: 1994-10-05
PRIOR PILING DATE: 1994-10-05
PRIOR PILING DATE: 1994-10-05
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                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 4
                                                                                                                                                                                                                                                                       Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 151
TYPE: PRT
ORGANISM: Escherichia coli
121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                          121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                   Conservative
                                                                                                                                                                                                                                                                    66.4%; Score 517; DB 5; Length 151; 66.2%; Pred. No. 1.2e-38; Live 22; Mismatches 29; Indels
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PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR PRILING DATE: 1998-05-06
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1989-05-04
PRIOR FILING DATE: 1989-05-04
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
                    NUMBER OF SOFTWARE:
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Best Local Similarity
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SEQ ID NO 2
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                                                           PRIOR APPLICATION NUMBER: US60/461,789
PRIOR FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US60/470,684
PRIOR FILING DATE: 2003-05-14
PRIOR APPLICATION NUMBER: US60/479,650
PRIOR FILING DATE: 2003-06-19
                                                                                                                                                                                                                         TITLE OF INVENTION: MARCAXS AS MODIFIERS OF THE APC AND AXIN PATHWAYS AND METHODS TITLE OF INVENTION: USE FILE REFERENCE: EXO4-003C-PC CURRENT APPLICATION NUMBER: PCT/US04/02338 CURRENT FILING DATE: 2004-01-28 PRIOR APPLICATION NUMBER: US60/443,484 PRIOR APPLICATION NUMBER: US60/443,484 PRIOR FILING DATE: 2003-01-29
                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US60/447,358 PRIOR FILING DATE: 2003-02-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Escherichia coli
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NO 49
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APPLICATION NUMBER: US 08/187,865
FILING DATE: 1994-01-28
APPLICATION NUMBER: US 08/318,519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82;
                  PatentIn
                                         SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTTTQHGGGNGAD
                                                                                                                                                                                                                                                                                                                                                                                          EXELIXIS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
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                    version 3.2
                                                         2003-06-19
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Pred. No. 6.9e-32;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-100-683-7608
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US-10-100-683-7608
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; ORGANISM: Hom-
PCT-US04-02338-49
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Best Local Similarity
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Best Local S
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SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: US 60/043,576
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CURRENT FILING DATE: 2002-03-19
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OR FILING DATE: 1997-04-11
OR APPLICATION NUMBER: US 60/047,601
OR FILING DATE: 1997-05-23
OR APPLICATION NUMBER: US 60/056,845
OR FILING DATE: 1997-08-22
OR APPLICATION NUMBER: US 60/043,580
OR FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/047,599
FILING DATE: 1997-05-23
APPLICATION NUMBER: US 60/056,664
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US
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FILING DATE: 1997-04-11
APPLICATION NUMBER: US 60/047,632
 298
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                                   115 VGQYGGN 121
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                                                                                                        76 GNGAD---VGQGADNSTIELTQNGFRNNATI-----
                                                                                                                                                                                 21 GVVPQ---WGGGGNHNGGGNSSGPDSTLSIYQ--YGSANAALALQSDARKSETTITQSGY 75
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35; Conserv
SGNHGGS 304
                                                                      GGGSSNSGGGSGSQSGSSGSSGSNGDNNNGSSSGGSGGSGGSRGDSGSESSWNGSSTGSS
                                                                                                                                             GMNPQGAPWGQGG---NGGPPNFGTNTQGAVAQPGYGSVRA----SNQNEGCTNPPPSGS
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30.4%; Pred. No. 2
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                                                                                                                                                                                                                                                          Length 443;
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                                                                                                          ---DOWNAKNSDIT 114
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US-10-767-701-45603
                                                                              US-10-093-037A-63
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CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 45603
                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                              TITLE OF INVENTION: ENZYMES HAVING GLYCOSIDASE ACTIVITY AND METHODS OF USE THEREOF FILE REFERENCE: 564462001402
CURRENT APPLICATION NUMBER: US/10/093,037A
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: US 09/910,579
PRIOR FILING DATE: 2001-07-20
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 09/134,078
PRIOR APPLICATION NUMBER: US 09/134,078
PRIOR PILING DATE: 1999-08-13
PRIOR PILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: US 08/949,026
PRIOR APPLICATION NUMBER: US 08/949,026
PRIOR FILING DATE: 1997-10-10
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kovalic, APPLICANT: Zhou, Y APPLICANT: Cao, Yo
                                                                                                                                                                                                        PRIOR FILING DATE: 1996-12-06
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                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                              TYPE: PRT
ORGANISM: Bankia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Sorghum bicolor
PEATURE:
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OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                  ENGTH:
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  Local Similarity 21.5
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39; Conservative
                                                                                                                                                                          FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Swanson, Ronald V. Mathur, Eric J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lam, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bylina, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/10767701
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                  10.9%;
    19;
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Score 85; DB
Pred. No. 6.8;
19; Mismatches
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Pred. No. 0.4;
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                  DB 6; Length 956; 6.8;
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    68;
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                                                                                                                                             RESULT
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Sequence 10327, Application US/10100683
GENERAL INFORMATION:
APPLICANT: Rosen, et al.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS900
CURRENT APPLICATION NUMBER: US/10/100,683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 10326
LENGTH: 386
TYPE: PRT
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PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: US 60/047,601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/040,162
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                                                                                                                                                                                                                                                                                                                                                            Local 5.
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APPLICATION NUMBER: US 60/043,314
FILING DATE: 1997-04-11
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                                                                                                                                                                                                                                            76 GNGAD----VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNN 122
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Pred. No.
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PCT-US03-02038-26
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application PC/TUS0302038
GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education and Research
TITLE OF INVENTION: Polycystic Kidney Disease Nucleic Acids
TITLE OF INVENTION: and Proteins
FILE REFERENCE: 07039/386W01
CURRENT APPLICATION NUMBER: PCT/US03/02038
CURRENT FILING DATE: 2003-01-23
PRIOR APPLICATION NUMBER: 60/351,110
PRIOR PILING DATE: 2002-01-23
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                    ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                         ENGTH: 1871
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ORGANISM: Homo sapiens
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FILING DATE: 1997-04-11
APPLICATION NUMBER: US 60/047,632
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: US 60/056,845
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 GGGSSNSGGGSGSQSGSSGSSNGDNNNGSSSGGSSSGSS-SGGSSGGSS 286
86 DNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNVDQLVTRVVTHEMAHANN 145
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                                                                                                                                         l Similarity
28; Conserv
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Similarity 29.1%;
                                                      WCAADSHKGSSETI-PKVTEVIRKYGSINGATRL-----TIKGEGFSQASQFNYGA
                                                                                           WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGA
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Pred. No. 31;
13; Mismatches
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Pred. No.
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PCT-US04-05654-1755
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US-10-451-467A-314
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GENERAL INFORMATI
                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Sherman, Bradley K

APPLICANT: Diachmann, Jose Luis
                 REPLICANT: Kumimoto, Roderick W
APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYNCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
                                                                                                                             APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: EP 01870002.1 PRIOR FILING DATE: 2001-01-04 PRIOR APPLICATION NUMBER: EP 01870003.9 PRIOR FILING DATE: 2001-01-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/451,467A CURRENT FILING DATE: 2003-06-19
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APPLICANT: REEKMANS, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG
TITLE OF INVENTION: YEAST AND FUNGI
FILE REFERENCE: JAB-1667
                                                                                                                                               PPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 43
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 STIELTONGFRNNATIDOWNAKNSDITVGOYGGNN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 GSNNNDSYGSNNNDS-----YGSNNNDSYGSNNDDSYGSSNKKKSSYGSNNDDSYGSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 GGNHNGGGNSSGPDSTLSIYQYGS-ANAALALQSDARKSETTITQSGYGNGADVGQGADN 87
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                                                                                     Gutterson, Neal
Yu, Guo-Liang
Broun, Pierre E
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                                                                                                                                             Century, Karen
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Jiang, Cai-Zhong
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                                                                                                                                                                                                  l III, Arnold N
                                                                                                                                                                                                                                                         Luc J
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PCT/US04/05654
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CURRENT FILING DATE:

2004-03-03

1.67

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PRIOR APPLICATION NUMBER: 10/374,780
PRIOR FILING DATE: 2003-02-25
PRIOR PPLICATION NUMBER: 10/675,852
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 2950
SOFTMARE: PATENTIN VERSION 3.2
SEQ ID NO 1755
LENGTH: 351
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                                                                                             Sequence 590, Application PC/TUS0405654
GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/779,461
CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 60/447,073
PRIOR FILING DATE: 2003-02-13
NUMBER OF SEQ ID NOS: 161
SOPTWARE: Patentin version 3.2
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 40, Application US/10779461 GENERAL INFORMATION:
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Best Local
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TITLE OF INVENTION: ANTIBODIES TO C-MET FOR
FILE REFERENCE: 00980/1
                                                APPLICANT:
                                                                  APPLICANT:
                                                                                 APPLICANT:
                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: artificial FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: phage display generated human antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 250
                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 SALAGVVPQWGGGGNHNGGG----NSSGPDSTLSIYQYGSANAALALQSDARKSETTITQ
                                                                                                                                                                                                                                                       60 QSDARKSE-TTITQSGYGNGADVGQ 83
                                                                                                                                                                                                                                                                                                                           9 FAAIVVSGSALAGVVPQWG------GGGNHNGGGNSSGPDSTLSIYQYGSANAALAL 59
                                                                                                                                                                                                                                                                                       YCAISPLRGLTADVFDVWGQGTLVTVSSGGGGSGGGGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SALARVVAGGGGGGGGDGDQWAWSSPSPSSS-----AAAAAARGVQERRREEQAMHEL
                         Jiang, Cai-Zhong
Heard, Jacqueline E
Haake, Volker
Creelman, Robert A
Ratcliffe, Oliver
                                                                                  Riechmann,
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Pred. No. 10;
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Pred. No. 8.
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LENGTH: 321
                                                                       Matches
                                                                                      Best Local Similarity
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Best Local Similarity
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CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374,780
PRIOR FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 10/675,852
PRIOR APPLICATION NUMBER: 10/675,852
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 2950
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                LENGTH: 382
TYPE: PRT
ORGANISM: E.
                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/492,709
PRIOR PILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
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SOFTWARE: FastSEQ for
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APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
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ORGANISM: Oryza sativa
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 158 GNTHGGNTSSGTSGYSSLNYRGAYGNTNVGYSRSGDS--SQIYYGMSGGIIAHADGITFG
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                                  30 GNHNGGGNSSGPDSTLSI-YQ--YGSANAALALQSDARKSETTITQSG----YGNGADVG 82
                                                                       38;
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                                                                                                                                                                                                    382
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Repetti, Peter
Century, Karen
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Keddie, James
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                                                                       Conservative
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27.7%; Pred
176 13;
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                                                                                        Score 76;
Pred. No.
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Pred. No. 11;
                                                                         Mismatches
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                                                                                                          DB 6; Length 382
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                                                                       Gaps
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APPLICANT: Pineda, Umalia
APPLICANT: Repetti, Peter
APPLICANT: Century, Karen
APPLICANT: Gutterson, Neal
APPLICANT: Gutterson, Neal
APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
APPLICANT: Wimimoto, Roderick W
APPLICANT: Neigrim, Marsha L
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT APPLICATION NUMBER: 10/374,780
PRIOR APPLICATION NUMBER: 10/374,780
PRIOR FILING DATE: 2003-02-25
PRIOR PPLICATION NUMBER: 10/675,852
PRIOR PPLICATION NUMBER: 10/675,852
PRIOR PILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 2950
SOFTWARE: Patentin version 3.2
SEQ ID NO 2748
LENGTH: 399
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: G1882
PCT-US04-05654-2748
9.6%; Score 75; DB 1; Length 399;
Search completed: March 11, 2004, 19:14:15 Job time : 6.3 secs
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PCT-US04-05654-2748
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APPLICANT: Sherman, Bradley K
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APPLICANT:
APPLICANT:
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                                                                             215 NSNNNNILGLGSSLPPLKLMPPLDFTDNFTLQYGAVSAPSYHIGGGSSGGAAALLNGFDQ 274
                                                                                                                                                                    155 GGGGGSTSSGNSKSQDSATSNDQYHHRAMANNQMGPPSSSSSLSSLLSSYNAGLIPGHDH 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 ADNVELDETVVTVIPTH 286
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                                                                                                                       77 --- NGADVGQGADNSTIBLTQN-GFRNNATIDQW--NAKNSDITVGQYGGNNAALVNYDQ 130
                                                                                                                                                                                                                 27 GGGGNHNGGGNSSGPDSTLSIYQY---GSANAALALQSDARKSETTITQSGYG----- 76
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Jiang, Cai-Zhong
Heard, Jacqueline E
Haake, Volker
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Keddie, James
Dubell III, Arnold N
Pineda, Omaira
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Listing first 45 summaries
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3: /cgn2 6/ptodata/2/paa/US080_C

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29: /cgn2 6/ptodata/2/paa/US00_C

31: /cgn2 6/ptodata/2/paa/US00_C

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/ cgn2_6/ptodata/2/paa/US01_COMB.pep:*
/ cgn2_6/ptodata/2/paa/US01_COMB.pep:*
/ cgn2_6/ptodata/2/paa/US081_COMB.pep:*
/ cgn2_6/ptodata/2/paa/US081_COMB.pep:*
/ cgn2_6/ptodata/2/paa/US082_COMB.pep:*
/ cgn2_6/ptodata/2/paa/US084_COMB.pep:*
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/ cgn2_6/ptodata/2/paa/US085_COMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd
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-60-324-109-305 -10-424-599-245 -10-282-122A-49 -09-678-411-8 -09-678-411-10	US-09-543-407-12 US-09-543-407-15 US-09-543-407-26 US-09-543-407-26 US-09-543-407-26 US-09-543-407-20 US-09-543-407-20 US-09-543-407-20 US-09-543-407-20 US-09-543-407-7 US-09-543-407-7 US-09-543-407-7 US-08-978-878-4 US-09-741-873B-4 US-09-252-691-8334 US-09-252-691-8334 US-09-543-407-37 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543	S-09-543-407-1
e 30520, e 245046, e 49412, e 8, Appl e 10, App	sequence 24, Appli Sequence 57, Appli Sequence 57, Appli Sequence 57, Appli Sequence 26, Appli Sequence 26, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 22, Appli Sequence 22, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 34, Appli Sequence 34, Appli Sequence 2, Appli Sequence 5834, Appl Sequence 5834, Appl Sequence 2, Appli Sequence 2, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 383, App Sequence 383, App Sequence 583421, App Sequence 583421, App Seq	equence 14,

ALIGNMENTS

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RESULT 1

US-09-543-407-14

Sequence 14, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Ray, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENVATION OF HETEROLOGOUS PEPTIDE SEQUENCES

FILE REFERENCE: 20043-406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14

LENGTH: 151

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA

OTHER INFORMATION: sequence containing the replacement fragment

OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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Regult No.

Score

Query Match Length DB

IJ

Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 24, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

APPLICANT: Kay, William W.

APPLICANT: Kay, William W.

APPLICANT: Kay, William W.

APPLICANT: HOST OF HETEROLOGOUS PER

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER

TITLE OF INVENTION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 24

LENGTH: 151

TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-24
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US-09-543-407-12
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            Sequence 12, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REPERENCE: 920043.406
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Best Local Similarity
Matches 151; Conserv
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Best Local Similarity
CURRENT APPLICATION NUMBER: US/09/543,407
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNNNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PRIFILE REFERENCE: 920043.406
CURRENT APPLICATION UNMEER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 151
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NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12
LENGTH: 151
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GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                     121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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121 NNAALVNOTASDSSVMVROVGFGNNATANOY
                                                                                         61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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                                                                                                                                                          SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQ---
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                                                                 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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Pred. No. 2.1e-66;
                                                                                                                                                                                                        Score 693; DB 19;
Pred. No. 4.4e-66;
3; Mismatches 11;
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     151
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RESULT 5
US-08-233-642A-57
; Sequence 57, Application US/08233642A
; GENERAL INFORMATION:
; APPLICANT: Kay, William W.

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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043, 406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 151
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US-09-543-407-30
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Matches
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642A
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920043.403C:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
TELEX: 3723836 SEEDAMBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Cen
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APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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STATE: Washington
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                 121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                        121 NNPALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tch 89.3%; al Similarity 90.7%; 137; Conservative
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Pred. No. 5.6e-66;
3; Mismatches 11;
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                                                                                                                                                 PEPTIDE
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                                                                                                                                                 SEQUENCES
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RESULT 8 US-09-543-407-18

Sequence 18, Application US/09543407 GENERAL INFORMATION: APPLICANT: White, Aaron P. APPLICANT: Doran, James L.

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; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-26
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                                                                                                                                                                                                               Query Match
Best Local S
Matches 123
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LENGTH: 151
TYPE: PRT
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Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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ORGANISM: Artificial Sequence
FEATURE:
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                          121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY
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NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                           SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                              MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                                                                                MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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81.5%;
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                                                                                                                                                                                                                                  Score 612; DB 19;
Pred. No. 2.5e-57;
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Pred. No. 2.1e-62;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
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Best Local
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS FILE REFERENCE: 920043,406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                          OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 151
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                       Local Similarity
                                                                                                                                                                  123;
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                                                                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                           SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                             MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                    Conservative
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                                                                                                                                                                                   78.6%;
81.5%;
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81.5%;
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                                                                                                                                                              Score 609; DB 19;
Pred. No. 5.2e-57;
6; Mismatches 22;
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Pred. No. 3.2e-57;
6; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HETEROLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPTIDE SEQUENCES
                                                                                                                                                                                                   Length 151;
                                                                                                                                                              Indels
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APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI

FILE REFERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 28

LENGTH: 151
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; APPLICANT: Kay, William W.
; APPLICANT: Kay, William W.
; TITLE OF INVENTION: BACCERIAL FIMBRIAL SYSTEM FOR
; TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
; FILE REFERENCE: 920043.406
; CURRENT APPLICATION UNMER: US/09/543,407
; CURRENT FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FRASTSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 131
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US-09-543-407-28
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US-09-543-407-31
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     Matches
                       Query Match
Best Local (
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Best Local
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                                                                                         OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                       Local Similarity
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     Conservative
                       77.8%;
80.8%;
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89.3%;
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     4.
 Score 603; DB 19;
Pred. No. 2.3e-56;
4; Mismatches 25
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Pred. No. 9e-57;
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   Indels
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MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60

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APPLICANT: White, Aaron P.
APPLICANT: CO11nson, S. Karen
APPLICANT: CO11nson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043_406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
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US-09-543-407-16
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CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 22
                                                                                                                                                                                                                                                                                            Sequence 16, Application US/09543407 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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TYPE: PRT
ORGANISM: Artificial
                                            ENGTH: 151
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81.5%;
      Sequence
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Pred. No. 3e-56;
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RESULT 15
US-08-978-878-4
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US-09-543-407-7
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                             Sequence 4, Application US/08978878
GENERAL INFORMATION:
APPLICANT: NORMARK, Staffan
APPLICANT: OLSEN, Arne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Best Local Similarity
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN FILE REFERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: SE 8801723-1
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM
TITLE OF INVENTION: PRESENTATION OF HETEROLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 151
TYPE: PRT
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OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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Pred. No. 2.9e-48;
0; Mismatches 27;
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Pred. No. 1.2e-53;
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EARLIER APPLICATION NUMBER: US 07/347,189
EARLIER FILING DATE: 1989-05-04
EARLIER APPLICATION NUMBER: US 07/789,437
EARLIER FILING DATE: 1991-11-06
EARLIER FILING DATE: 1991-11-06
EARLIER APPLICATION NUMBER: US 07/970,846
EARLIER APPLICATION NUMBER: US 08/187,865
EARLIER APPLICATION NUMBER: US 08/187,865
EARLIER APPLICATION NUMBER: US 08/318,519
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-00-05
EARLIER FILING DATE: 1994-00-05
EARLIER FILING DATE: 1995-06-28
EARLIER APPLICATION NUMBER: US 08/495,959
EARLIER FILING DATE: 1995-06-28
INUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTING DATE: 2.0
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Search completed: March 11, 2004, 19:13:10 Job time: 172.3 secs
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; ORGANISM: Escherichia coli
US-08-978-878-4
                                                                                                                                                                                                                                                                                                                                                                               Query Match 67.7%; Score 525; DB 13; Length 151; Best Local Similarity 68.2%; Pred. No. 6.1e-48; Matches 103; Conservative 21; Mismatches 27; Indels 0;
                                                                                           121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                            121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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// cgn2_6/ptcdata/1/paa/USO7_NEW_COMB.pep:*

// cgn2_6/ptcdata/1/paa/USO8_NEW_COMB.pep:*

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US-09-741-873C-2
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e 2086, Ap
e 58818, Ap
e 58870, A
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e 10327, Appl
s 40, Appl
s 40, Appl
s 40104, Ap
s 40104, Ap
s 40104, Ap
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s 40104, Appl
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68	83	68.5	69	69	70	70	70	70	70	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	71
8.8	8.8	8.8	8.9	8.9	9.0	9.0	9.0	9.0	9.0	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.2
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence
30, Appl	59665, A	314, App	1, Appli	6, Appli	1466, Ap	34, Appl	59, Appl	51583, A	35046, A	398, App	402, App	400, App	1755, Ap	396, App	392, App	32417, A	51685, A	45219, A

ALIGNMENTS

Sequence 4, Application US/09741873C GENERAL INFORMATION:

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APPLICANT: NOTWALLOW:
APPLICANT: Oleen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As
FILE REFERENCE: 012899-084
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/790,846
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-03
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
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Best Local Similarity
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TYPE: PRT
ORGANISM: Escherichia coli
121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                           121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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68.2%; Pred. No. 3e-40;
cive 21; Mismatches
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US-10-767-701-42696 US-10-603-150-2

Sequence Sequence

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CURRENT APPLICATION NUMBER: PCT/US04/0238
CURRENT FILING DATE: 2004-01-28
PRIOR APPLICATION NUMBER: US60/443,484
PRIOR FILING DATE: 2003-01-29
PRIOR PILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: US60/447,358
PRIOR FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US60/461,789
PRIOR FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US60/470,684
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US-09-741-873C-2
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 49, Application PC/TUS0402338 GENERAL INFORMATION: APPLICANT: EXELIXIS, INC.
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                                                            NUMBER OF SEQ ID NOS: 54
                                                                                  PRIOR APPLICATION NUMBER: US60/479,650 PRIOR FILING DATE: 2003-06-19
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Best Local Similarity
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                                                                                                                                PRIOR FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MAPCAXS AS MODIFIERS OF THE APC AND AXIN PATHWAYS AND METHODS TITLE OF INVENTION: USE
                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.0
EQ ID NO 2
LENGTH: 131
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TITLE OF INVENTION: Pibronectin Binding Protein
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
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FILING DATE: 1992-11-03
APPLICATION NUMBER: US 08/187,865
FILING DATE: 1994-01-28
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                                             PatentIn version 3.2
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; FEATURE:
; OTHER INFORMATION: G1152 Paralogous to G1146
PCT-US04-05654-2086
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                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 2950
SOFTWARE: PatentIn version
SEQ ID NO 2086
LENGTH: 1048
                                                                                                                                                                                                                                   Query Match
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Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 10/374,780 PRIOR FILING DATE: 2003-02-25 PRIOR APPLICATION NUMBER: 10/675,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: PCT/US04/05654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kumimoto, Roderick W
APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYMOCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLICANT:
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                                                                                                                                                                                                                     Local
214 TITPEVTSRGVNRAVMKQLV 233
                             121 LVTRVVTHEMAHASVMVRQV 140
                                                             154 EQLSVEQGAPSQAIQPIPSSSKAFKFPMRPGKGQSGKRCIVKANHFFAELPDKDLHHYDV 213
                                                                                                77 NGADVGQGADNSTIE--
                                                                                                                                                                27 GGGGNHNGGGNSSGPDSTLSI-----
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                                                                                                                                                                                                     36;
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                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35;
                                                                                                                                                                                                                                                                                                                                                                                     PatentIn version 3.2
                                                                                                                             GGYGGGRGGGPSSGPPQRQSVPELHQATSPTYQAVSSQPTLSEVSPTQVPEPTVLAQQF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yu, Guo-Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Broun, Pierre E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repetti, Peter
Century, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Creelman,
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                                                                                                                                                                                                   Conservative
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25.7%;
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                                                                                                                                                                                                                 Score 85.5;
Pred. No. 5.
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                                                                                           -LTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                            YOYGSANAALALOSDARKSETTITOSGYG 76
                                                                                                                                                                                                                          DB 1;
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                                                                                                                                                                                                                              Length 1048;
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MEDIUM TYPE: CD/ROM ISO9660

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US-10-100-683-7608
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Sequence 5818, Applitus
GENERAL INFORMATION:
GENERAL INFORMATION: A Doucette-Stamm
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
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GENERAL INFORMATION:
APPLICANT: Rosen, 6
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Human Secreted Proteins FILE REFERENCE: PS900 CURRENT APPLICATION NUMBER: US/10/100,683 CURRENT FILING DATE: 2002-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Remaining Prior Application data removed - See File Wrapper or PALM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: US 60/043,576
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APPLICATION NUMBER: US 60/047,601
FILING DATE: 1997-05-23
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APPLICATION NUMBER: US 60/047,632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-05-23
APPLICATION NUMBER: US 60/056,664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/047,599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/043,580 FILING DATE: 1997-04-11
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COMPUTER READABLE FORM:
                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                     298 SGNH 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 VGQY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 GGGSSNSGGGSGSGSGSGSGSNGDNNNGSSSGGSGGSGGSRGDSGSESSWNGSSTGSS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 GMNPQGAPWGQGG--NGGPPNFGTNTQGAVAQPGYGSVRA-----SNQNEGCTNPPPSGS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 GNGAD---VGQGADNSTIELTQNGFRNNATI--------DQWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GVVPQ---WGGGGNHNGGGNSSGPDSTLSIYQ--YGSANAALALQSDARKSETTITQSGY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31; Conservative
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                                                              STATE: Massachusetts
                                                                                   CITY: Waltham
                                                                                                             STREET:
                                         COUNTRY: USA
                                                                                                                             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/10100683
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                                                                                                           100 Beaver Street
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%; Pred. No. 7.9;
17; Mismatches
                                                                                                                                                                                               and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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NAME/KEY: misc feature;
LOCATION: (B) LOCATION 1...318;
SEQUENCE DESCRIPTION: SEQ ID NO: 5818:
US-10-417-884A-5818
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; OTHER INFORMATION: Clone ID: 6858533.pep
US-10-767-701-58970
                                                                                                                                                                        NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 58970
LENGTH: 125
TYPE: PRT
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                                                                                                                                                                                                                                                              TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(53535)B CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei
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                                                            NAME/KEY: unsure
LOCATION: (1)..(125)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                ORGANISM: Sorghum bicolor
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mes 30; Conserv
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LENGTH: 318 amino acids
TYPE: amino acid
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FILING DATE: 30-Jun-1998
APPLICATION UNMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/417,884A
FILING DATE: 17-Apr-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: YES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 S-TTASSAKVVAGGDLQDGTYKLEEKNYSNGYR---AVFEMVVKDGKITESKYDNV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 SETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQL 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489
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OPERATING SYSTEM: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                            David K.
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25.9%; Pred. No. 6.5;
:ive 14; Mismatches
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US-10-100-683-10326
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                                                                                                                                                                                                                                                                                            RESULT 9
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; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C82834_1.pep
US-10-767-701-45603
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                                                                                                                                                                                                                                   Sequence 10326, Application US/10100683 GENERAL INFORMATION:
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Best Local S
Matches 30
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SEQ ID NO 45603
                                               PRIOR APPLICATION NUMBER: US 60/043,576 PRIOR FILING DATE: 1997-04-11 PRIOR APPLICATION NUMBER: US 60/047,601
                                                                                                                                          APPLICANT: Rosen, et al.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: P8900
CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
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                                                                                                        PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR FILING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(535)B CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
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ORGANISM: Sorghum bicolor
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NAME/KEY: unsure
LOCATION: (1)...(234)
OTHER INFORMATION: unsure at all Xaa locations
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mes 37; Conserv
                                     FILING DATE:
               APPLICATION NUMBER: US 60/056,845
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1997-08-22
                                    1997-05-23
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25.9%; Pred. No.
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Pred. No. 5.4;
10; Mismatches
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US-10-100-683-10327
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US-10-100-683-10327
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                                                                                   SOFTWARE: PatentIn Ver. SEQ ID NO 10327
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10326
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Best Local (
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CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: US 60/043,576
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: US 60/047,601
                                                                                                                              Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 13468
                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/056,892
PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/047,632 PRIOR FILING DATE: 1997-05-23
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                ORGANISM: Homo sapiens
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                                                            LENGTH: 386
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APPLICATION NUMBER: US 60/056,664
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/043,580 FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                           FILING DATE: 1997-04-11
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FILING DATE: 1997-04-11
APPLICATION NUMBER: US 60/047,632
FILING DATE: 1997-05-23
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                                                                                                                                                                                                                                                                                                         LING DATE: 1997-08-22
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Pred. No. 10;
13; Mismatches
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; ORGANISM: Bankia gouldi
US-10-093-037A-63
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GENERAL INFORMATION:
APPLICANT: Jay M. Short
APPLICANT: Bylina, Edwar
APPLICANT: Swanson, Rona
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                                                                                                                                               Sequence 40, Application US/10779461
GENERAL INFORMATION:
APPLICANT: MORTON, Philip A
TITLE OF INVENTION: ANTIBODIES TO C-MET FOR
FILE REFERENCE: 00980/1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 63
CURRENT APPLICATION NUMBER: US/10/779,461
CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 60/447,073
PRIOR FILING DATE: 2003-02-13
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 40
LENGTH: 250
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Best Local Similarity
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PRIOR FILING DATE: 1996-12-06
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PRIOR APPLICATION NUMBER: US 08/949,026
PRIOR FILING DATE: 1997-10-10
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PRIOR FILLING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 09/134,078
PRIOR FILING DATE: 1998-08-13
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CURRENT APPLICATION NUMBER: US/10/093,037A
CURRENT FILING DATE: 2002-03-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/056,916
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                                                                                                                                                                                                                                                                                                                                                                                                                                     72 QSGYGNGADVGQGADNSTIEL--TQNGFRNNATI-------
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Swanson, Ronald V.
Mathur, Eric J.
Lam, David E.
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19.8%; Pred. No. 31;
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                                                                                                                                                                       THE TREATMENT OF CANCERS
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RESULT 13
US-10-771-241-299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FASTSEQ for Windows Version SEQ ID NO 299
LENGTH: 382
                                                                                                                                                                                                                 Sequence 47075, Application US/10767701 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 299, Application US/10771241 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 47075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/771,241
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION TITLE OF INVENTION: ESCHERICHIA COLIFILE REFERENCE: ELITRA.001C1
                                                                                                                                                                                           APPLICANT: Kovalic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zyskind, Judith APPLICANT: Forsyth, R. Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: artificial
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: phage display generated human antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      VGQYDQLVTRVVTHEMAHASVMVRQVG-----FGNNA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                 QPLGDTMVLVKAPGADNVKIE-NQTGIHTDWRGYAILPFATEYRENRV--ALNANSLADN 272
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                                                                                                                                                                                             David K.
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25.0%; Pred. No.
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Pred. No.
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FILE OF INVENTION: LIBRARIES

FILE REFERENCE: DYAX/002 CIP2

CURRENT APPLICATION NUMBER: US/10/045,674A

CURRENT FILING DATE: 2001-10/25

PRIOR APPLICATION NUMBER: 06/199,069

PRIOR FILING DATE: 2001-04-17

PRIOR FILING DATE: 2001-04-17

PRIOR FILING DATE: 2001-04-17

NUMBER OF SEQ ID NOS: 635

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 591

LENGTH: 424

TYPE: PRT
ORGANIAM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: M13 protein
FORMATION: Sequence
US-10-045-674A-591
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US-10-045-674A-591
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FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-C24509_1.pep
US-10-767-701-47075
                                                                                                                                                                                                                                                      Query Match 9.7%;
Best Local Similarity 30.3%;
Matches 37; Conservative
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GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
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Best Local Similarity 28.4%;
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TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAM.
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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TYPE: PRT
359 FR 360
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                                      97
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                                                                                                                          64 R-KSETTITQ-----
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                                    FR 98
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Search completed: March 11, 2004, 19:14:15 Job time : 5.3 secs

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Gapop 10.0 , Gapext 0.5
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1: /cgn2 6/prodata/2/paa/vcTuS

2: /cgn2 6/prodata/2/paa/US06

3: /cgn2_6/prodata/2/paa/US07
/ Cgn2_6/ptodata/2/paa/US081_COMB.pep: *
/ Cgn2_6/ptodata/2/paa/US081_COMB.pep: *
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/ Cgn2_6/ptodata/2/paa/US099_COMB.pep: *
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/ Cgn2_6/ptodata/2/paa/US092_COMB.pep: *
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-09-739-449-885	-09-791-537-3286	-09-791-537-3076	-09-791-537-9484	-09-791-537-11	-09-791-537-2922	-09-791-537-1113	-09-791-537-2922	07-965-673A-1	-09-543-407-	-60-360-039-2063	-10-369-493-	-09-543-407-	-10-417-886-5833	-09-252-691C	-09-252-691-583	-09-543-407-3	-09-543-407-3	-09-543-407-3	-09-543-407-3	-09-741-873B-	US-08-978-878-2	-10-417-886-583	-09-252-691C-58	-09-252-691-58	-60-444-37	-60-352-946-	-09-741-873B	-08-978-878-	US-09-543-407-7	-08-233-642A-	9-543-407-3	S-09-543-407-	-09-543-407-2	9-543-407-2	-09-543-407-2	-543-407-2	-09-543-40	-09-543-407-1	-09-543-407-	-543-407-	-543-407-1	08-233-642A-5	-09-543-407-	US-09-543-407-16	
equence 885	æ	equence 3076	equence 94843	nce 11137	equence 2922	equence 11137	equence 292	quence 10,	equence 6, App	equence 20638,	equence 20638,	equence 8, Appl	equence 583	equence 5833,	equence 583	equence 39,	e 32,	equence 37, App	equence 35,	equence 2, Appl	e 2,	equence 5834, A	equence 5834, A	equence 583	equence 2,	equence 2, Appl	equence 4, Appl	equence 4, Appl	equence 7	quence 55,	e 34,	equence 30,	equence 22	equence 28,	equence 20,	equence 24,	quence 26,	equence 14,	equence 31,	e 12,	equence 18,	quence 57, App	e 5, Appl	equence 16, Ap	

ALIGNMENTS

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RESULT 1

US-09-543-407-16

Sequence 16, Application US/09543407

Sequence 16, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

FILE REFERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 16

LENGTH: 151

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA

OTHER INFORMATION: sequence containing the replacement fragment

OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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Regult No.

Score

Query Match Length DB

IJ

Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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US-08-233-642A-57
US-08-233-642A-57
; Sequence 57, Application US/08233642A
; GENERAL INFORMATION:
APPLICANT: Kay, William W.
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES

"TMMSER OF SEQUENCES: 58
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US-09-543-407-5
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
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Best Local Similarity
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FITTLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
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Best Local Similarity
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STREET: C. Seattle
                                             ADDRESSEE:
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                   3: Seed and Berry
6300 Columbia Center, 701 Fifth Avenue
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90.1%;
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Pred. No. 4.5e-65;
3; Mismatches 12;
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| Sequence 18, Application US/09543407 | GENERAL INFORMATION: APPLICANT: White, Aaron P. | APPLICANT: White, Aaron P. | APPLICANT: Collinson, S. Karen | APPLICANT: Collinson, S. Karen | APPLICANT: Collinson, S. Karen | TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR | TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEP | FILE REFERENCE: 920043.406 | CURRENT APPLICATION UMMBER: US/09/543,407 | CURRENT APPLICATION UMMBER: US/09/543,407 | CURRENT FILING DATE: 2000-04-05 | NUMBER OF SEQ ID NOS: 59 | SOFTWARE: FRASESEQ for Windows Version 4.0 | SEQ ID NO 18 | LENGTH: 151
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      Best Local Similarity Matches 131; Conserv
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Best Local Similarity 89.4%;
Matches 135; Conservative 2
                                                                                                  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragmer OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEFHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: King, Joshua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642A
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 151 amino acids
TYPE: amino acid
TOPOLOGY: linear
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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98104-7092
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                         81.6%;
Score 618; DB 19;
Pred. No. 1.4e-60;
0; Mismatches 0;
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Pred. No. 1.6e-64;
3; Mismatches 13
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                                         Length 151;
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Conservative

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Indels

40;

Gaps

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Sequence 31, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEO ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 31

LENGTH: 131
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US-09-543-407-12
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GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043,406
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Best Local S
Matches 121
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE: FEATURE: OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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Similarity 80.1%;
21; Conservative
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Pred. No. 2.6e-56;
7; Mismatches 23;
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TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOI
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOU:
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 151
TYPE: PRT
Sequence 26, Application US/09543407
(GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
CURRENT APPLICATION UMMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
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Best Local Similarity
Matches 113; Conserv
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
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80.8%;
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Pred. No. 4.4e-56;
6; Mismatches 23;
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Pred. No. 2.8e-56;
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APPLICANT: COllinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 151
TYPE: PRT
RESULT 10
US-09-543-407-20
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Best Local Similarity
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Best Local Similarity
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TYPE: PRT
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80.8%; Pred. No. 5.7e-56;
tive 5; Mismatches 24;
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Pred. No. 9.5e-56;
5; Mismatches 23;
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Sequence 20,

Application US/09543407

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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: COllinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043.406
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
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                                                                                                                         Matches 121;
                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28, Application US/09543407 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 9
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 20
                                                                                                                                                                                                             OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FITTLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
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                                                                                                                                                                                                                                                                                                                                           LENGTH: 151
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                            local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                     MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGFDSTLSIYQYGSANAALALQ
SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                   MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                       Conservative
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                                                                                                                                      75.0%;
80.1%;
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                                                                                                                     4.
                                                                                                                 Score 568; DB 19;
Pred. No. 5.8e-55;
4; Mismatches 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEPTIDE SEQUENCES
                                                                                                                                                         Length 151;
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APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
FITTLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR FILE REFERENCE: 920043.406
CURRENT APPLICATION UNMBER: US/99/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEO ID NOS: 59
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 151
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APPLICANT: Woran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT PELICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT PILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOPTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 22
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 30, Applica GENERAL INFORMATION:
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Best Local Similarity 80.:
Matches 122; Conservative
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OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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                                                                                                                    TYPE: PRT
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; Pred. No. 7.5e.
5; Mismatches
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7.5e-55;
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APPLICANT: COllinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                      US-08-233-642A-55
; Sequence 55, Application US/08233642A
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-09-543-407-34
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Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                          APPLICANT: Kay, William W.
APPLICANT: Collinson, S. Karen
APPLICANT: Clouther, Sharon C.
APPLICANT: Doran, James L.
                                                                                                                                                                                                   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
                                                                                                                  ADDRESSEE: Seed and
                                                                                                                                                           NUMBER OF SEQUENCES:
                                  COUNTRY:
                                                       CITY: Seattle
STATE: Washing
                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 74.8%;
Local Similarity 80.8%;
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                     98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNAT 102
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READABLE FORM
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                                                         Washington
                                                                                               6300 Columbia Center,
                                        U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                     Seed and Berry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.2%; Score 554; DB 19; 100.0%; Pred. No. 1.4e-53; tive 0; Mismatches 0;
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Pred. No. 9.7e-55;
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                                                                                                    701 Fifth Avenue
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us-09-543-407-16.rapm
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA;
APPLICATION DATA;
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 920043.403C3
REFERENCE/DOCKET NUMBER: 920043.403C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 622-4900
TELEPAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: protein
US-08-233-642A-55 Search completed: March 11, 2004, 19:13:10 Job time : 171.3 secs Query Match 64.3%; Score 487; DB 6; Length 120; Best Local Similarity 97.9%; Pred. No. 5.2e-46; Matches 95; Conservative 2; Mismatches 0; Indels 0; Gaps

В Ś 밁

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                        Length DB
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US-09-741-873C-2
US-10-974-158-34
US-10-767-701-40444
PCT-US03-35645-44
US-10-767-701-42417
US-10-767-701-42417
US-10-763-150-2
US-10-763-150-2
US-10-7641-678-38
PCT-US04-02188-185
US-10-764-425-185
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US-10-781-979-11
  US-09-126-816C-6
PCT-US04-05654-334
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34, Appl
34, Appl
40444, A
44, Appl
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63	63.5	63.5	63.5	63.5	63.5	64	64	64.5	64.5	64.5	65	65	65.5	65.5	65.5	66	66.5	67
8.3	8.4	8.4			8.4									8.7				8.9
179	526	467	263	175	154	1645	198	1221	795	135	1230	620	3668	772	178	708	172	595
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US-10-767-701-35342	PCT-US04-04280-9	US-10-771-241-381	PCT-US04-05654-126	US-10-767-701-59665	US-10-767-701-39935	US-10-451-467A-452	US-10-767-701-59434	US-10-417-884A-3959	US-10-417-884A-5429	US-10-091-007A-38	US-10-786-892-150	US-10-767-701-46258	US-10-746-795A-4	US-10-417-884A-5724	US-10-767-701-32700	US-10-417-884A-6047	US-10-767-701-49464	US-10-786-892-166
Sequence 35342, A	Sequence 9, Appli	Sequence 381, App	Sequence 126, App	Sequence 59665, A	Sequence 39935, A	Sequence 452, App	Sequence 59434, A	Sequence 3959, Ap	Sequence 5429, Ap	Sequence 38, Appl	Sequence 150, App	Sequence 46258, A	Sequence 4, Appli	Sequence 5724, Ap	Sequence 32700, A	Sequence 6047, Ap	Sequence 49464, A	Sequence 166, App

ALIGNMENTS

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APPLICANT: NOTMARK, Staffan

APPLICANT: Olsen, Arne

FILE REFERENCE: 01289-084

CURRENT APPLICATION PIDONECTIN Binding Protein As

FILE REFERENCE: 01289-084

CURRENT APPLICATION NUMBER: US/09/741,873C

CURRENT APPLICATION NUMBER: E801723-1

PRIOR PILING DATE: 1998-05-06

PRIOR PILING DATE: 1998-05-06

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR FILING DATE: 1997-11-06

PRIOR APPLICATION NUMBER: US 07/789,437

PRIOR FILING DATE: 1991-11-06

PRIOR APPLICATION NUMBER: US 07/970,846

PRIOR APPLICATION NUMBER: US 08/187,865

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PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR FILING DATE: 1994-01-28

PRIOR PILLING DATE: 1994-01-28

PRIOR PILLING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 11

SOPTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 151
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                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 100; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 151
TYPE: PRT
ORGANISM: Escherichia
                                           121
                                                                                       61
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                                                                                                                                                                                                                        1 MKILKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                       GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                        NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                   MKLLKVAAIAAIVFSGSAVAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
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                                                                                                                                                                                                                                                                           63.5%; Score 481; DB 5; Length 151; 66.2%; Pred. No. 2.6e-41; rive 19; Mismatches 32; Indels
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                                                               SOFTWARE: P
SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34, Application US/10004115B GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                      APPLICANT: ITO, NOBUYA
APPLICANT: WAKITA, RYUHEI
TITLE OF INVENTION: PROCESS FOR PRODUCING OPTICALLY ACTIVE
TITLE OF INVENTION: 4-HALO-3-HYDROXYBUTANOATE
FILE REFERENCE: 7372-72249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                         PRIOR APPLICATION NUMBER: JP 2001-175175 PRIOR FILING DATE: 2001-06-11
                                                                                                                                                                 PRIOR APPLICATION NUMBER: JP 2001-026594 PRIOR FILING DATE: 2001-02-02
                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/004,115B
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: JP 2000-372704
PRIOR FILING DATE: 2000-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09741873C GENERAL INFORMATION:
                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: JP 2001-006144 PRIOR FILING DATE: 2001-01-15
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APPLICANT: MATSI
ORGANISM: Corynebacterium sp.
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                                            LENGTH: 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION UNMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
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APPLICANT: Oleen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
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APPLICATION NUMBER: US 07/347,189
REILING DATE: 1989-05-04
APPLICATION NUMBER: US 07/789,437
FILING DATE: 1991-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/970,846
FILING DATE: 1992-11-03
APPLICATION NUMBER: US 08/187,865
FILING DATE: 1994-01-28
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APPLICATION NUMBER: US 08/978,878
FILING DATE: 1997-11-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SHIMIZU, MASATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MATSUMURA,
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Pred. No. 1.1e-34;
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US-10-767-701-40444
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                                                                                                                                                                                                                                               Sequence 44, Application PC/TUS0332645 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 40444
LENGTH: 358
CURRENT APPLICATION NUMBER: PCT/US03/32645
CURRENT FILING DATE: 2003-10-15
NUMBER OF SEQ ID NOS: 234
SOFTWARE: PatentIn version 3.0
BEQ ID NO 44
LENGTH: 1531
                                                                                                         APPLICANT: Progulske-Fox, Ann
TITLE OF INVENTION: Identification of Actinobacillus actinomycetemcomitans Antigens
TITLE OF INVENTION: in the Diagnosis, Treatment, and Monitoring of Periodontal Dise
FILE REFERENCE: MBHB01-662B
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                                                                                                                                                                                     APPLICANT: Handfield, Martin
APPLICANT: Hillman, Jeffrey
APPLICANT: Progulske-Fox, Ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Ot
TITLE OF INVENTION: Plants and Uses Thereof For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Sorghum bicolor
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                                                                                                                                                                                                                                                                                                                                                                    278 TEAENSOGDSSSGVNGSSEETS----NKGDGATVTSN 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 SATASSGTGSGDDKGNSSDSTPAEENTETASGDDEKGMETGTTTEAVHSKEENSENSSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305 LIDLAHAGIFDISVETFSLDNGAEAYRRLAAGTLSGRAVVV 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 THEMAHASGPDST---LSIYQYGSANAALALQSDAR------KSE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity 22.3
35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTITQSGYGNGADVGQGADNSTIELT-----QNGFRNNATID-----QWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                                                           VGQYG--GNNAALVNQTASDSSVMVRQVGFGNNATAN 149
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Pred. No. 0.06
26; Mismatches
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Pred. No. 1.
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Sequence 4417, Application US/10767701

Sequence 42417, Application US/10767701

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(33535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 42417

LENGTH: 386
TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-C47268_1.pep

US-10-767-701-42417
                                             RESULT 7

US-10-093-037A-63

; Sequence 63, Application US/10093037A

; GENERAL INFORMATION:
; APPLICANT: Jay M. Short
; APPLICANT: Bylina, Edward
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Lam, David E.
; TITLE OF INVENTION: ENZYMES HAVING GLYCOSIDASE ACTIVITY AND METHODS OF USE THEREOF
; FILE REFERENCE: 564462001402
; FILE REFERENCE: 564462001402
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Best Local S
Matches 28
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Best Local Similarity
CURRENT APPLICATION NUMBER: US/10/093,037A CURRENT FILING DATE: 2002-03-06 PRIOR APPLICATION NUMBER: US 09/910,579
                                                                                                                                                                                                                                                                                                                                                                                              141
                                                                                                                                                                                                                                                                                                                                                                                                                                          129 NSNVNISSS---NSSPTPHTNRSVFDTLESSSRGSQKTVNQETSSDNNKNRPERNSTQEE 185
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                                                                                                                                                                                                                                                                                                                                                     GISHSAAA 193
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21.9%; Pred. No. 5.5;
ative 25; Mismatches 55; Indels
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; Pred. No. 24;
27; Mismatches
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PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 09/134,078
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 08/949,026
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: US 60/056,916
PRIOR FILING DATE: 1996-12-06
NUMBER OF SEO ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 63
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GENERAL INFORMATION:
APPLICANT: Robert G. Wisotzkey
TITLE OF INVENTION: MAGED3-Like Gene Disruptions,
TITLE OF INVENTION: Compositions and Methods Rel
                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2
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CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US 60/391,205
PRIOR FILING DATE: 2002-06-24
NUMBER OF SEQ ID NOS: 4
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TYPE: PRT
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les 37; Conserv
                                                                          563 VLNGRAGFGGALNT----NATFGGVLNGSAGFGGAMNTNATFG--GALNSNAGFGGAIS
                                                                                                                                                           519 SFSGVLNSSASFGGAINT------SAGFGSTLN----SSASFGSALSTSASFGG 562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 AQAGDEIIIAPGNYNFQDKIQGAFNRSVYLYGSANGNSTNPIILRGESATNPPVFSGLDY 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 SVVQAGQGVSGLISNKLTASGEIVKNIIQNWDTETSTGPKTT----QCSTIECIRAAMET 357
                                                                                                                  68 TTITQSGYGNGADVGQGADNSTIELTQNG-----FRNNATIDQWNAKNSDITVG---- 116
                                                                                                                                                                                                                                        40;
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                                                                                                                                                                                               8 AFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARKSE 67
                                  --- QYGG--NNAA----LVNQTASDSSVMVRQVGFGN--NATAN 149
TSTNFGGALNNSAGFGGAMNTSASFGGVLNNSAGFGGAINTSAN
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                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                             9.7%;
                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                             Score 73.5;
Pred. No. 27;
                                                                                                                                                                                                                                          Mismatches
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18;
                                                                                                                                                                                                                                                                                DB 6;
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5
                                                                                                                                                                                                                                                                              Length 1160;
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                                                                                                                                                                                                                                        45;
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                                                                              615
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; TYPE: PRT
; ORGANISM: Phanerochaete chrysosporium
US-10-641-678-38
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US-10-641-678-38
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US-10-767-701-47075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-10-767-701-47075
                                                                                                                         SOFTWARE: Fa
SEQ ID NO 38
LENGTH: 449
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 38, Application US/10641678 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 47075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 47075, Application US/10767701 GENERAL INFORMATION:
                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/458,696
PRIOR FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: US 60/456,368
PRIOR EILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: US 60/404,063
PRIOR FILING DATE: 2002-08-16
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                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: GC772-3
CURRENT APPLICATION NUMBER: US/10/641,678
CURRENT FILING DATE: 2003-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION UNMBER: US/10/767,701
CURRENT APPLICATION UNMBER: US/10/767,701
                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/458,853
PRIOR FILING DATE: 2003-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Stahlberg, Jerry
TITLE OF INVENTION: Novel Variant Hypocrea jecorina CBH1
TITLE OF INVENTION: Cellulases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Day, Anthony, G.
APPLICANT: Goedegebuur, Frits
APPLICANT: Gualfetti, Peter
APPLICANT: Mitchinson, Colin
                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 SAGAASSGTAGSASAGAGAASS-----GTTAGAGVSTTGASSVATTVGVWTSAVAIGD 176
                                                                                                                         449
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                                                                                                                                                             FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARKS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEKADD 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAAAGAASGSAAAG-----SASGSAAT-----GSGSAGAAGSSTTLAS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shaw, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sandgren, Mats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neefe, Paulien
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  9.5%;
26.1%;
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  Score 72;
Pred. No.
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Pred. No. 2
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  DB 6;
11;
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                  Length 449;
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CURRENT APPLICATION NUMBER: PCT/US04/02188
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: 60/442,582
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 191
SOFTWARE: Patentin version 3.2
SEQ ID NO 185
LENGTH: 583
TYPE: PRT
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                                                                                                                   ; TYPE: PRT; ORGANISM: Homo sapiens US-10-764-425-185
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PCT-US04-02188-185
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                                                                                                                                                                                           SOFTWARE: PatentIn version 3.2 SEQ ID NO 185
                                                            Query Match
Best Local
                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                  APPLICANT: Taylor, Ian
TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
FILE REFERENCE: 5151
CURRENT APPLICATION NUMBER: US/10/764,425
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: 60/442,582
PRIOR APPLICATION NUMBER: 60/442,582
PRIOR FILING DATE: 2003-01-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 185,
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bayer Pharmaceuticals Corporation APPLICANT: Eveleigh, Deepa APPLICANT: Bigwood, Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 185,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bayer Pharmaceuticals Corporation
APPLICANT: Eveleigh, Deepa
APPLICANT: Bigwood, Douglas
APPLICANT: Taylor, Ian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPPLICANT: Taylor, Ian
                                                                                                                                                                           ENGTH: 583
                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 NSKLSLTPNCSSTLNITQSQIHFLSPDSFVNNSHGANNELELVTCLSSD 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213
27 VTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 SDITVGQYG------GNNAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 NGALYFVAMDADGGKSK----YPGNRAGAKYGTGYCDSQCPRDVQFINGQANVQGWNATS 212
                                        32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 VTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGAD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 29.4
32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/10764425
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                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.4%; Score 71.5; D
29.4%; Pred. No. 17;
ative 16; Mismatches
                                                        9.4%;
                                        16;
                                      Score 71.5; D
Pred. No. 17;
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Mismatches
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                                                                        DB 6;
                                      50;
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                                                                        Length 583;
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                                      Indels 11;
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                                    Gaps
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86
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US-10-771-241-364
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US-10-767-701-44555
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                                                                                                              ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C21806_1.pep
US-10-767-701-44555
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Query Match
Best Local Similarity 28.0
Marches 23; Conservative
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44555, Application US/10767701 GENERAL INFORMATION:
                                                                                                                                                                                                                               SEQ ID NO 44555
LENGTH: 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.4%; Score 71.5; D
Best Local Similarity 22.7%; Pred. No. 29;
Matches 34; Conservative 19; Mismatches
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APPLICANT: Forsyth, R. Allyn
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
TITLE OF INVENTION: ESCHERICHTA COLI
FILE REFERENCE: ELITRA .001C1
CURRENT APPLICATION NUMBER: US/10/771,241
CURRENT APPLICATION NUMBER: 09/492,709
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Plants and Uses Ther FILE REFERENCE: 38-21 (53535)8
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
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                                                                                                                                                               FEATURE:
                                                                                                                                                                                   TYPE: PRT
ORGANISM: Sorghum bicolor
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                        9.3%; Score 70.5; Di
28.0%; Pred. No. 8.1;
tive 13; Mismatches
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Pred. No. 29;
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                                                                    DB 6; Length 281;
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Search completed: March 11, Job time: 6.3 secs
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SEQ ID NO 462
LENGTH: 829
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: EP 01870002.1
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: EP 01870003.9
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: JAB-1667
CURRENT APPLICATION NUMBER: US/10/451,467A
CURRENT FILING DATE: 2003-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: REEKMANS, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIPH GENES FOR DRUG TARGET IDENTIFICATION IN
TITLE OF INVENTION: YEAST AND FUNGI
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                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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Local Similarity 27.4%; Pred. No.
hes 32; Conservative 17; Mismatc
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                                                                                     GFPIPGSPDETTRPNS----IFGGHTRGLFSSRLSESQSVLYQQYAIADD-TVGDY 731
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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860.386 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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l: /cgn2_6/ptodata/2/paa/
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                     /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
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quence 358,	e 357,	e 358,	equence 514	equence 20566	e 25957,	equence 25818,	equence	equence 21553,	6	equence 8,	equence 20	e 20	equence 58	equence 58	equence 58	equence 39	equence 32	equence 37	equence 35	equence 2	ρ 2,	equence 58	₽ 583	equence 583	equence 34	quence 55,	equence	quence 2, Appl	equence 4. Appl	quence 4	equence 7. Appl	ر د د	equence 28, App	8 31,	equence 24, App	equence 14, App	equence 12, App	equence 16, App	equence 20	се 26, Арр	quence 57, Appl	quence 5,	equence 18, App

ALIGNMENTS

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RESULT 1

US-09-543-407-18

Sequence 18, Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BRCTERIAL FIMERIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 18

LENGTH: 151

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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Result No.

Score

Query Match Length DB

IJ

Description

SUMMARIES

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APPLICANT: White, AARON P.
APPLICANT: White, AARON P.
APPLICANT: COllinson, S. Karen
APPLICANT: COllinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEP
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 151
TYPE: PRT
ORGANISM: Salmonella enteritidis
US-09-543-407-5
                                                                                                                                                                                            US-08-233-642A-57
; Sequence 57, Application US/08233642A
; GENERAL INFORMATION:
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Best Local
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                                   NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                    APPLICANT: KAY, William W.
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
                                                                                    TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLATITLE OF INVENTION: BASED VACCINES
   ADDRESSEE:
STREET: 6
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                                                                                                                                                                                                                                                                                                                                                                             SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                           SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                                                                                                                                           NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09543407
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E: Seed and Berry
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.6%;
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Pred. No. 1.4e-65;
3; Mismatches 11
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FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 151
TYPE: PRT
ORGANISM: Artificial Sequence
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                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26, Applicat GENERAL INFORMATION:
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Best Local Similarity 90.1%;
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: White, Aaron P. APPLICANT: Doran, James L.
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
                                                                                       FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 92.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
LENGTH: 151 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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OPERATING SYSTEM:
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98104-7092
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Y: U.S.A.
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                    86.5%;
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Score 675; DB 19;
Pred. No. 7.3e-64;
0; Mismatches 0;
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Pred. No. 4.8e-65;
3; Mismatches 12;
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Best Local Similarity 81. Matches 136; Conservative

<u>,</u>

30;

Gaps

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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTE
TITLE OF INVENTION: PRESENTATION OF HETEROL
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTMARE: FASESEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 151
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US-09-543-407-20
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 151
                                                                                                                                                                                                                                                   Sequence 16, Application US/09543407 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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                                                                                                                                                                                                                                                                                                                                                                     RUNATIDQWNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----YDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF
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73.6%;
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Pred. No. 3.6e-58,
0; Mismatches (
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                                                                                                                                     OF HETEROLOGOUS
                                                                                                                                                       SYSTEM
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RESULT 8 US-09-543-407-14

Sequence 14, Application US/09543407 GENERAL INFORMATION:

APPLICANT: White, Aaron P. APPLICANT: Doran, James L.

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US-09-543-407-12
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                                                                                                                                                                                                Query Match
Best Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 151
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DOYAN, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
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OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
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                                  NNAALVNOTASDSSVMVROVGFGNNATANOY 151
                                                                      SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                         SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
NNAALVNYDQLVTRVVTHEMAHANNATANQY
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80.8%;
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Pred. No. 3.4e-57;
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Pred. No. 9.8e-58;
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US-09-543-407-24
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Best Local
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LENGTH: 151
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Best Local :
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APPLICANT: Doran, James L
APPLICANT: Collinson, S.
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NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
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APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
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CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
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TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
                                                                                                                                                                                                                                                               OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                  124;
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                                SDÄRKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                               MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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Pred. No. 1.2e-56;
5; Mismatches 22;
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Pred. No. 5
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CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 151
Query Match
Best Local Similarity
Matches 122; Conserv
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Best Local Similarity
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LENGTH: 131
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APPLICANT:
                                                                               FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
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SOFTWARE: FastSEQ for Windows Version 4.0
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Kay, William W.
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80.8%;
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••
     Score 601; DB 19;
Pred. No. 6.6e-56;
4; Mismatches 25;
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Pred. No. 2.6e-56;
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   Gaps
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1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ 60

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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-09-543-407-30
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CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Applica
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             Sequence 30, Applica GENERAL INFORMATION:
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Matches 123;
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 151
TYPE: PRT
ORGANISM: Artificial Sequence
TYPE: PRT
ORGANISM: Artificial
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81.5%;
    Sequence
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Pred. No. 8.4e-56;
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US-08-978-878-4
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                                                                                                                                          Sequence 4, Application US/08978878 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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APPLICANT: NORMARK, Staffan
APPLICANT: OLSEN, Arne
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN
FILE REFERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: SE 8801723-1
EARLIER FILING DATE: 1988-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 81.9
Matches 123; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: R
OTHER INFORMATION: G
OTHER INFORMATION: G
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CURRENT APPLICATION NUMBER: US/09/543,407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: White, Aaron P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 151
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                                                                                                                                                                                                                                                                                                                       TDÁRNSDLTÍTÓHGGGNGÁÐVGÓGSDÐSSÍÐLTÓRGFGNSATLÞÓWNGKNSEMTVKQFGG
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                                                                                                                                                                                                                                                   GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
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81.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.1%; Score 523; DB 19; 68.9%; Pred. No. 1.6e-47; tive 20; Mismatches 27
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Pred. No. 1.1e-55;
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                                                                                        WELL
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Database :
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             March 11, 2004, 18:35:05; Search time 5.3 Seconds (without alignments) 376.014 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125546 seqs, 13197846 residues
Pending_Patente_AA, New:*

| Cgm2_6/ptodata/1/paa/USO6_NEW_COMB.pep:*
| Cgm2_6/ptodata/1/paa/USO7_NEW_COMB.pep:*
| Cgm2_6/ptodata/1/paa/USO7_NEW_COMB.pep:*
| Cgm2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*
| Cgm2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*
| Cgm2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*
| Cgm2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                125546
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

26		24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	89	7	6	₅	4.	ω	2	1	NO.	Result	
69	69.5	70	70.5	71	71.5	71.5	71.5	72	72	73	73	73	74	74.5	76.5	76.5	77.5	77.5	78.5	79.5	•	81.5	82.5	444	520	score		
		9.0		9.1	•	•	•	•	•	9.4	•	9.4	9.5	9.6	•	9.8	9.9	9.9	10.1	10.2	10.4	10.4	10.6	56.9	66.7	Match		d
245	449	1160	173	391	772	386	386	654	654	1327	386	310	305	430	348	179	443	234	480	956	533	424	434	131	151	Length		
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US-10-779-461-19	US-10-641-678-38	US-10-603-150-2	US-10-767-701-39649	PCT-US04-05654-336	US-10-417-884A-5724	US-10-100-683-10327	US-10-100-683-10326	US-10-764-425-156	PCT-US04-02188-156	PCT-US04-02338-49	US-10-767-701-42417	PCT-US04-05654-1412	PCT-US04-05654-1406	US-10-451-467A-314	US-10-004-115B-34	US-10-767-701-35342	US-10-100-683-7608	US-10-767-701-45603	PCT-US04-05654-1498	US-10-093-037A-63	US-10-045-674A-527	US-10-045-674A-591	US-10-045-674A-594	US-09-741-873C-2	US-09-741-873C-4			
19,	e 38	Sequence 2, Appli	e 39649	e 336, 1	Sequence 5724, Ap	æ	1032	156,	e 156,	49,	e 4241	1412	e 1406	e 314,	e 34,		7608	Sequence 45603, A	1498	e 63,	527,	Sequence 591, App	594,	e 2,	Sequence 4, Appli	Description	-	

8.8 633 6 8.8 1133 6 8.8 1346 1 8.7 292 1 8.6 6 321 6 8.5 221 6 8.5 221 6 6 8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	Δ,	44	43					38	37	36						30	29	28	27
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PCT-US04-05-94-334 US-10-781-979-11 US-10-781-979-11 US-10-782-020-8 PCT-US04-05092-23 PCT-US04-05654-1756 PCT-US04-05654-2080 US-10-767-701-4044 PCT-US04-05654-2586 US-10-767-701-58351 PCT-US04-05654-2338 PCT-US04-05654-2338 PCT-US04-05654-338 PCT-US04-05654-338	442 1	245 6	221 6	342 6	317 1	317 1	147 6	878 6	321 1	310 6	433 1	358 6	292 1	364 1	346 1	135 1	633 6	633 6	5/4 L
	PCT-US04-05654-338	US-10-779-461-59	US-10-767-701-41435	US-10-767-701-46086	PCT-US04-05654-2370	PCT-US04-05654-2038	US-10-767-701-58351	US-10-771-241-364	PCT-US04-05654-590	US-10-786-850-4	PCT-US04-05654-2586	US-10-767-701-40444	PCT-US04-05654-2080	PCT-US04-05654-1756	PCT-US04-02242-58	PCT-US04-05092-23	US-10-782-020-8	US-10-781-979-11	PCT-0504-05654-334
	338, App	59, Appl	41435, A	46086, A	2370, Ap	2038, Ap	58351, A	364, App	590, App	4, Appli	2586, Ap	40444, A	2080, Ap	1756, Ap	58, Appl	23, Appl	8, Appli	11, Appl	334, App

ALIGNMENTS

APPLICANT: Normark, Staffan

APPLICANT: Olsen, Arne

FILLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

FILE REFERENCE: 012889-084

CURRENT APPLICATION NUMBER: US/09/741,873C

CURRENT FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: SE 8801723-1

PRIOR APPLICATION NUMBER: US 08/978,878

PRIOR APPLICATION NUMBER: US 08/978,878

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR APPLICATION NUMBER: US 07/789,437

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PRIOR APPLICATION NUMBER: US 07/789,437

PRIOR APPLICATION NUMBER: US 08/187,865

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PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR APPLICATION NUMBER: US 08/318,519

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PRIOR APPLICATION NUMBER: US 08/318,519

PRIOR APPLICATION NUMBER: US 08/318,519

PRIOR APPLICATION NUMBER: US 08/318,519 S 밁 Ś Ş RESULT 1 US-09-741-873C-4 밁 US-09-741-873C-4 SEQ ID NO 4 LENGTH: 151 TYPE: PRT ORGANISM: Escherichia coli Sequence 4, Application US/09741873C GENERAL INFORMATION: Matches 103; Query Match SOFTWARE: PatentIn version 3.0 Local Similarity 121 GNGAAVDOTASNSSVNVTOVGFGNNATAHOY 151 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151 61 61 SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWAKNSDITVGQYGG 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ 60 TDARNSDITITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG MKLLKVAAIAAIVFSGSAVAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ Conservative 66.7%; Score 520; DB 5; Length 151; 68.2%; Pred. No. 4.8e-40; Live 21; Mismatches 27; Indels 21; Gaps 120 120 60 0

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CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 594
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PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR PRIOR DATE: 1980-05-06
PRIOR PPLICATION NUMBER: US 08/978,878
PRIOR PPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1980-05-04
PRIOR PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/790,446
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR FILING DATE: 1992-11-03
PRIOR PRIOR DATE: 1992-11-03
PRIOR PRIOR DATE: 1992-11-03
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APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAM.
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
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                                                                                                                                                                                           TITLE OF INVENTION: LIBRARIES FILE REFERENCE: DYAX/002 CIP2
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NUMBER OF SEQ ID NOS: 11
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APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well
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ORGANISM: Escherichia coli
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FILING DATE: 1994-01-28
APPLICATION NUMBER: US 08/318,519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GFGNNATAHQY 131
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COHEN, EDWARD H.
NASTRI, HORACIO G.
ROOKEY, KRISTIN L.
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65.6%; Pred. No. 2.
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APPLICANT: ROCKEY KRISTIN L.

APPLICANT: HOOT, RENE
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.

APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.

TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
CONTENTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
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Best Local :
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SEQ ID NO 591
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Best Local Similarity
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APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Unknown Organism
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mes 32; Conserv
                                                       140 VGFGNNA
                                                                                                                     318
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                                                                                                                                                                   DVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQ 139
                                                                                                                                                                                                                                                                                            GGG--GNHNGGGNSSGP-DYDQLVT----RVVTHEMAHALQSDARKSETTITQSGYGNGA 79
                                                                                                                                                                                                                                        GGGSEGGGSGGGSGSGDFDYEKMANANKGAMTENADENALQSDA-KGKLDSVATDYGAAI 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----QVGDGDNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/10045674A
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                                                       146
353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description of Unknown Organism: M13
                                                                                                                                                                                                                                                                                                                                                                 10.4%; Score 81.5; D)
25.2%; Pred. No. 3.8;
tive 19; Mismatches
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24.1%; Pred. No. 3
                                                                                                                     GFIGDVS--
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SOPTWARE: PatentIn Ver. 2
SEQ ID NO 527
LENGTH: 533
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               -10-093-037A-63
                                                           PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 09/134,078
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 08/949,026
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: US 60/056,916
                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/093,037A CURRENT PILING DATE: 2002-03-06
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TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAM.
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/045,674A CURRENT FILING DATE: 2001-10-25
                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/910,579
                                                                                                                                                                                                                                                      FILE REFERENCE: 564462001402
                                                                                                                                                                                                                                                               APPLICANT: LAM, DAVIG E.
TITLE OF INVENTION: ENZYMES HAVING GLYCOSIDASE ACTIVITY AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jay M. Short
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 06/198,069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS OTHER INFORMATION: protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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                   LING DATE: 19 F SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGSEGGGSGSGSGSGDFDYEKMANANKGAMTENADENALQSDA-KGKLDSVATDYGAAI 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGG--GNHNGGGNSSGP-DYDQLVT----RVVTHEMAHALQSDARKSETTITQSGYGNGA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGDGDNS 462
                                                                                                                                                                                                                                                                                                                Bylina, Edward
Swanson, Ronald V.
Mathur, Eric J.
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                                                                                                                                                                                                                                                                                                David E.
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                                         1996-12-06
Windows Version 4.0
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Pred. No. 5
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LENGTH: 956
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SEQ ID NO 1498
                                                                                                       Matches
                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kumimoto, Roderick W
APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374,780
PRIOR APPLICATION NUMBER: 10/374,780
PRIOR APPLICATION NUMBER: 10/675,852
PRIOR APPLICATION NUMBER: 10/675,852
                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 2950
                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE:
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TYPE: PRT
ORGANISM: Bankia gouldi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT:
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                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                 ENGTH: 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318 LTASGEIVKNIIQNW------DTETSTGPK----TTQCSTIECIRAAMETAQAGDEIII 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427 GDYWNIKDIEFKTGSKGIVLDNSNGSKLKNLVVHDIGEEAIHLRD-GSSNNS 477
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98
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                                                           WGGGGNHNGGGNSSGPDYDQLVTRVVTHBMAHALQSDARKSETTITQSGYGNGADVGQGA
DNSTIELTQNGFRNNATID---QWNAKNSDITVGQYGGNNAALVNQTASDSS 134
                                   WPDTDSEQGGGGGGAAYFGELEEALVHQVA-TLRRRAQQTATT-TTSHHGHTTPFSTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sherman, Bradley K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Century, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gutterson, Neal
Yu, Guo-Liang
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Jiang, Cai-Zhong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dubell III, Arnold
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                                                                                                    10.1%; Score 78.5; Diarity 26.8%; Pred. No. 8.3; Conservative 19; Mismatches
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22.1%; Pred. No. 16;
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                                     102
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RESULT 9
US-10-100-683-7608
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                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: US 60/043,576
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: US 60/047,601
PRIOR APPLICATION NUMBER: US 60/047,601
PRIOR FILING DATE: 1997-08-23
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C82834_1.pep US-10-767-701-45603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-767-701-45603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7608, Application US/10100683 GENERAL INFORMATION:
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SEQ ID NO 45603
LENGTH: 234
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ORGANISM: Sorghum bicolor
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(234)
OTHER INFORMATION: unsure (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 45603, Application US/10767701
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                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: PS900
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen, et al.
TITLE OF INVENTION: Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kovalic, APPLICANT: Zhou, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                             APPLICATION NUMBER: US 60/056,664 FILING DATE: 1997-08-22
                 FILING DATE: APPLICATION
                                                         APPLICATION NUMBER: US 60/043,314
                                                                                                                         FILING DATE: 1997-05-23
                                                                                                                                           APPLICATION NUMBER: US 60/047,599
                                                                                                                                                                 APPLICATION NUMBER: US 60/043,580 FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 GAYAQGGAQGGGGGGGQYGGSGS 134
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34; Conservative
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Can. Yongwei
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NUMBER: US 60/047,632 : 1997-05-23
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23.8%; Pred. No. 4.2;
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RESULT 11
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US-10-767-701-35342
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                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(53535)B CURRENT APPLICATION NUMBER: US/10/767,701 CURRENT FILING DATE: 2004-01-29 NUMBER OF SEQ ID NOS: 63128 SEQ ID NO 35342 LENGTH: 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 35342, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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SEQ ID NO 7608
LENGTH: 443
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                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                  140 VGFGNNA 146
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                                                                                                                                                87 NSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTA-----SDSSVMVRQ 139
                                                                                                                                                                                                                 27 GGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGAD 86
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                                                  NGYGTKS 102
                                                                                                                   DNT-----SSSSSGDGWGGSKSS--
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Pred. No. 3
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5; Mismatches
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Pred. No. 9
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                                                                                                                 GGÝGGWDEILDNNTAAAQEAKRSSNSFSAGN
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US-10-004-115B-34

Sequence 34, Application US/10004115B GENERAL INFORMATION:

APPLICANT: ASAKO, HIROYUKI APPLICANT: MATSUMURA, KEN APPLICANT: SHIMIZU, MASAT

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US-10-451-467A-314
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                                                                                                                                          ; ORGANISM: Saccharomyces cerevisiae US-10-451-467A-314
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                                                             Matches
                                                                               Query Match
Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2003-06-19
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PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: JP 2001-006144
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: JP 2001-026594
PRIOR FILING DATE: 2001-02-02
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TITLE OF INVENTION: PROCESS FOR PRODUCING OPTICALLY ACTIVE
TITLE OF INVENTION: 4-HALO-3-HYDROXYBUTANOATE
FILE REFERENCE: 17372-72249
CURRENT APPLICATION NUMBER: US/10/004,115B
CURRENT FILING DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: EP 00870318.3 PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LUYTEN, WÄLTER HERMAN MARIA LOUIS
APPLICANT: REEKMANS, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIE GENES FOR DRUG TARGET IDENTIFICATION
TITLE OF INVENTION: YEAST AND FUNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CONTRERAS, ROLAND HENRI
APPLICANT: EBERHARDT, INES
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NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 732
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: EP 01870002.1 PRIOR FILING DATE: 2001-01-04
                                                                                                                                                                                     TYPE: PRT
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ORGANISM: Corynebacterium
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26 WGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGA 85 : | |:: | |: | |: | |: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 ---GQGADNSTIELTQNGFRNNATIDQWNAKNS-----DITVGQYGGNNAA- 124
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                                                             h 9.6%; Score 74.5; D
Similarity 21.1%; Pred. No. 17;
27; Conservative 23; Mismatches
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Pred. No. 8.4;
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                                                             Indels 21;
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PCT-US04-05654-1412
FCT-US04-05654-1412
FCQUENCE 1412, Application PC/TUS0405654
FGENERAL INFORMATION:
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SEQ ID NO 1406
LENGTH: 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kumimoto, Roderick W
APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374,780.
PRIOR APPLICATION NUMBER: 10/675,852
PRIOR APPLICATION NUMBER: 10/675,852
PRIOR PILING DATE: 2003-09-30
PRIOR FILING DATE: 2003-09-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 2950
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Oryza sativa FEATURE:
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Local Similarity 24.0%;
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                                                                                                    156 A.156
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                                                                                                                                                                         105 SANTLRAHILE----
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                                                                                                                                                                                                                                                                            27 GGGGN------HNGGGNSSGPDYD------QLVTR-------VVTHE
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Jiang, Cai-Zhong
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                                                                                                                                                                                                                                                                                                              Conservative
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Pred. No.
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Sherman, Bradley K

Riechmann, Jose Luis Jiang, Cai-Zhong

Jacqueline E

Haake, Volker Creelman, Robert A

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RESULT 15
US-10-767-701-42417
(SEQUENCE 42417, Application US/10767701
; SEQUENCE 42417, Application US/10767701
; GENERAL INFORMATION:
   APPLICANT: Kovalic, David K.
   APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; FILE REFERENCE: 38-21(53535)B
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; OTHER INFORMATION: Orthologous to G1073
PCT-US04-05654-1412
             CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 42417
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Best Local :
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PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 2950
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APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.2
EQ ID NO 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 10/374,780 PRIOR FILING DATE: 2003-02-25
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ORGANISM: Glycine max
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) NO 42417
TH: 386
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Century, Karen
Gutterson, Neal
Yu, Guo-Liang
Broun, Pierre B
Kumimoto, Roderick W
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                                                                                                                                      Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                       ORGANISM: Sorghum bicolor FEATURE:
138 ---NSSPTPHTNRSVFDTLESSSRGSQKTVNQETSSDNNKMRPERNSTQEEGISHSAAA 193
                                    96 GFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVM-----VRQVGFGNNATA 148
                                                                         87 GTGSDQAVSR------H--QPELKRTTTTITGKGHQTTGSLGEELLIPLDNSNVNISSS
                                                                                                           40 GPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQ----GADNSTIELTQN 95
                                                                                                                                                  Conservative
                                                                                                                                                                 9.4%;
                                                                                                                                                  24; Mismatches
                                                                                                                                                                 Score 73;
Pred. No.
                                                                                                                                                  46; Indels
                                                                                                                                                                                  Length 386
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Search completed: March 11, 2004, 19:14:17
Job time: 6.3 secs

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Result
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Maximum DB seq length: 200000000
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                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
       Score
Query
Match Length DB
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Gapop 10.0 , Gapext 0.5
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'Cgm2_6/ptodata/2/paa/US08_COMB.pep:*
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-09-573-655B-	S-09-573-655B-34	-09-573-655A-66	-09-573-655A-349	-09-570-581A-18	09-935-625-2515	-09-935-625-7945	-09-935-625-251	8-09-935-625-794	-09-708-427-765	-09-708-427-765	-09-708-427-765	-60-360-039-2	S-10-369-493-2063	8-09-803-110-885	S-09-739-449-885	-09-543-407-3	-09-543-407	9-543-407-3	-09-543-407-3	S-09-741-873B-	-08-978-878-2	-10-417-886-583	9-252-691C-58	-09-252-691-58	S-09-543-407	8-233-642A-5	-60-444-371	-352-946-2	-09-741-873	-08-978-878-	-09-543-4	1-104-545-40-	S-09-543-407-	-09-543-407-2	-09-543-407	9-543-4	-09-543-407-2	-09-543-407-1	S-09-543-40 7- 2	-08-2	S-09-543-407-5	S-09-543-407-2	US-09-543-407-20
equence 667,	quence 349,	equence 667,	349,	: 1851, A	25157,	7945, A	25158,	7946, A	9 7655, A	7656	7657, A	e 20638,	20638,	equence 8854	equence 885	39,	2	37,	35,	2, Appl	2, App	5834, A	5834,	5834, A	Sequence 34,	quence 55, Appl	equence 2, Appl	e (equence 4. Appl	equence ', Appl	equence to, App	equence 30, App	Sequence 31, Appl	equence 24, App	equence 14,	Φ	equence 22, App	equence 18,	equence 28, App	57,	equence 5, Appl	quence 26,	equence 20, App

ALIGNMENTS

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US-09-543-407-20

; Sequence 20, Application US/09543407
; General Information:
; APPLICANT: White, Aaron P.
; APPLICANT: White, Aaron P.
; APPLICANT: Collinson, S. Karen
; APPLICANT: Kay, William W.
; TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
; TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
; FILE REFERENCE: 920043.406
; CURRENT APPLICATION NUMBER: US/09/543,407
; CURRENT FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Artificial Sequence
    FEATURE:
    OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
    OTHER INFORMATION: sequence containing the replacement fragment
    OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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RESULT 3
US-09-543-407-5
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 151
                                                                                                                                                                 Sequence 5, Application US/09543407 GENERAL INFORMATION:
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Best Local Similarity
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               APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
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APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: White, Aaron P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                               113 ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
APPLICATION NUMBER: US/09/543,407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Pred. No. 3.8e-68;
0; Mismatches 0;
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                                        PEPTIDE SEQUENCES
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RESULT 4
US-08-233-642A-57
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Query Match
Best Local Similarity
Matches 136; Conserv
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Matches
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 5
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                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                               FILING DATE: 26-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                               TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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ADDRESSEE: Seed and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "."
                                                                                                                                                                                       TELEPHONE: (200) 682-6031
                                                                                                                                                                                                                                                 NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity hes 137; Conserv
                                                                                                   TOPOLOGY:
                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/233,642A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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N FOR SEQ ID NO: 57:
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                                                                                                                                  151 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collinson, S. Karen
Clouthier, Sharon C.
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88.4%; Score 684; DB 6; Length 151; 90.1%; Pred. No. 1.9e-65; tive 3; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METHODS AND COMPOSITIONS FOR SALMONELLA-
                                                                                                                                                                                                                                                    920043.403C3
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Pred. No. 5.6e-66;
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                                                                                                                                                                                                                                                                                                                                                                                 Version
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Sequence 18, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI

FILE REFERENCE: 920043.406

CURRENT APPLICATION UNMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 18

LENGTH: 151
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APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, Karen
APPLICANT: Collinson, Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEF
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 151
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US-09-543-407-28
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Best Local S
Matches 136
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81.9%;
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Pred. No. 4.7e-63;
0; Mismatches 0
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RESULT 8
US-09-543-407-12
; Sequence 12, Application US/09543407
; GENERAL INFORMATION:
; APPLICANT: White, Aaron P.
; APPLICANT: Doran, James L.
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Best Local S
Matches 129
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 151
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: White, Aaron P. APPLICANT: Doran, James L.
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ORGANISM: Artificial Sequence
FEATURE:
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FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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                                                                                                                                                ----DQWNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
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73.6%;
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Pred. No. 2.2e-58;
0; Mismatches 0;
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Pred. No. le-58;
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APPLICANT: White, Maron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
ITILE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
ITITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 151
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-09-543-407-14
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 151
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Best Local
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APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
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ORGANISM: Artificial Sequence
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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ
                          SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                            MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                 Conservative
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81.5%;
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80.8%; Pred. No. 1.
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                                                                                                                                                           Score 609; DB 19;
Pred. No. 2.7e-57;
6; Mismatches 22;
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FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 131
TYPE: PRT
ORGANISM: Salmonella enteritidis
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                                                                                                                          US-09-543-407-31
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US-09-543-407-31
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US-09-543-407-24
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Best Local S
Matches 124
                                              Matches
                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 31, Application US/09543407 GENERAL INFORMATION:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 24
LENGTH: 151
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: PRESENTAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT FILICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
mes 124; Conserv
                                          117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                          Conservative
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                                                           77.8%;
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82.1%;
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                                      Score 602; DB 19;
Pred. No. 1.3e-56;
3; Mismatches 11;
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Pred. No. 5.
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5.7e-57;
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                                                                              Length 131;
                                        Indels
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT TILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
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US-09-543-407-16
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US-09-543-407-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 123; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                   TYPE: PRT
 ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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81.5%;
Sequence
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Pred. No. 5.4e-56;
5; Mismatches 23;
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US-08-978-878-4
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US-09-543-407-7
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                                                                                                                                                 Sequence 4, Application US/08978878 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 122;
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN FILE REFERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: SE 8801723-1
EARLIER FILING DATE: 1988-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                            APPLICANT: NORMARK, Staffan APPLICANT: OLSEN, Arne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 151
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APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PE
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Applicat GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPELICANT: White, Aaron P.
APPLICANT: Doran, James L.
                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                            Local Similarity
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121 NNAALVNOTASDSSVMVROVGFGNNATANOY 151
                                                                 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNNNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                          TDÁRNSDLTITQHGGGNGÁDVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                        MKLLKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
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80.8%;
                                                                                                                                                                                                                          68.2%;
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                                                                                                                                                                                                                            Score 528; DB 19;
Pred. No. 1.6e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 574; DB 19;
Pred. No. 1.7e-53;
6; Mismatches 23;
                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                           27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEPTIDE SEQUENCES
                                                                                                                                                                                                                                               Length 151;
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PREPARATION

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EARLIER APPLICATION NUMBER: US 07/347,189
EARLIER FILING DATE: 1993-05-04
EARLIER APPLICATION NUMBER: US 07/789,437
EARLIER FILING DATE: 1993-11-06
EARLIER FILING DATE: 1992-11-03
EARLIER FILING DATE: 1992-11-03
EARLIER FILING DATE: 1992-11-03
EARLIER APPLICATION NUMBER: US 08/187,865
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-10-05
EARLIER APPLICATION NUMBER: US 08/318,519
EARLIER FILING DATE: 1994-10-05
EARLIER FILING DATE: 1994-00-05
EARLIER APPLICATION NUMBER: US 08/495,959
EARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.0
SOFTWARE: PATENTIN Ver. 2.0
SOFTWARE: SCHENTIN VER. 2.0
SOFTWARE: SCHENTIN VER. 2.0
CORGANISM: ESCHERICHIA COLI
Search completed: March 11, 2004, 19:13:12 Job time: 172.3 secs
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                                                                                  121 GNGAAVDOTASNSSVNVTOVGFGNNATAHOY 151
                                                                                                            121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                               Length 151;
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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                                                          is derived by analysis of the total
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2004
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  PCT-US04-03808-14
US-10-93-037A-63
US-09-126-816C-6
US-09-126-816C-6
US-10-767-701-37968
PCT-US04-05654-2748
US-10-603-150-2
PCT-US04-05654-34
US-10-701-2338-9
PCT-US04-05654-34
US-10-771-701-37368
PCT-US04-05654-1755
US-10-767-701-40820
US-10-767-701-45219
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US-09-741-873C-2

US-10-767-701-35342

US-10-779-461-40

US-10-045-674A-591

PCT-US04-05654-2586

US-10-045-674A-527
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US-10-045-674A-594
US-10-417-884A-6047
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                                                                                          Sequence 4, Appli
Sequence 2, Appli
Sequence 35342, A
Sequence 354, Appl
Sequence 591, App
Sequence 527, App
Sequence 590, App
Sequence 594, App
Sequence 6047, App
Sequence 614, Appl
Sequence 614, Appl
Sequence 6, Appli
Sequence 6, Appli
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65	65.5	65.5	65.5	65.5	65.5	65.5	65.5	65.5	65.5	65.5	66	66	66	66	66.5	66.5	66.5	66.5
8.4	8.5	8.5	8.5	8.5	8.5	8.5	8.5	8.5	8.5	8.5	8.5	8.5	8.5	8.5	8.6	8.6	8.6	8.6
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US-10-767-701-59520	PCT-US04-05654-1838	US-10-600-070-170	US-10-600-070-169	US-10-417-884A-5134	US-10-695-499-70	US-10-600-070-119	PCT-US04-05654-120	US-10-417-884A-5818	US-10-779-461-43	US-10-767-701-48913	US-10-151-553-2	US-10-786-850-2	US-10-767-701-43919	US-10-767-701-42650	US-10-786-892-138	PCT-US04-05654-1466	US-10-767-701-37331	US-10-004-115B-34
Sequence 59520,	Sequence 1838, A	Sequence 170, App	Sequence 169, App	4	Sequence 70, Appl	Sequence 119, Ap	Sequence 120, App	Sequence 5818, Ap	Sequence 43, Appl	Sequence 48913,	Sequence 2, Appl	Sequence 2, Appl:	Sequence 43919,	Sequence 42650,	Sequence 138, App	Sequence 1466, Ap	Sequence 37331,	Sequence 34, Appl

ALIGNMENTS

US-09-741-873C-4

Application US/09741873C

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; CRGANISM: Escherichia coli
US-09-741-873C-4
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PRIOR FILING DATE: 1998-05-06
PRIOR PELICATION NUMBER: US 08/978,878
PRIOR PELICATION NUMBER: US 07/347,189
PRIOR PILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR PILING DATE: 1989-05-04
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR PILING DATE: 1991-11-06
PRIOR PILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR PILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
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Best Local Sim
Matches 103;
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GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.0 SEQ ID NO 4 LENGTH: 151
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                                     121
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                                                                             TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQNNGKNSEMTVKQFGG
  GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
                       NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                  SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                         MKLLKVAAIAAIVFSGSAVAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
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                                                                                                                                                                                                                                                          67.8%; Score 525; DB 5; 68.2%; Pred. No. 2.4e-41;
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                                     151
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; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C65560_1.pep
US-10-767-701-35342
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                                                                                                                                                                                                                                                       Sequence 35342, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 (55535)
FILE REFERENCE: 38-21 (55535)
     Matches
                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 35342
LENGTH: 179
                       Query Match
Best Local :
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Best Local Similarity
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PRIOR
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PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1997-11-26
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APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its
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ORGANISM: Escherichia coli
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PRIOR APPLICATION NUMBER: SE 8801723-1
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OR APPLICATION NUMBER: US 07/789,437
OR FILING DATE: 1991-11-06
OR APPLICATION NUMBER: US 07/970,846
OR FILING DATE: 1992-11-03
OR APPLICATION NUMBER: US 08/187,865
OR FILING DATE: 1994-01-28
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   33; Conserv
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     Conservative
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                   9.9%;
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64.9%;
   13;
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                 Score 76.5;
Pred. No. 3
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Pred. No. 2.7e-34;
 Mismatches
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                                   DB 6; Length 179;
   46;
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 Indels
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35;
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US-10-779-461-40
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Best Local
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LENGTH: 250
TYPE: PRT
ORGANISM: artificial
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                                              APPLICANT: HONGENBOOM, HENDRICUS R. J. M.
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMI
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
FILE OF INVENTION: LIBRARIES
FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-10-25
CURRENT FILING DATE: 2001-10-25
CURRENT APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
                                                                                                                                                                                                                                                                                                  APPLICANT: LADNER, ROBERT C. APPLICANT: COHEN, EDWARD H.
                                                                                                                                                                                                                                                            APPLICANT:
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CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 60/447,073
PRIOR FILING DATE: 2003-02-13
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SOFTWARE: PatentIn version 3.2
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ROOKEY,
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KRISTIN L.
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Pred. No. 9;
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                                                                       PCT-US04-05654-2586
                                                                                                                                                 PRIOR APPLICATION NUMBER: 10/675,852
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 2950
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2586
LENGTH: 433
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 591
                Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374,780
PRIOR FILING DATE: 2003-02-25
                                                                                                                                                                                                                                                                                                                     APPLICANT: Yu, Guo-Liang
APPLICANT: Broun, Pierre E
APPLICANT: Kumimoto, Roderick W
APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
FILE REFERENCE: MBI-0047 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                         TYPE: PRT
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                                                                                     OTHER INFORMATION: G1337
                                                                                                       FEATURE:
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Jiang, Cai-Zhong
Heard, Jacqueline E
Haake, Volker
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Ratcliffe, Oliver
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Dubell III, Arnold N
9.5%; Score 73.5; I
ilarity 22.7%; Pred. No. 18;
Conservative 17; Mismatches
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25.7%; Pred. No. 18;
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                                   Length 433;
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FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 527
LENGTH: 533
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US-10-045-674A-527
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                                                                                                    RESULT 8
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Sequence 590, Application PC/TUS0405654
GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
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Best Local (
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TITLE OF INVENTION: NO
TITLE OF INVENTION: OF
TITLE OF INVENTION: OF
TITLE OF INVENTION: OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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T: HOET, RENE
T: HOGENBOOM, HENDRICUS R. J. M.
T: HOOGENBOOM, HENDRICUS R. J. M.
T: HOOGENBOOM, HENDRICUS R. J. M.
TINVENTION: NOVEL METHODS OF CONCRUCTING LIBRARIES COMPRISING
INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMI
TINVENTION: OF PEFFICES, POLYPEPTIDES OR PROTEINS AND THE NOVEL.
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COHEN, EDWARD H.
NASTRI, HORACIO G.
ROOKEY, KRISTIN L.
                                                                                                                                                                                                                                                  KGKLDSVAT-----DYGAAID-----
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25.7%; Pred. No. 24;
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APPLICANT:

Riechmann, Jose Luis Jiang, Cai-Zhong Heard, Jacqueline I Haake, Volker

APPLICANT:

Creelman, I Ratcliffe,

Robert A

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CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374,780
PRIOR FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 10/675,852
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 2950
SOFTWARE: Patentin version 3.2
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SEQ ID NO 590
                                                                                                                            SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 594,
                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/045,674A CURRENT FILING DATE: 2001-10-25 PRIOR APPLICATION NUMBER: 06/198,069 PRIOR FILING DATE: 2000-04-17 PRIOR APPLICATION NUMBER: 09/837,306 PRIOR FILING DATE: 2001-04-17 NUMBER: OF SEQ ID NOS: 635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                       APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAM
TITLE OF INVENTION: OF ERPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LADNER, APPLICANT: COHEN,
                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                        FILE REFERENCE: DYAX/002 CIP2
OTHER INFORMATION: Description of Artificial Sequence: M13-III OTHER INFORMATION: protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                           ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLICANT: Kumimoto, Roderick W
PPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYMCTEOTIDES AND POLYPEPTIDES IN PLANTS
TILE REFERENCE: MBI-0047 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICANT:
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                                                                                                           434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 AAIVVSGSALAGVVPQW----GGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKY 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATID--QWNAKNSDITVGQYGGNNA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAYASSADNIARLLQGWMRPGGG----GGGNGKGPEAS-----GSTSTTATTQQQPQ-- 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/10045674A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Broun, Pierre E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yu, Guo-Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Century, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repetti, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dube1
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Dubell III, Arnold N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                RENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROBERT C.
EDWARD H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HORACIO G.
KRISTIN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.4%; Score 73; DB 1; Length 321; 23.5%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -CSGEGAASASASASQSGAAAAATAQTPECSTETSKMATGGGAGGPA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42;
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; INAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-417-884A-6047
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US-10-417-884A-6047
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6047,
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                                                                                                                                                                                                                                                                                          TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6047:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQUENCE 6047, Application US/10417884A
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532
FILING DATE: 30-Unn-1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: JULY 2, 1997
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                     FEATURE:
                                                                                                                                                                            HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (781)893-5007
                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 NSOMAQVGDGDNS 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 SVMVROVGFGNNA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 ĠĠSĠGGSĠĠSEGĠ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 GGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGAD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 9.4%;
1 Similarity 25.6%;
34; Conservative 1
                                                                                                                                                                                                                                                 LENGTH: 708 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/417,884A
FILING DATE: 17-Apr-2003
                                                                                                                                                    ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 100 Beaver Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
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9.3%;
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Score 72;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 72.5;
Pred. No. 2
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                                                                           6047:
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
DB
48;
                  6
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Length 708;

RESULT 11 PCT-US04-0

-US04-03808-14

APPLICANT:

밁 ફ 밁 ঠ 밁 ঠ

430

Matches

43;

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; ORGANISM: Gallus gallus PCT-US04-03808-14
                                                                                                                                                                                                                                                                                                                               Sequence 63, Application US/10093037A
GENERAL INFORMATION:
APPLICANT: Jay M. Short
APPLICANT: Bylina, Edward
APPLICANT: Swanson, Ronald V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 14
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GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
                                                                                                         FILE REFERENCE: 564462001402
CURRENT APPLICATION NUMBER: US/10/093,037A
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: US 09/910,579
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 09/134,078
PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 38586-332
CURRENT APPLICATION NUMBER: PCT/US04/03808
CURRENT FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: US 60/445,672
PRIOR FILING DATE: 2003-02-07
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                            TITLE OF INVENTION: ENZYMES HAVING GLYCOSIDASE ACTIVITY AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Nell Peptide Expression Systems and TITLE OF INVENTION: Formation Activity of Nell Peptide
                                                                  PRIOR APPLICATION NUMBER: US 08/949,026 PRIOR FILING DATE: 1997-10-10
                    APPLICATION NUMBER: US 60/056,916 FILING DATE: 1996-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           545 KISEITGKANNYTDGKVSEINSQLTASINEVDTTAKDA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 TIDOWNAKNSDITVGQYGGNNAAL-----VNQTASDSSVMVRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                486 ATKG-AVQIEWLKLEKGNTRTPNISEYKYRGTGMRDSNNPKDYVWDLAPEYVEDNLATDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 LRNKYE--FTILVTLKQAHLNSGVIFSIHHLDHRYLELESSGHRN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 DARKYDQLVTRVVTHEMAHAGQGA-----DNSTJELTQNGFRN 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LKVAAFAAIVVSGSALAGV--VPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                   Bylina, Edward
Swanson, Ronald V.
Mathur, Eric J.
Lam, David E.
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29.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 72; DB 1;
Pred. No. 58;
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                                                                                                                                                                                                                       RESULT 14
US-10-767-701-37968
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US-10-093-037A-63
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SEQ ID NO 63
LENGTH: 956
                                                                                                                                                                          Sequence 37968, Application US/10767701 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09126816C GENERAL INFORMATION:
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(53535)B CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
                                                                                                           APPLICANT: Kovalic, Davi
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/EP97/00426
PRIOR FILING DATE: 1997-01-31
PRIOR APPLICATION NUMBER: 96 101 469.3
PRIOR FILING DATE: 1996-02-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 98501/254992/bet
CURRENT APPLICATION NUMBER: US/09/126,816C
CURRENT FILING DATE: 1998-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VON EICHEL-STREIBER, CHRISTOPH APPLICANT: BOQUET, PATRICE APPLICANT: THELESTAM, MONICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHOD OF INACTIVATION OF RAS SUBFAMILY PROTEINS AND TITLE OF INVENTION: AGENTS THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Clostridium sordellii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27;
                                                                                                                                                                                                                                                                                                                                                      96 GFRNNAT----IDOWNAKNSDITYGQYGGNNAALVN 127
                                                                                                                                                                                                                                                                                                                                                                                                  57 DNYLNTYKKSGRNKAL-----KKFKEYLTMEVL-----ELKNNSLTPVEKNLHFIWI 103
                                                                                                                                                                                                                                                                                                                                                                                                                                           42 DSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIBLTQN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 RVVTHEMAHAGQGADNSTIEL--TQNGFRNNATI------
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19.8%; Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.2%; Score 71.5; DB 5;
28.1%; Pred. No. 2.5e+02;
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Mismatches
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Query Match Best Local

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Matches

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US-10-093-037A-63 RESULT 12

SEQ

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APPLICANT: Gutterson, Neal
APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
APPLICANT: Eroun, Pierre E
APPLICANT: Kumimoto, Roderick W
APPLICANT: Kumimoto, Roderick W
APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374,780
PRIOR APPLICATION NUMBER: 10/675,852
PRIOR APPLICATION NUMBER: 10/675,852
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 2950
SOFTWARE: Patentin version 3.2
SEQ ID NO 2748
LENGTH: 399
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PCT-US04-05654-2748
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                                                                                                                                               Query Match 9.2%; Score 71; DB 1; Length 399; Best Local Similarity 22.0%; Pred. No. 28; Matches 44; Conservative 13; Mismatches 53; Indels
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APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
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EQ ID NO 37968
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OTHER INFORMATION: G1882
                                                                                                                                                                                                                                                                                               ORGANISM: Arabidopsis thaliana
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26; Conserv
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                                                                GGGGGSTSSGNSKSQDSATSNDQYHHRAMANNQMGPPSSSSSLSSLLSSYNAGLIPGHDH 214
                                                                                                       GGGGNHNGGGNSSGPDSTLSIYQY------GSANAALALQSDARKYD------
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Century, Karen
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Reuber, T. Lynne
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------QLVTRVVTHEMAHAGQGADNSTIELTQNGFR 98
                                                                                                                                                 Indels
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328 SASSAMV----
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                                                                ----DOWNFPATNOLPLGGLDPFDQQHQMEQQNPGYGLVTGSGQYRPKNIFHNLISSSS 327
---TATASQ 340
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Search completed: March 11, Job time: 5.3 secs 2004, 19:14:17

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Score
Match Length DB
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/ cgn2_6/ptodata/2/paa/US082_COMB.pep:*
/ cgn2_6/ptodata/2/paa/US084_COMB.pep:*
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/ cgn2_6/ptodata/2/paa/US085_COMB.pep:*
/ cgn2_6/ptodata/2/paa/US085_COMB.pep:*
/ cgn2_6/ptodata/2/paa/US086_COMB.pep:*
/ cgn2_6/ptodata/2/paa/US089_COMB.pep:*
/ cgn2_6/ptodata/2/paa/US090_COMB.pep:*
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/ cgn2_6/ptodata/2/paa/US093_COMB.pep:*
/ cgn2_6/ptodata/2/paa/US093_COMB.pep:*
/ cgn2_6/ptodata/2/paa/US093_COMB.pep:*
/ cgn2_6/ptodata/2/paa/US095_COMB.pep:*
/ cgn2_6/ptodata/2/paa/US096_COMB.pep:*
/ cgn2_6/ptodata/2/paa/US096_COMB.pep:*
/ cgn2_6/ptodata/2/paa/US099B_COMB.pep:*
/ cgn2_6/ptodata/2/paa/US099B_COMB.pep:*
/ cgn2_6/ptodata/2/paa/US099B_COMB.pep:*
/ cgn2_6/ptodata/2/paa/US100_COMB.pep:*
/ cgn2_6/ptodata/2/paa/US101_COMB.pep:*
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/cgn2_6/ptodata/2/paa/USO6_
/cgn2_6/ptodata/2/paa/USO7_
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2 6/ptodata/2/paa/US080_COMB.pep:*
2 6/ptodata/2/paa/US081_COMB.pep:*
                                                                           SUMMARIES
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US-10-369-493-20638 US-60-360-039-20638 US-60-360-039-20638 PCT-US01-05992-146 US-09-793-306-146 US-09-793-306-146 US-09-739-449-8854 US-09-739-449-8854	US-09-543-407-22 US-09-543-407-28 US-09-543-407-28 US-09-543-407-30 US-09-543-407-20 US-09-543-407-12 US-09-543-407-14 US-09-543-407-16 US-09-543-407-16 US-09-543-407-16 US-09-543-407-17 US-09-543-407-17 US-09-543-407-7 US-08-978-878-4 US-09-543-407-7 US-08-978-878-4 US-09-543-407-7 US-08-978-878-4 US-09-543-407-3 US-09-543-407-3 US-09-543-407-37 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-543-407 US-09-5	
Sequence 2038, A Sequence 2038, A Sequence 2038, A Sequence 146, App Sequence 147, App Sequence 147343, Sequence 8854, Ap	Sequence 22, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 30, Appl Sequence 20, Appli Sequence 11, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 17, Appli Sequence 4, Appli Sequence 4, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 534, Appli Sequence 5834, Appli Sequence 5834, Appli Sequence 31, Appli Sequence 32, Appli Sequence 33, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 383, Appli Sequence 383, Appli Sequence 5833, Appli Sequence 5833, Appli Sequence 5833, Appli Sequence 5833, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 23, Appli Sequence 23, Appli Sequence 21, Appli Sequence 21, Appli Sequence 22, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli	

ALIGNMENTS

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APPLICANT: White, Aaron P.

APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

FILE REFERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/99/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 22

LENGTH: 151

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
US-09-543-407-22
; Sequence 22, Application US/09543407
; GENERAL INFORMATION:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                               ORGANISM: Artificial Sequence FEATURE:
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Description

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Sequence 28, Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER
TITLE OF INVENTION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
TYPE: PRT
TYPE: PRT
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            Sequence 5, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043,406
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Best Local Similarity 91.1
144; Conservative
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CURRENT APPLICATION NUMBER: US/09/543,407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragmer OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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                                                                                                                                                                                                                                                                                  114
                                                                                                                                                                                                                                                                                                  114 TVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                           61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHA------DQNNAKNSDI 113
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                                                                                                                                                                                                                                                                     TVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                  SDARKSETTITQSGYGNGAD-----YDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.8%; Score 712; DB 19;
91.1%; Pred. No. 9.1e-68;
vative 0; Mismatches 0;
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                                   PEPTIDE SEQUENCES
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; MOLECULE TYPE: protein US-08-233-642A-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-233-642A-57
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Query Match
Best Local Similarity
Matches 136; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642A
FILING DATE: 26-APR-1994
CLASSIPICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920043.403
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 57, Applicat GENERAL INFORMATION:
                                                                                                                                                                            TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 6300 Co
CITY: Seattle
STATE: Washingt
                                                                                                                     TOPOLOGY:
                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 98104-7092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
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                                                                                                                                      amino acid
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                                                                                                                                                             151 amino acids
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Collinson, S. Karen
Clouthier, Sharon C.
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Conservative

2

Score 677; DB 6; Length 151; Pred. No. 5.2e-64; Mismatches 13; Indels

0

Gaps

0

87.2%; 90.1%;

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Sequence 20, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PREFILE REFERENCE: 920043,406

CURRENT APPLICATION UNMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOPTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 20

LENGTH: 151
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US-09-543-407-20
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US-09-543-407-30
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Best Local S
Matches 136
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-543-407-30
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CURRENT FILING DATE: 2000-04-05
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OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tch 84.7%;
al Similarity 81.9%;
136; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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59
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Pred. No. 7.4e-62;
0; Mismatches 0;
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RESULT 8 US-09-543-407-12

Sequence 12, Application US/09543407 GENERAL INFORMATION: APPLICANT: White, Aaron P. APPLICANT: Doran, James L.

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NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 151
TYPE: PRT
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Doran, James L.
APPLICANT: Collingon, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/543,407
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
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                           HEMAHADQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                         SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT
                                                                                                                                                MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                            SDARKSETTITQSGYGNGADVGQGAD-----
 HEMAHA----
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                                                                                                                                                                                                                      78.5%; Score 609; DB 19; 73.6%; Pred. No. 1.1e-56; ive 0; Mismatches 0;
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Pred. No. 8.9e-58;
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                                                                                                                                                                                                                                                           Length 151;
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Best Local S
Matches 122
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 151
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APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM
TITLE OF INVENTION: PRESENTATION OF HETEROLOC
FILE REFERENCE: 920043.406
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                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
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OTHER INFORMATION: sequence containing the replacement fragme
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major
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                                                                                                                                                                    Similarity
                                SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
                                                                     MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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                                                                                                                                                     Conservative
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                                                                                                                                                                77.6%;
81.5%;
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                                                                                                                                             Score 602; DB 19;
Pred. No. 6e-56;
5; Mismatches 23;
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Pred. No. 3.6e-56;
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                                                                                                                                                                                DB 19;
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                                                                                                                                                                                Length 151;
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CURRENT APPLICATION NUMBER: US/09/543,407; CURRENT FILING DATE: 2000-04-05; NUMBER OF SEQ ID NOS: 59; SOFTWARE: FASTSEQ for Windows Version 4.0; SEQ ID NO 26; LENGTH: 151
TYPE: PRT
TYPE: Artificial Sequence; FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: White, Maron P.
; APPLICANT: Doran, James L.
; APPLICANT: Collinson, S. Karen
; APPLICANT: Kay, W4111
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US-09-543-407-18
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                                                                                                                                              TILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/09543407 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Callinson, S. Karen
APPLICANT: Xay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
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TYPE: PRT
ORCANISM: Artificial Sequence
ORCANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragmen
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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81.5%;
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Pred. No. 7.7e-56;
4; Mismatches 24
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Query Match

77.3%;

Score 600;

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19;

Length 151

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Sequence 31, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PERILE REFERENCE: 920043.406

CURRENT APPLICATION MUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 31

TUDE: DEF.
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Matches
                                        CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 151
                                                                                                                                                                                                                                                                                 Sequence 16, Applica GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collingon, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Salmonella
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hes 123; Conservative
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89.3%;
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Pred. No. 2.8e-55;
2; Mismatches 12;
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5; Mismatches 23;
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RESULT 15
US-08-978-878-4
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                                                                                                                                                          Sequence 4, Application US/08978878 GENERAL INFORMATION:
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SEQ ID NO 7
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Best Local Similarity
Matches 122; Conser
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Best Local Similarity
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS FILE REFERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: SE 8801723-1
EARLIER FILING DATE: 1988-05-06
                                                                                                                   APPLICANT: NORMARK, Staffan APPLICANT: OLSEN, Arne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 151
TYPE: PRT
ORGANISM: Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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Pred. No. 3.4e-52;
5; Mismatches 24;
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Pred. No. 3e-47;
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EARLIER APPLICATION NUMBER: US 07/347,189

EARLIER FILING DATE: 1989-05-04

EARLIER APPLICATION NUMBER: US 07/789,437

EARLIER APPLICATION NUMBER: US 07/970,846

EARLIER APPLICATION NUMBER: US 08/187,865

EARLIER FILING DATE: 1994-10-28

EARLIER FILING DATE: 1994-10-103

EARLIER FILING DATE: 1994-10-28

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EARLIER FILING DATE: 1995-06-28

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EARLIER FILING DATE: 1995-06-28

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EARLIER FILING DATE: 1994-10-26

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Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/1/paa/USO9_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/USO0_NEW_COMB.pep:*
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US-09-741-873C-2
US-10-767-701-45603
US-10-451-467A-314
US-10-79-461-19
US-10-79-461-6
US-10-767-701-35342
US-10-767-701-32417
US-10-767-701-41-29
PCT-US04-02338-49
US-10-779-461-40
US-10-779-461-40
US-10-767-701-61402
US-10-767-701-61402
US-10-767-701-61402
US-10-767-701-61404
PCT-US04-05654-2744
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US-10-779-461-18
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US-10-779-461-18
US-10-045-674A-559
PCT-US04-05654-2748-594
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US-10-100-683-7608
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4, Appli
45603, A
314, App
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6, Appli
33342, A
33347, Appli
61422, A
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61422, A
591, Appl
6142, Appl
6142, Appl
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527, Appl
527, Appl
52748, Ap
1755, Ap
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1964, Appl
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US-10-093-037A-63	US-10-764-425-187	PCT-US04-02188-187	US-10-767-701-44940	US-10-767-701-32700	US-10-603-163-2	PCT-US04-05654-1466	PCT-US04-05654-1844	US-10-779-461-30	US-10-779-461-59	PCT-US04-05654-1743	PCT-US04-02242-58	US-10-767-701-61575	US-10-641-678-45	PCT-US04-05654-590	US-10-779-461-22	US-10-190-902B-10	US-10-603-150-2	US-10-417-884A-5134
Sequence 63, Appl	Sequence 187, App	Sequence 187, App	Sequence 44940, A	Sequence 32700, A	Sequence 2, Appli	Sequence 1466, Ap	Sequence 1844, Ap	Sequence 30, Appl	Sequence 59, Appl	Sequence 1743, Ap	Sequence 58, Appl	Sequence 61575, A	Sequence 45, Appl	Sequence 590, App	Sequence 22, Appl	Sequence 10, Appl	Sequence 2, Appli	Sequence 5134, Ap

ALIGNMENTS

US-09-741-873C-4

Sequence 4, Applicat GENERAL INFORMATION:

Application US/09741873C

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CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1999-11-26
PRIOR FILING DATE: 1999-05-04
PRIOR FILING DATE: 1989-05-04
PRIOR FILING DATE: 1989-05-04
PRIOR PRICING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR PRILING DATE: 1991-11-03
PRIOR PRICING DATE: 1992-11-03
PRIOR PRICING DATE: 1992-11-03
PRIOR PRICING DATE: 1992-11-03
PRIOR PRICING DATE: 1992-11-03
PRIOR PRICING DATE: 1994-01-28
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR PRICING DATE: 1994-01-28
PRIOR PRICING DATE: 1994-01-30
PRIOR PRICING DATE: 1994-10-05
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Matches 104
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APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein
FILE REFERENCE: 012889-084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 151
TYPE: PRT
ORGANISM: Escherichia coli
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                               NNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                  66.8%; Score 518; DB 5; 68.9%; Pred. No. 8.6e-39; ive 18; Mismatches 29
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; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C82834_1.pep US-10-767-701-45603
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                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Kovalic,
APPLICANT: Zhou, Yi
APPLICANT: Cao, Yon
                                                                                                                                                                                                  SEQ ID NO 45603
LENGTH: 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 45603, Application US/10767701
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Best Local Similarity
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                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
                                                                                                                                                                                                                                                                                    APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
FILE REFERENCE: 38-21(53535)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/741,873C CURRENT FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: SE 8801723-1 PRIOR FILING DATE: 1998-05-06
                                                          NAME/KEY: unsure
LOCATION: (1)..(234)
OTHER INFORMATION: unsure at all Xaa locations
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                                                 FEATURE:
                                                                                                                                                        ORGANISM: Sorghum bicolor
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TITIE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
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APPLICANT: Olsen, Arne
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FILING DATE: 1992-11-03
APPLICATION NUMBER: US 08/187,865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1989-05-04
APPLICATION NUMBER: US 07/789,437
FILING DATE: 1991-11-06
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FILING DATE: 1997-11-26
APPLICATION NUMBER: US 07/347,189
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                                                                                                                                     Sequence 19, Application US/10779461 GENERAL INFORMATION:
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APPLICANT: MORTON, Philip A
TITLE OF INVENTION: ANTIBODIES TO C-MET FOR
FILE REPERBNCE: 00980/1
CURRENT APPLICATION NUMBER: US/10/779,461
CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 60/447,073
PRIOR FILING DATE: 2003-02-13
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Best Local Similarity
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TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
TITLE OF INVENTION: YEAST AND FUNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CONTRERAS, ROLAND HENRI
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TYPE: PRT
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                                                                                                                                                                                                                                                      249 YGSN 252
                                                                                                                                                                                                                                                                                           142 FGNN 145
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                                                                                                                                                                                                                                                                                                                                                               86 -- DNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALVNQTASDS--SVMVRQVG 141
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                                                                                                                                                                                                                                                                                                                                                                                                         GSSNNNDSYGSNNNDS
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LUYTEN, WALTER HERMAN MARIA LOUIS
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Pred. No. 2.9;
L4; Mismatches
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MOTTON, Philip A
TITLE OF INVENTION: ANTIBODIES TO C-MET FOR THI
FILE REFERENCE: 00980/1
CURRENT APPLICATION NUMBER: US/10/779,461
CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 60/447,073
PRIOR PILING DATE: 2003-02-13
PRIOR PILING DATE: 2003-02-13
NUMBER OF SEQ ID NOS: 161
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                                                                                                                                                                                                                                                                             RESULT 7
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US-10-779-461-6
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US-10-779-461-19
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 (5.5358)
CURRENT APPLICATION INVESER: US/10/767,701
CURRENT APPLICATION AND ADDITION OF SEQ ID NOS: 63128
SEQ ID NO 35142
LENGTH: 179
                                                                                                                                                                                                                  Sequence 35342, Application US/10767701 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOPTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 250
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SOFTWARE: PatentIn versio
SEQ ID NO 19
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Best Local :
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Best Local Similarity
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ORGANISM: artificial
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                                                                                                                                                                                                                                                                                                                                                                                                                  113 WGRGTLVTVSSGGGGGGGGGGGGG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 KWGQGTLVTVSSGGGGSGGGGSGGG
                                                                                                                                                                                                                                                                                                                                      163 GSSSDIGDYNHVSWYQQHPGKAPKLMIYDVNKWPSGVPDRFSGSKSGNTASL 214
                                                                                                                                                                                                                                                                                                                                                                             76
                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 WG-----GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSE-TTITQSGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 SGYGNGADVGQGADN-YDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAAL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 QWG------GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ---SDARKSETTITQ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                           GNGADVG--QGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAAL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S--GSSSNIGNNAVNWYQQLPGKAPKLLIYYNDLLPSGVSDRFSGSKSGTSASL
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Pred. No. 3
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TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR TITLE OF INVENTION: ESCHERICHIA COLI FILE REFERENCE: ELITRA.001C1
CURRENT APPLICATION NUMBER: US/10/771,241
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR PRICH DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ. ID NOS: 485
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US-10-767-701-32417
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                                                                                                                                                                                                                     Sequence 299, Application US/10771241
GENERAL INFORMATION:
APPLICANT: Syskind, Judith
APPLICANT: Forsyth, R. Allyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(5355)B CURRENT APPLICATION NUMBER: US/10/767,701 CURRENT FILING DATE: 2004-01-29 NUMBER OF SEQ ID NOS: 63128 SEQ ID NO 32417
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Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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les 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                          191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 GSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQY-GSANAALALQSDARKSETTITQSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 GGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                  YGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNA 123
                                                                                                                                                                                                                                                                                                                                                                                            SGTNAGPG-GAGSY---
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29.4%; Pred. No. 4.8;
cive 14; Mismatches
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Pred. No. 3.
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RESULT 11
US-10-779-461-40
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; ORGANISM: E. Coli
US-10-771-241-299
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                                                                                                                                                        Sequence 40, Application US/10779461 GENERAL INFORMATION:
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Matches
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Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
           PRIOR APPLICATION NUMBER: 60/447,073
PRIOR FILING DATE: 2003-02-13
NUMBER OF SEQ ID NOS: 161
                                                                  APPLICANT: MORTON, Philip A
TITLE OF INVENTION: ANTIBODIES TO C-MET FOR THE TREATMENT OF CANCERS
FILE REFERENCE: 00980/1
CURRENT APPLICATION NUMBER: US/10/779,461
CURRENT FILING DATE: 2004-02-13
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SOFTWARE: PatentIn
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PRIOR FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US60/461,789
PRIOR FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US60/470,684
PRIOR FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: MAPCAXS AS MODIFIERS OF THE APC AND AXIN PATHWAYS AND METHODS TITLE OF INVENTION: USE FILE REPERENCE: EXO4-003C-PC CURRENT APPLICATION NUMBER: PCT/US04/02338 CURRENT FILING DATE: 2004-01-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US60/479,650 PRIOR FILING DATE: 2003-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 54
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PRIOR FILING DATE: 2003-01-29
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27; Conserv
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                                                                                                                                                                                                                                                              -----AGVSSTAPLGPGA 169
                                                                                                                                                                                                                                                                                                                             VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEA-
                                                                                                                                                                                                                                                                                               KSETTITQSGYGNGADVGQGA 85
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26.1%; Pred. No. 9.
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US-10-045-674A-591
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US-10-767-701-61422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-767-701-61422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE: ; OTHER INFORMATION: phage display generated human antibody US-10-779-461-40
                                                                                                                                                                                    Sequence 591, Application US/10045674A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 61422
LENGTH: 134
TYPE: PRT
 TITLE OF
TITLE OF
TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 61422, Application US/10767701 GENERAL INFORMATION:
                                                                                                           APPLICANT: LANNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: WASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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LENGTH: 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei
                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(53535)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 250
TYPE: PRT
ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: 9306804.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                     124 VQTN 127
                                                                                                                                                                                                                                                                                                                                      108 AKNS 111
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                                                                                                                                                                                                                                                                                                                                                                                                               48 YQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28;
T: HOOGENBOOM, HENDRICUS R. J. M.
INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMI
INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
INVENTION: LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 AAVLAGASLDTSPVTFHAGYMPLFGGGNLVPSPGGRSVRLKLDRHTGSGFVS-----KSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 AIVVSGSAL-----AGVVPQWGGGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 YCAISPLRGLTADVFDVWGQGTLVTVSSGGGGSGGGGSGGG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 FAAIVVSGSALAGVVPQWG------GGGNHNGGGNSSGPDSTLSIYQYGSANAALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                          NASTRI, HORJ
ROOKEY, KRIS
HOET, RENE
                                                                                                                                                                                                                                                                                                                                                                            YHHGFFSASIKLPDD---DTAGVVVAFYLSNADVFPG--NHDEVDFELLGNRRGH--EWR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhou, IIII.
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23.4%;
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Pred. No. 4.1;
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                                     FAMILY
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CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEO ID NOS: 635
SOPTWARE: PATENTIN Ver. 2.1
SEO ID NO 527
LENGTH: 533
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 591
LENGTH: 424
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                                                                                                                                       ; PEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vector pCES5; OTHER INFORMATION: protein sequence
US-10-045-674A-527
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                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HOET, RENE
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OP INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OP INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMI
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DYAX/002 CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO
APPLICANT: ROOKEY, KRISTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Unknown Organism
PEATURE:
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15 SGSALAGVVPQWGG--GGNHNGGGNSSGPDSTLSIYQ-YGSANAAL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 R-KSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.7%;
Similarity 25.0%;
36; Conservative 15
                                                                                9.7%;
Similarity 25.0%;
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                                                                 Conservative
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                                                               15; Mismatches 48; Indels 45;
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Pred. No. 16
                                                                                  Score 75.5;
Pred. No. 22;
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                                                                                                      DB 6;
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                                                                                                    Length 533;
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Search completed: March 11, Job time: 6.3 secs
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US-10-767-701-56903
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GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yinua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 56903
LEEGTH: 174
TYUEF. DET
                                                                                                                                                                                                                                                                                                                          Matches
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                                                                               118 TAVTVGNEVLSGTNAAML
                                                                                                                       111 SDITVGQ--YGGNNAALV 126
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                                                                                                                                                                 66 ADAR-----VLRAFAGSGVDFTVGVP--DRLVPRMATDPSA-AASWVRSNLLPHLPATSI 117
                                                                                                                                                                                                       61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKN------
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                                                                                                                                                                                                                                                                                    3 LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNG--GGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                              6 MLAAAAAFAVLAPPAASSGPTPAPPALGINYGQVADNLPPPQAALLLLRALNATRVKLYD
                                                                                                                                                                                                                                                                                                                                               9.7%;
Similarity 26.1%;
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                    2004, 19:14:18
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Pred. No. 6.2;
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                                                                                                                                                                                                                                                                                                                            59; Indels
                                                                                                                                                                                                                                                                                                                                                                  Length 174;
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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein search, using sw model
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ALIGNMENTS	73-464-1219	-60-167-217-1497	-09-614-150A-149	-09-614-150-	-60-191-681-1901	-60-191-637-24	-09-614-150A-240	9-614-150-2408	-09-543-407-	-09-914-543-	-09-543-407-6	-10-417-886-583	09-252-6910	-09-252-691-5833	-60-360-039-206	-10-369-493-2063	-09-543-407-3	-543-407-3	-09-543-407-3	-09-543-407-3	9-741-873B-	-08-978-878-2	9-543-407-34	-10-417-886-5	9-252-691C-5	S-09-252-691-58	08-233-642A-5	-60-444-371-	60-352-946-2	S-09-741-873E	-08-978-87	-09-543-407-7	09-543-407-	-09-543-407-3	-09-543-407-2	-09-543-407-1	-09-543-407-	-09-543-407-2	US-09-543-407-1	08-233-642A-	9-543-407-5	-09-543-407-3	S-09-543-407-	-09-543-407-
	1219	1497	1491	14916,	19019,	2417	24084,	24084,	8,	44,	6	583	5833,	583	20638,	20	39	32	37	35 35	ຸນ	N	34	58	5834	5834	quence 55, Appl	equence 2, Appl	equence 2	equence 4. Appl	Sequence /, Appli	equence to, App	equence 28, App	equence 31, App	equence 20,	equence 18,	26, App		Sequence 12, App	quence 57, Appl	equence 5,	quence 30.	equence 14	equence 24,

ALIGNMENTS

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WESULT 1

US-09-543-407-24

US-09-543-407-24

Sequence 24, Application US/09543407

GENERAL INFORMATION:
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
ITILE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
ITILE OF INVENTION: NUMBER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FASCISQ for Windows Version 4.0

SEQ ID NO 24

LENGTH: 151

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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Regult No.

Score

Query Match Length DB

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Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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APPLICANT: Doran, James L.

APPLICANT: Kay, William W.

ITITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

ITITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEITLE REFERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 14
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US-09-543-407-30
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US-09-543-407-14
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                                                                                                                                               Sequence 30, Application US/09543407 GENERAL INFORMATION:
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Best Local
                   APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                         APPLICANT: White, Aaron P. APPLICANT: Doran, James L APPLICANT: Collinson, S. APPLICANT: Kay, William W
CURRENT APPLICATION NUMBER: US/09/543,407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 151
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91.1%;
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Pred. No. 9.2e-68;
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FILE REFERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 151

TYPE: PRT
ORGANISM: Salmonella enteritidis
US-09-543-407-5
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NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for W
SEQ ID NO 30
LENGTH: 151
                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Best Local Similarity
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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 121
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                   HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                      SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                 SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                   MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNAT----
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                                                                                                                                                                                                          Conservative
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59
Windows Version
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                                                                                                                                                                                                                       Score 690; DB 19;
Pred. No. 3.4e-65;
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Pred. No. 2.9e-66;
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US-08-233-642A-57
; Sequence 57, Application US/08233642A
; GENERAL INFORMATION:
; APPLICANT: Kay, William W.

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APPLICANT: COllinson, S. Karen
APPLICANT: KAY, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENVATION OF HETEROLOGOUS PER
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEO ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 151
                                                                                                                                                                                                                                                                                                      RESULT 6
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Best Local S
Matches 138
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642A
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein -08-233-642A-57
                                                                                                                                                                                                         APPLICANT: White, Aaron P. APPLICANT: Doran, James L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
TELEY, 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
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REFERENCE/DOCKET NUMBER: 920043.403C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: King, Joshua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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6300 Columbia Center,
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Clouthier, Sharon C.
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Pred. No. 4.4e-65;
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US-09-543-407-26
US-09-543-407-26
; Sequence 26, Application US/09543407
; GENERAL INFORMATION:
; APPLICANT: White, Aaron P.
; APPLICANT: Doran, James L.
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                                                                                                          RESULT 8
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Best Local S
Matches 128
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LENGTH: 151
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragmen
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FABUSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                              HEMAHADQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
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79.8%;
                                                                                                                                                                                                                                                                                                                                                                                                               78.6%; Score 609; DB 19; 73.6%; Pred. No. 1.6e-56;
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Pred. No. 1.9e-61;
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CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 151
                                                                                                                                                                                            Query Match
Best Local
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: White, Aaron P. APPLICANT: Doran, James L
                                                                                                                                                                                                                                                                            OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragmen OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragmer
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Collinson, S. Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                             61
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                                                                                                                                                                                              Similarity
                                                                                                                        MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                               MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                        SDARKSETTITOSGYGNGADVGOGADNSTIELTONGFRNNATIDOWNAKNYDQLVTRVVT 120
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                                                                                                                                                                          Conservative
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82.1%;
                                                                                                                                                                                            78.5%;
82.1%;
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                                                                                                                                                                                            Score 608; DB 19;
Pred. No. 2.1e-56;
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Pred. No. 1.6e-56;
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                                                                                                                                                                                                                 DB 19;
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                                                                                                                                                                                                              Length 151;
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; TYPE: PRT; ORGANISM: Salmonella enteritidis US-09-543-407-31
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US-09-543-407-31
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                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 31
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Matches
    Matches 118;
                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 31, Application US/09543407 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
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                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragmer OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 151
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                           ENGTH: 131
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    Conservative
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                     77.8%;
90.1%;
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82.1%;
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Score 603; DB 19;
Pred. No. 5.9e-56;
2; Mismatches 11
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Pred. No. 3.4e-56;
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                                                                                                                                                                                                                                                                                           PEPTIDE SEQUENCES
                                       Length 131;
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Indels
0;
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Gaps
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21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD 80

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APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEFILE REFERENCE: 92043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
                              APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEF
FILE REFERENCE: 92004, 406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 151
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US-09-543-407-16
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Pred. No. 1.5e-55;
3; Mismatches 25;
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                                                                                                                                                                             RESULT 15
US-08-978-878-4
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; ORGANISM: Escherichia
US-09-543-407-7
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                                                                                                                                             Sequence 4, Application US/08978878 GENERAL INFORMATION:
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SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 106;
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Best Local Similarity
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Best Local Similarity
APPLICANT: NORMARK, Staffan
APPLICANT: OLSEN, Arne
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN
FILE REFERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: SE 8801723-1
EARLIER FILING DATE: 1988-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
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NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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Pred. No. 2.3e-48;
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Pred. No. 7.2e-53;
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EARLIER APPLICATION NUMBER: US 07/347,189
EARLIER FILING DATE: 1989-05-04
EARLIER FILING DATE: 1991-11-06
EARLIER FILING DATE: 1991-11-06
EARLIER APPLICATION NUMBER: US 07/970,846
EARLIER FILING DATE: 1992-11-03
EARLIER APPLICATION NUMBER: US 08/187,865
EARLIER APPLICATION NUMBER: US 08/187,865
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER APPLICATION NUMBER: US 08/318,519
EARLIER FILING DATE: 1994-10-05
EARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIAN DATE: 1995-06-28
INDO 4
LENGTH: 151
TYPE: PAT
ORGANISM: Escherichia coli
US-08-978-878-4
Search completed: March 11, 2004, 19:13:13 
Job time : 172.3 secs
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Listing first 45 summaries
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Perfect score:
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Gapop 10.0 , Gapext 0.
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  US-10-771-241-299
US-10-771-41-364
PCT-US04-05654-590
US-10-100-683-10326
US-10-100-683-7608
US-10-707-461-40
US-10-767-701-40104
US-10-045-674A-527
PCT-US04-02188-187
US-10-767-701-45603
US-10-767-701-426-41
US-10-767-701-426-41
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US-10-767-701-426-41
US-10-767-701-426-41
US-10-603-150-2
US-10-603-150-2
PCT-US04-05654-1756
PCT-US04-05654-1756
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US-09-741-873C-2
PCT-US04-02338-49
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2 9, Appli
3 299, App
5 290, App
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5 10326, A
7 1008, Ap
7 1009, Appli
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5 291, Appli
5 2010, Appli
6 4014, Appli
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68	68.5	68.5	69	69	69.5	70	70	70	70	70	70	70.5	70.5	70.5	70.5	70.5	70.5	70.5
8.8	8.8				9.0			9.0	9.0	9.0	9.0	9.1	9.1	9.1	9.1	9.1	9.1	9.1
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Sequence 59665, A	Sequence 30, Appl	Sequence 47075, A	Sequence 26, Appl	Sequence 6, Appli	Sequence 1755, Ap	Sequence 1466, Ap	Sequence 45219, A	Sequence 2748, Ap	Sequence 59, Appl	Sequence 51583, A	Sequence 35046, A	Sequence 2086, Ap	Sequence 63, Appl	Sequence 398, App	Sequence 402, App	Sequence 400, App	Sequence 396, App	Sequence 392, App

ALIGNMENTS

US-09-741-873C-4

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Sequence 4, Application US/09741873C
GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT APPLICATION NUMBER: SE 8801723-1
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/790,846
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR FILING DATE: 1994-01-28
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-01-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 151
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Best Local Similarity
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TYPE: PRT
ORGANISM: Escherichia
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CURRENT APPLICATION NUMBER: PCT/US04/02338
CURRENT FILING DATE: 2004-01-28
PRIOR APPLICATION NUMBER: US60/443,484
PRIOR FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: US60/447,358
PRIOR APPLICATION NUMBER: US60/461,789
PRIOR PILING DATE: 2003-02-11
PRIOR FILING DATE: 2003-04-10
PRIOR FILING DATE: 2003-04-10
PRIOR FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US60/470,684
PRIOR FILING DATE: 2003-05-14
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PCT-US04-02338-49
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PRIOR PELICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR FILING DATE: 1992-11-03
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-10-05
PRIOR SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.2 SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 49, Application PC/TUS0402338 GENERAL INFORMATION: APPLICANT: EXELIXIS, INC.
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Best Local (
                                                                PRIOR APPLICATION NUMBER: US60/479,650 PRIOR FILING DATE: 2003-06-19
                                           NUMBER OF SEQ ID NOS: 54
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                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: EX04-003C-PC
                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: MAPCAXS AS MODIFIERS OF INVENTION: USE
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PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1989-05-04
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APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
CURRENT FILING DATE: 2000-12-22
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TYPE: PRT
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US-10-771-241-299
                                                                                                                                       Sequence 364, Application US/10771241 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FAS
SEQ ID NO 299
LENGTH: 382
TYPE: PRT
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PCT-US04-02338-49
         APPLICANT: Zyskind, Judith
APPLICANT: Forsyth, R. Allyn
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA.001C1
CURRENT APPLICATION NUMBER: US/10/771,241
CURRENT FILING DATE: 2004-02-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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PRIOR APPLICATION NUMBER: 09/492,709
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Best Local
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CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/117,405 PRIOR FILING DATE: 1999-01-27
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TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA.001C1
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APPLICANT: Forsyth, R. Ali
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                                                                                                                                                                                                                                                            276
                                                                                                                                                                                                                                                                                               104
                                                                                                                                                                                                                                                                                                                      216 QPLGDTMVLVKAPGADNVKIENQTGIHTDWRGYAILPFATEYRENRVALNANSLADNVEL
                                                                                                                                                                                                                                                                                                                                                                                              158 GNTHOGNTSSGTSGYSSLNYRGAYGNTNVGYSRSGDS--SQIYYGMSGGIIAHADGITFG
                                                                                                                                                                                                                                                                                                                                                                      83 Q-----
                                                                                                                                                                                                                                                                                                                                                                                                                             30 GNHNGGGNSSGPDSTLSI-YQ--YGSANAALALQSDARKSETTITQSG----YGNGADVG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 HEMAHANQTASD----SSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG------DVSRVKRLVDA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLYTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 VAAFAAI-VVSGSALAGYVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
                                                                                                                                                                                                                                                  D-----ETVVTVIPTHGAIARATFNAQIGGKVLMTLKYGNKS 312
                                                                                                                                                                                                                                                                                     DQWNAKNYDQLVTRVVTH-EMAHANQTASDSSVMVRQVGFGNNA 146
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42; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.5%; Score 81; DB 6; Length 382; 23.2%; Pred. No. 4.1;
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28.4%;
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SOFTWARE: FastSEQ for Windows Version SEQ ID NO 364

ENGTH: 878

92

NUMBER OF SEQ ID NOS: 485

PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27

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; ORGANISM: E. Coli
US-10-771-241-364
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SEQ ID NO 590
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Query Match
Best Local Similarity
Matches 32; Conserv
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                                                                                                                                                                                    PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 2950
SOFTWARE: PatentIn version 3.
                                                                                                                                                                                                                                                                                        APPLICANT: Kumimoto, Roderick W
APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
                                                                  ORGANISM: Oryza sativa FEATURE:
OTHER INFORMATION: G3384
-US04-05654-590
                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 10/374,780 PRIOR FILING DATE: 2003-02-25
                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 10/675,852
                                                                                                                                    LENGTH: 32
TYPE: PRT
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Riechmann, Jose Luis
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Jiang, Cai-Zhong
Heard, Jacqueline E
Haake, Volker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANQ 150
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Yu, Guo-Liang
Broun, Pierre E
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Reuber, T. Lynne
                                                                                                                                                                                                                                                                                                                                                                                                                                                Century, Karen
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Dubell III, Arnold N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratcliffe, Oliver
 Conservative
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                                                                                                                                                                                         version 3.2
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9.9%; Score 76.5; Di
22.5%; Pred. No. 8.2;
ative 19; Mismatches
                                                                                  Orthologous to
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 42;
                                Length 321;
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   49;
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Gaps
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RESULT 8
US-10-100-683-10327
Sequence 10327, Application US/10100683
GENERAL INFORMATION:
APPLICANT: Rosen, et al.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: P8900
CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
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PRIOR APPLICATION NUMBER: US 60/043,314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: US 60/056,664
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PRIOR FILING DATE: 1997-03-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/047,599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1997-08-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 386
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                                                                                                                                                                                                                                                                 GNGAD---VGQGADNSTIELTQNGFRNNAT 102
                                                                                                                                                                                                                                                                                                          GMNPQGAPWGQGG--NGGPPNFGTNTQGAVAQPGYGSVRA----SNQNEGCTNPPPSGS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PECSTETSKMATGGGAGGPAPA 294
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Pred. No. 10;
13; Mismatches
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US-10-100-683-10327
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GENERAL INFORMATION:
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PRIOR FILING DATE: 1997-03-07
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CURRENT FILING DATE: 2002-03-19
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TITLE OF INVENTION: Human Secreted Proteins
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                                           PRIOR FILING DATE: 1997-08-22
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: US 60/056,892
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APPLICATION NUMBER: US 60/047,632
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APPLICATION NUMBER: US 60/056,664
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ICATION NUMBER: US 60/043,314
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CATION NUMBER: US 60/043,580
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NUMBER: US 60/043,314
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tive 13; Mismatches
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US-10-767-701-40104
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; OTHER INFORMATION: phage display generated human antibody
US-10-779-461-40
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US-10-779-461-40
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                                                   SEQ ID NO 40104
LENGTH: 205
TYPE: PRT
                                                                                                                                                                                                                                                             Sequence 40104, Application US/10767701 GENERAL INFORMATION:
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Best Local :
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SEQ ID NO 40
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                                                                                                                    TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(53535)B CURRENT APPLICATION NUMBER: US/10/767,701 CURRENT FILING DATE: 2004-01-29
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CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 60/447,073
PRIOR FILING DATE: 2003-02-13
                                                                                                      NUMBER OF SEQ ID NOS: 63128
                                                                                                                                                                                                              APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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TITLE OF INVENTION: ANTIBODIES TO C-MET FOR THE TREATMENT OF CANCERS
FILE REFERENCE: 00980/1
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TYPE: PRT
                                  ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: artificial
                    FEATURE:
OTHER INFORMATION: Clone ID:
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                                                                                                                                                                                                                                                                                                                                                                                                        60 QSDARKSE-TTITQSGYGNGADVGQ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                          95 YCAISPLRGLTADVFDVWGQGTLVTVSSGGGGSGGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GVVPQ----WGGGGNHNGGGNSSGPDSTLSIYQ--YGSANAALALQSDARKSETTITQSGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 GNGAD---VGQGADNSTIELTQNGFRNNAT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443
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                                                                                                                                                                                                 Zhou, rangwei
                                                                                                                                                                                                                                                                                                                                                                       PASASGSPGQSITISCTGTSSDIGR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGSSNSGGGSGSGSGSGSNGDNNNGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/10779461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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SORBI-28MAY03-C44145_1.pep
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Pred. No. 6.
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6;
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US-10-767-701-40104

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RESULT 13
US-10-045-674A-527
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                                                                                    Sequence 527, Application US/10045674A GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 635
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 591
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
           APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-10-25
PRIOR ADDITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAM:
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/837,306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LADNER, ROBERT C. APPLICANT: COHEN, EDWARD H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Descript OTHER INFORMATION: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 424
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                                                                                                                                                                                                                                                                            303 KGKLDSVATDYGAAIDGFIGDVSGLANGNGATGDFAGSNSQMAQVGDG-DNSPL---MNN
                                                                                                                                                                                                                                                                                                                                                     243 SGGGSEGGGSEGGGSEGGGSGGGGGGGGGGGGGGGGGANANKGAMTENADENALQSDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Similarity 22.2%;
                                                                                                                                                                                                                                         FR 98
                                                                                                                                                                                                      FR 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NASTRI, HORACIO G. ROOKEY, KRISTIN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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RENE
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                                                                                                                                                                                                                                                                                                                                                                                                                                               9.7%;
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Pred. No. 16;
8; Mismatches
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PCT-US04-02188-187
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                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
PCT-US04-02188-187
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                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn
SEQ ID NO 187
LENGTH: 588
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SEQ ID NO 527
LENGTH: 533
                                                                                                                                                       Matches
                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 187, Application PC/TUS0402188 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 191
                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 5151
CURRENT APPLICATION NUMBER: PCT/US04/02188
CURRENT FILING DATE: 2004-01-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: 60/442,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bigwood, Douglas
APPLICANT: Taylor, Ian
TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bayer Pharmaceuticals Corporation APPLICANT: Eveleigh, Deepa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION UMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAM:
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DYAX/002 CIP2
                                                                                                                                                                                                                                                                        TYPE: PRT
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                                        83
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    33
                                                                                                              23 VPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVG 82
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                                      QGADNSTIEL-TQNGFRNNATIDQWNA-KNYDQLVTRVVTHEMAHANQTASDSSVMVRQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FR 469
-GANDELIPFQDEGGEEQEPSSDSASAQRDLDEVKSSLVNES---ENQSSSSDSEAERR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eveleigh, Deepa
Bigwood, Douglas
                                                                                                                                                       Conservative
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                                                                                                                                                                     9.5%; Score 74; DB 26.1%; Pred. No. 29;
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Pred. No.
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                                                                                                                                                                                           DB 1;
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RESULT 15

(Sequence 187, Application US/10764425)

(Sequence 187, Application US/10764425)

(Sequence 187, Application US/10764425)

(Sequence 187, Application US/10764425)

(SEXERAL IMPORMATION:

APPLICANT: Eveleigh, Despa
APPLICANT: Eveleigh, Despa
APPLICANT: Taylor, Ian
APPLICANT: Taylor, Ian
APPLICANT: Taylor, Ian
APPLICANT: MIMBER: US/10/764,425

(CURRENT FILING DATE: 2004-01-23

PRIOR APPLICATION NUMBER: US/10/764,425

(CURRENT FILING DATE: 2003-01-24

NUMBER OF SEQ ID NOS: 191

SEQ ID NO 187

PRIOR FILING DATE: 2003-01-24

NUMBER OF SEQ ID NOS: 191

SEQ ID NO 187

(CORGANISM: Homo Sapiens)

(CORGANISM: Homo Sapiens)

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
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Perfect score:
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Pending Patents AA Main:*

1: /cgn2-6/ptodata/2/paa/US06_COMB.pep:*
2: /cgn2-6/ptodata/2/paa/US06_COMB.pep:*
4: /cgn2-6/ptodata/2/paa/US07_COMB.pep:*
5: /cgn2-6/ptodata/2/paa/US081_COMB.pep:*
5: /cgn2-6/ptodata/2/paa/US081_COMB.pep:*
6: /cgn2-6/ptodata/2/paa/US081_COMB.pep:*
7: /cgn2-6/ptodata/2/paa/US083_COMB.pep:*
9: /cgn2-6/ptodata/2/paa/US083_COMB.pep:*
11: /cgn2-6/ptodata/2/paa/US084_COMB.pep:*
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18: /cgn2-6/ptodata/2/paa/US097_COMB.pep:*
19: /cgn2-6/ptodata/2/paa/US097_COMB.pep:*
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21: /cgn2-6/ptodata/2/paa/US097_COMB.pep:*
22: /cgn2-6/ptodata/2/paa/US097_COMB.pep:*
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28: /cgn2-6/ptodata/2/paa/US097_COMB.pep:*
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20: /cgn2-6/ptodat
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Copyright (c) 1993 - 2004 Compugen Ltd.
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RESULT 1

US-09-543407-26

US-09-543407-26

Sequence 26, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

FILE REFERENCE: 920043,406

CURRENT FILING DATE: 2000-04-05

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 26

LENGTH: 151

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE

FEATURE: INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment

OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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Result No.

Score

Query Match Length DB

ä

Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

```
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
ITILE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043,406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 151
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                     Sequence 5, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
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CURRENT APPLICATION NUMBER: US/09/543,407
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. K
APPLICANT: Kay, William W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                             113
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                                                                                                                                                                                                                                                                                                                                                                         SDARKYDQLVTRVVTHEMAHA------GQGADNSTIELTQNGFRNNATIDQWNAKNSD 112
                                                                                                                                                                                                                                                                                                                                                                                                   -----YDQLVTRVVTHEMAHAGYGNGADVGQQGADNSTIELTQNGFRNNATIDQWNAKNSD 112
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100.0%; Pred. No. 1.8e-75;
tive 0; Mismatches 0;
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Pred. No. 1.3e-67;
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RESULT 4
US-08-233-642A-57
; Sequence 57, Applicat
; GENERAL INFORMATION:
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Best Local S
Matches 137
Query Match
Best Local Similarity
Matches 136; Conserv
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 5
                                                                                                                                                                      TELEX: 3723836 SEEDANBERRY INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION UNDER: 35,570
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 151
TYPE: PRT
ORGANISM: Salmonella
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                   TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 98104-7092
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 5
NUMBER OF SEQUENCES: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Seed and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 26-APF CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                     151 amino acids
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Clouthier, Sharon C.
Doran, James L.
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SYSTEM: PC-DOS/MS-DOS
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Windows Version
                87.9%;
90.1%;
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                                                                                                                                                                                                                                                           920043.403C3
Score 687; DB 6
Pred. No. 3e-65;
2; Mismatches
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Pred. No. 8.7e-66;
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                                DB 6; Length 151;
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Gaps

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APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEF

FILE REFERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT APPLING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 18

LENGTH: 151

TYPE: PRT

ORGANISM: Artificial Sequence
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 151
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Best Local (
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OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragmen
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 81.9%;
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Pred. No. 5.9e-64;
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Query Match
Best Local Similarity
Watches 128; Conserv
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                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 12
LENGTH: 151
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
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                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 122; Conserv
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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ORGANISM: Artificial Sequence
FEATURE:
121
                             121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                       61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                   1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHUGGGNSSGPDSTLSIYQYGSANAALYDQ
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                                                                                                 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKVSDITVGQYGG
NNAALVNYDQLVTRVVTHEMAHANNATANQY
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                                                                                                                                                                                                                               Conservative
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73.6%;
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80.8%; Pred. No. 2.2e-57;
tive 6; Mismatches 23;
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Pred. No. 1e-57;
0; Mismatches 0;
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US-09-543-407-14
; Sequence 14, Application US/09543407
; GENERAL INFORMATION:
; APPLICANT: White, Aaron P.
; APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

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APPLICANT: LOTAN, James L.

APPLICANT: COllinson, S. Karen

APPLICANT: Kay, William W.

ITILE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

ITILE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

FILE REFERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 24

LENGTH: 151

TYPE: PRT

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Best Local (
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 151
                                                                                                                                                              Matches
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Best Local Similarity
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TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
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TYPE: PRT
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                      FEATURE:
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OTHER INFORMATION: sequence containing the replacement fragmer
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT
                      61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                               1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60
                                                                                                                                                                              Similarity
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                                                                        MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                       Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                            77.9%;
82.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.3%;
81.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 612; DB Pred. No. 3.6e. 5; Mismatches
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                                                                                                                                                          4; Mismatches
                                                                                                                                                                          Score 609; DB 19; Pred. No. 7.5e-57;
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.6e-57;
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                                                                                                                                                          Indels
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RESULT 11
US-09-543-407-22
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                                                                                    US-09-543-407-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: White, Aaron P.
APPLICANT: Collingon, S. Karen
APPLICANT: Collingon, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE REFERENCE: 920043.406
FILLE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
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US-09-543-407-31
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                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 151
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22, Applica GENERAL INFORMATION:
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LENGTH: 131
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      Matches
                   Query Match
Best Local 9
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Best Local Similarity 89.3%;
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                         APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                               OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
    123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 GFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GEGNNATANOY 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGAD
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                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09543407
    Conservative
                   76.9%;
81.5%;
  Score 601; DB
Pred. No. 5.5e
4; Mismatches
  4.
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Pred. No. 1.7e-56;
2; Mismatches 12;
                   DB 19;
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    Indels
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Gaps
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1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60

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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 151
                                   FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 151
                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/09543407 GENERAL INFORMATION:
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Best Local 9
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                                                                                                                                                                        APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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81.5%;
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pred. No. 7e-56;
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RESULT 15
US-08-978-878-4
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SOFTWARE: FastSEQ for
SEQ ID NO 7
                                                                                                                                           Sequence 4, Application US/08978878 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 104;
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APPLICANT:
APPLICANT:
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FILE REFERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: SE 8801723-1
EARLIER FILING DATE: 1988-05-06
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                                                                                       TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS
                                                                                                       APPLICANT: NORMARK, Staffan APPLICANT: OLSEN, Arne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                       61 TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
                                                                                                                                                                                                                                                                                                                                                61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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Kay, William W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.98;
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Pred. No. 1.4e-47;
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Pred. No. 2.1e-53;
5; Mismatches 24;
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EARLIER APPLICATION NUMBER: US 07/347,189
EEARLIER FILING DATE: 1980-05-04
EEARLIER APPLICATION NUMBER: US 07/789,437
EEARLIER APPLICATION NUMBER: US 07/789,437
EARLIER APPLICATION NUMBER: US 07/970,846
EEARLIER APPLICATION NUMBER: US 08/197,865
EARLIER FILING DATE: 1992-11-03
EEARLIER FILING DATE: 1994-10-05
EARLIER FILING DATE: 1995-06-28
EARLIER FILING DATE: 1995-06-28
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Result
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Maximum Match 100%
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Perfect score:
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2004 Compugen Ltd
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US-10-100-683-7608
PCT-US04-05654-336
US-10-100-683-10326
US-10-100-683-10327
US-10-004-115B-34
US-10-004-115B-34
US-10-003-150-2
US-10-003-150-2
US-10-603-150-2
US-10-603-150-2
US-10-627-556-396
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US-10-627-556-400
US-10-627-556-400
US-10-627-556-398
US-10-767-701-45448
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PCT-US04-04499-132
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US-09-741-873C-2
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    Sequence 4, Appli
Sequence 2, Appli
Sequence 45603, Ap
Sequence 4603, Ap
Sequence 49, Appl
Sequence 35342, Ap
Sequence 3136, App
Sequence 10326, Ap
Sequence 10327, Appl
Sequence 314, Appl
Sequence 314, Appl
Sequence 3, Appl
Sequence 2, Appli
Sequence 364, Appl
Sequence 396, Appl
Sequence 396, Appl
Sequence 400, Appl
Sequence 400, Appl
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Sequence 410, Appl
Sequence 45448, Ap
Sequence 187, Appl
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70 9.0 305 1 PCT-US04-05654-1406 70 9.0 399 1 PCT-US04-05654-2748 70 9.0 434 6 US-10-045-674A-594 69 8.8 215 6 US-10-767-701-43375 69 8.8 245 6 US-10-779-461-59 69 8.8 616 6 US-10-79-461-59 69 8.8 616 6 US-10-79-461-59 69 8.8 616 6 US-10-786-850-1 68.5 8.8 431 6 US-10-786-850-1 68.5 8.8 433 1 PCT-US04-05654-2586 68.5 8.8 433 1 PCT-US04-05654-338 68.5 8.8 433 1 PCT-US04-05654-338 68.5 8.8 433 1 PCT-US04-05654-338 68.7 195 6 US-10-767-701-32144 68 8.7 195 6 US-10-767-701-32144 68 8.7 351 1 PCT-US04-05654-1755 68 8.7 636 6 US-10-767-701-37968 67.5 8.6 201 1 PCT-US04-05654-136 67.5 8.6 358 6 US-10-767-701-41094 67.5 8.6 358 6 US-10-767-701-440444 67.5 8.6 358 6 US-10-767-701-440444 67.5 8.6 358 6 US-10-767-701-440444
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PCT-USO4-05654-1406 PCT-USO4-05654-2748 US-10-045-674A-594 US-10-767-701-43375 US-10-779-461-59 US-10-467-243-1 US-10-786-850-1 US-10-786-850-1 US-10-045-674A-591 PCT-USO4-05654-2586 PCT-USO4-05654-238 PCT-USO4-05654-238 US-10-767-701-32144 PCT-USO4-05654-1755 US-10-767-701-37968 US-10-767-701-37968 US-10-767-701-34044 PCT-USO4-05654-136 US-10-767-701-41094 US-10-767-701-41094 US-10-767-701-41094 US-10-767-701-41094 US-10-767-701-41094 US-10-767-701-41094 US-10-767-701-41094 US-10-767-701-41094 US-10-76554-1844

ALIGNMENTS

RESULT 1 US-09-741-873C-4

밁 Ś 밁 δ 밁 Ş CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR PILING DATE: 1997-11-26
PRIOR PILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR PILING DATE: 198-05-04
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR FILING DATE: 1994-01-28
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR FILING DATE: 1994-01-28 US-09-741-873C-4 Sequence 4, Application US/09741873C GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein
FILE REFERENCE: 012889-084 SEQ ID NO 4 Matches 103; Query Match Best Local & PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0 LENGTH: 151 TYPE: PRT ORGANISM: Escherichia 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYGG
61 TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQMNGKNSEMTVKQFGG 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ Similarity 68.2 03; Conservative GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151 MKILKVAAIAAIVFSGSAVAGVVPQYGGGGHHGGGGHNSGFNSELNIYQYGGGHSALALQ 66.5%; Score 520; DB 5; 68.2%; Pred. No. 1.4e-40; tive 19; Mismatches 29 coli 151 Āθ Length 151; Well Indels Αs Its 0 Preparation Gaps 120 60 60 120 0

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; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C82834_1.pep
US-10-767-701-45603
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US-09-741-873C-2
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                                                                                                                                                            NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 45603
LENGTH: 234
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 45603, Application US/10767701 GENERAL INFORMATION:
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                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                                                              APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei
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PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR FILING DATE: 1992-11-03
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PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1989-05-04
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                                                    NAME/KEY: unsure
LOCATION: (1)..(234
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 07/789,437
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                                                                                                                                    ORGANISM: Sorghum bicolor
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Pred. No. 1.5e-33;
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Best Local :
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Best Local Similarity
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CURRENT FILING DATE: 2002-03-19
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PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: US 60/056,892
PRIOR FILING DATE: 1997-08-22
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PRIOR APPLICATION NUMBER: US 60/043,576
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                                                                                                                                                                                                                                                                                                                                          ENGTH: 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1997-05-23
APPLICATION NUMBER: US 60/056,664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/047,599
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                                 114 TVGQYGGN 121
                                                                       243 NSGGGSGSQSGSSGSGS
                                                                                                                                         185 GMNPQGAPWGQGG--NGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSS
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                                                                                                       72 HAGYGNGADVGQGADNSTIELTQNGFRNNATI------
                                                                                                                                                                         21 GVVPQ---WGGGGNHNGGGNSSGPDSTLSIYQ--YGSANAALYDQLVTRVVTH----EMA 71
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SSGNHGGS 304
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                                                                                                                                                                                                                Conservative
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Pred. No. 2.3;
20; Mismatches
                                                                       NGDNNNGSSSGGSGGSGGSRGDSGSESSWNGSSTGS
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; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C65560_1.pep
US-10-767-701-35342
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PCT-US04-02338-49
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PCT-US04-02338-49
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CURRENT APPLICATION NUMBER: PCT/US04/02338
CURRENT FILING DATE: 2004-01-28
PRIOR APPLICATION NUMBER: US60/443,484
PRIOR FILING DATE: 2003-01-29
PRIOR FILING DATE: 2003-02-11
PRIOR FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US60/447,358
PRIOR FILING DATE: 2003-02-11
PRIOR FILING DATE: 2003-04-10
PRIOR FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US60/470,684
PRIOR APPLICATION NUMBER: US60/479,650
PRIOR APPLICATION NUMBER: US60/479,650
PRIOR APPLICATION NUMBER: US60/479,650
PRIOR APPLICATION NUMBER: US60/479,650
PRIOR FILING DATE: 2003-06-19
                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 35342
LENGTH: 179
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GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: MAPCAX8 AS MODIFIERS OF THE APC AND AXIN PATHWAYS AND METHODS
TITLE OF INVENTION: USE
                                                                                                                                                                                   Matches
                                                                                                                                                                                                        Query Match
Best Local (
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LENGTH: 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 (53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
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                                                                                                                                                                                                                                                                                                                                           ORGANISM: Sorghum bicolor
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                                         87 NSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTA-----SDSSVMVRQ 139
                                                                                                                                  27 GGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGADVGQGAD
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DNT----SSSSSGDGWGGSKSS--
                                                                                         GGRGNRYSGGTSS-----YYEGRRGRRSYQSRVSN-----DFVDAASTAVGAD
                                                                                                                                                                                Conservative
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GGYGGWDEILDNNTAAAQEAKRSSNSFSAGN 95
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PCT-US04-05654-336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374,780
PRIOR FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 10/675,852
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 2950
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 336
LENGTH: 391
TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                 Sequence 10326, Application US/10100683 GENERAL INFORMATION:
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: US 60/043,576
PRIOR FILING DATE: 1997-04-11
                                                                                                          APPLICANT: Rosen, et al.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS900
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APPLICANT: Pilgrim, Marsha L
ITTLE OF INVENTION: POLYMCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
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                                                                                                                                                                                                                                                                                113 KRRREVEEGGAKAVKAANTLTVDQYFSGGSSTSKVREASSNMSGPGPTYEYTTTATAS 170
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                                                                                                                                                                                                                                                                                                               98 RNNATIDQWNAK----NSDITVGQY--GGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                        57 SSSSSSLISGFSREMEMSAIVSAL-THVVAGNVPQHQQGGGGGGGGTSNSS---SSSGQ 112
                                                                                                                                                                                                                                                                                                                                                                                             38 SSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGF 97
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Repetti, Peter
Century, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reuber, T. Lynne
Keddie, James
Dubell III, Arnold N
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Haake, Volker
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Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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LENGTH: 386
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                  PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/043,314
PRIOR ETILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: US 60/047,632
PRIOR TLING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: US 60/056,892
PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/056,845
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/043,580
PRIOR FILING DATE: 1997-04-11
PRIOR ETITING DATE: 1097-04-11
PRIOR ETITING DATE: 1097-04-11
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CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
                                                                                                                                                         PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: US 60/056,664
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/043,576
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: US 60/047,601
PRIOR FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/040,162 PRIOR FILING DATE: 1997-03-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/047,632
PRIOR TILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: US 60/056,892
PRIOR FILING DATE: 1997-08-22
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APPLICATION NUMBER: US (
FILING DATE: 1997-08-22
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FILING DATE: 1997-05-23
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Similarity 25.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen, et al
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  Application data
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Pred. No. 6.8;
21; Mismatches
  removed -
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See File Wrapper or PALM.
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US-10-451-467A-314
                RESULT 11
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US-10-004-115B-34
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                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: JP 2000-372704
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: JP 2001-006144
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: JP 2001-026594
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: JP 2001-175175
PRIOR APPLICATION NUMBER: JP 2001-175175
PRIOR FILING DATE: 2001-06-11
NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 34
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CURRENT APPLICATION NUMBER: US/10/004,115B
CURRENT FILING DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WAKITA, RYUHEI
TITLE OF INVENTION: PROCESS FOR PRODUCING OPTICALLY ACTIVE
TITLE OF INVENTION: 4-HALO-3-HYDROXYBUTANOATE
FILE REFERENCE: 7372-72249
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                                                                  296 WGARNELIELIDLAHAGIFDISVETFSLDNGAEAYRRLAAGTLSGRAVVV
                                                                                                     106 WNAKNS----
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                                                                                                                                                                      51 GSANAALYDQLVTRVVTHEMAHAGYGNGADV-----GQGADNSTIELTQNGFRNNATIDQ 105
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                                                                                                                                                                                                                       Similarity
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SHIMIZU, MASATOSHI
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Pred. No. 6.8;
21; Mismatches
                                                                                                   DITYGQYGGNNAA----LVNQTASDSSVMV
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Pred. No. 7.3;
L5; Mismatches
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Sequence 314, Application US/10451467A GENERAL INFORMATION:
APPLICANT: CONTERRAS, ROLAND HENRI APPLICANT: EBERHARDT, INES

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PRIOR APPLICATION NUMBER: EP 00870318.3
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: EP 01870002.1
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: EP 01870003.9
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 732
SOFTWARE: Patentin version 3.1
SEQ ID NO 314
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                                                                                                                                                                 ; ORGANISM: Bankia gouldi
US-10-093-037A-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       뭉
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-451-467A-314
                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 63 LENGTH: 956
                                                                     Query Match 9.6%; Score 75; DB 6; Length 956; Best Local Similarity 24.2%; Pred. No. 35; Matches 31; Conservative 17; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 63, Applica GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ENZYMES HAVING GLYCOSIDASE ACTIVITY AND METHODS OF USE THEREOF FILE REPERENCE: 564462001402
CURRENT APPLICATION NUMBER: US/10/093,037A
CURRENT FILING DATE: 2002-03-06
FRIOR APPLICATION NUMBER: US 09/910,579
PRIOR FILING DATE: 2001-07-20
PRIOR FILING DATE: 2001-07-20
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 08/949,026
PRIOR PRIOR FILING DATE: 1998-10-10
PRIOR PRIOR DATE: 1998-10-10
PRIOR PRIOR DATE: 1998-10-10
PRIOR FILING DATE: 1996-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jay M. Short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: JAB-1667
CURRENT APPLICATION NUMBER: US/10/451,467A
CURRENT FILING DATE: 2003-06-19
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: REEKMANS, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
TITLE OF INVENTION: YEAST AND FUNGI
                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 GFGNN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 SYGSN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 DSYGSSNKKKSSYGSSNN----DSYGSNNDD----SYGSNNNDSYGSNNDDSYGSSNKKKS 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148
30 GNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGADVGQGADNST 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 GGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGADVGQGADN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSNNNDSYGSNNNDS-----YGSNNDDSYG-----SSNKNKSSYGSNNDDSYGSNND 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----STIBLTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS--SVMVRQV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bylina, Edward
Swanson, Ronald V.
Mathur, Eric J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lam, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/10093037A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.7%;
llarity 25.6%;
Conservative 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 76; DB; Pred. No. 11; 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
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                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                     30;
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                                                                        Gaps
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CURRENT APPLICATION UNMBER: US/10/771,241
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: 09/49,709
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 485
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 364
LENGTH: 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-10-771-241-364
                                                                 ; ORGANISM: E. US-10-771-241-364
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US-10-603-150-2
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 364, Application U
GENERAL INFORMATION:
APPLICANT: Zyskind, Judith
APPLICANT: Forsyth, R. Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10603150 GENERAL INFORMATION:
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                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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TITLE OF INVENTION: MAGED3-Like Gene Disruptions
TITLE OF INVENTION: Compositions and Methods Re
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FORSYTH, R. Allyn
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA.001C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/391,205
PRIOR FILING DATE: 2002-06-24
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/603,150
CURRENT FILING DATE: 2003-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 9.6%;
Local Similarity 28.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       616 TSTNFGGALNNSAGFGGAMNTSASFGGVLNNSAGFGGAINTSAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 --- QYGG--NNAA----LVNQTASDSSVMVRQVGFGN--NATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  566 ---GRAGFGGALNT----NATFGGVLNGSAGFGGAMNTNATFG--GALNSNAGFGGAIS 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 QVGFGNNA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                471 D-GSSNNS 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 VFSGLDYNNGYLLSIEGDYWNIKDIEFKTGSKGIVLDNSNGSKLKNLVVHDIGEEAIHLR 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               369 GNYNFQDKIQGAFNR-SVYLYGSANGNSTNPIILR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 AIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTL-SIYQYGSA--NAALYDQLVTRVVT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 HEMAHAGYGNGADVGQGADNSTIBLTQNG-----FRNNATIDQWNAKNSDITVG---- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AISTSFSGVLNSSASFGGAIN----TSAGFGSTLNSSASFGSALSTSASFGGVLN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/10771241
9.4%;
28.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 75; DB
Pred. No. 45;
Score 73.5;
Pred. No. 43;
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                       DB 6;
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Best Local Similarity

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GENERAL INFORMATION:
APPLICANT: LEDBETTER, MARTHA
APPLICANT: HAYDEN-LEDBETTER, MARTHA
APPLICANT: THOMPSON, PETER A.
ITITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF
FILE REFERENCE: 49076.000004.CIP2
CURRENT APPLICATION NUMBER: US/10/627,556
CURRENT FILING DATE: 2003-07-26
PRIOR APPLICATION NUMBER: 60/367,358
PRIOR FILING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: 60/367,358
PRIOR APPLICATION NUMBER: 60/367,358
PRIOR FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 60/367,358
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/385,691
PRIOR FILING DATE: 2001-06-03
NUMBER OF SEQ ID NO3: 699
SOFTWARE: PATENT ON SEC ID NO 392
LENGTH: 273
TYPE: PRI
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: amino acid sequence
US-10-627-556-392
Search completed: March 11, 2004, 19:14:19 Job time : 5.3 secs
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US-10-627-556-392
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Best Local S
Matches 23
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                                                                                                                                                                                                                                                   y Match 9.3%; Score 72.5; DB 6; Length 273;
Local Similarity 25.8%; Pred. No. 13;
hes 23; Conservative 15; Mismatches 36; Indels 1
                                                                               127 KLEIKGGGGSGGGGSGGVQLQQSG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        762 TNTLADNVDL-----DNAVAN 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 NQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      708 VTLGOPLNDTVVLVKAPGAKDAKVE-NOTGVRTD-----WRGYAVLPYATEYRENRVALD 761
                                                                                                                     68 HEMAHAGYGNGADVGQGADNSTIELTONG 96
                                                                                                                                                                    75
                                                                                                                                                                                                           15 SGSALAGVVPOWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALY------DQLVTRVVT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 ADVGQ------GADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Conservative
                                                                                                                                                               ASNIVSGIPPRESGSG-----SGIDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Mismatches
                                                                                                                                                                                                                                                   36; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45; Indels
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein - protein search, using sw model
                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     Score
Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          March 11, 2004, 18:33:51 ; Search time 171.3 Seconds (without alignments) 860.386 Million cell updates/sec
                                                                                                                                                                                                                                                         6019581 seqs, 976053577 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
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775
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/cgn2_6/ptodata/2/paa/
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/cgn2_6/ptodata/2/paa/US086_COMB.pep:*
/cgn2_6/ptodata/2/paa/US089_COMB.pep:*
/cgn2_6/ptodata/2/paa/US099_COMB.pep:*
/cgn2_6/ptodata/2/paa/US09_COMB.pep:*
/cgn2_6/ptodata/2/paa/US09_COMB.pep:*
/cgn2_6/ptodata/2/paa/US09_COMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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equence 108562, equence 50616, equence 23883, equence 29231,	H- 8878888	equence 58: equence 2, equence 35: equence 37: equence 39: equence 39: equence 58: equence 58:	equence 5, Appi quence 20, App equence 26, App equence 26, App equence 11, App equence 14, App equence 24, App equence 24, App equence 4, Appi equence 4, Appi equence 2, Appi equence 2, Appi equence 2, Appi equence 34, Appi equence 34, Appi equence 34, Appi equence 34, Appi equence 34, Appi equence 34, Appi equence 34, Appi equence 34, Appi equence 34, Appi equence 34, Appi equence 34, Appi	equence 28, equence 22,

ALIGNMENTS

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WESULT 1

US-09-543-407-28

US-09-543-407-28

US-09-543-407-28

Sequence 28, Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043-406

CURRENT APPLICATION UNDERSE: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 28

LENGTH: 151

TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
FORTURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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US-09-543-407-5
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 151
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              APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: White, Aaron P. APPLICANT: Doran, James L APPLICANT: Collinson, S. APPLICANT: Kay, William W
CURRENT APPLICATION NUMBER: US/09/543,407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                           Application US/09543407
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Pred. No. 7.2e-68;
0; Mismatches 0;
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Pred. No. 1.2e-74;
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SEQ ID NO 5
LENGTH: 151
TYPE: PRT
ORGANISM: Salmonella enteritidis
US-09-543-407-5
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US-08-233-642A-57
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Best Local Similarity 90.1%;
Query Match 87.5%;
Best Local Similarity 89.4%;
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/233,642A
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
CCLASSIFICATION: 424
                                                                                                                                               TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Seed and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS AND CO
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                                                                                  MOLECULE TYPE:
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STREET: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: Washington
                                                                                                    TOPOLOGY:
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                                                                                                                                 LENGTH:
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Collinson, S. Karen
Clouthier, Sharon C.
Doran, James L.
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59
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Pred. No. 9.5e-65;
1; Mismatches 14;
     Score 678; DB 6;
Pred. No. 3.3e-64;
1; Mismatches 15
                                                                                                                                                                                                                                                      920043.403C3
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                                                                                                                                                                                                                                                                                                                                                                                        Version
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                                  Length 151;
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Sequence 26, Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
ITILE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CURRENT APPLICATION UNMBER: US/09/543,407
CURRENT APPLICATION UNMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 151
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US-09-543-407-20
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CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 151
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Best Local S
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
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Local Similarity 81.9%;
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Pred. No. 1.7e-62;
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RESULT 8
US-09-543-407-12
Sequence 12, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
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US-09-543-407-30
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LENGTH: 151
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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Best Local Similarity
Matches 129; Conserv
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Best Local (
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CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEO ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
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Pred. No. 1.2e-
0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 151
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FAStSEQ for Windows Version 4.0
SEQ ID NO 14
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Best Local (
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APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
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APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
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OTHER INFORMATION: sequence containing the replacement fragmen
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major
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                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 151
                                                                                                                                                                                           Local Similarity
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                            SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
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  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                    MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ
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                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                             sequence containing the replacement fragmer encoding PT3 from GP63 of Leishmania major.
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80.1%;
                                                                                                                                                                                         77.8%;
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Pred. No. 2.3e-56;
5; Mismatches 25
                                                                                                                                                                     Score 603; DB 19;
Pred. No. 3.8e-56;
4; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
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APPLICANT: DOZAN, JAMES L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BRCTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043.406
CURRENT APPLICATION UMMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-09-543-407-18
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                                                                                                                                                                                                     SEQ ID NO 24
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                                                                                                                                                                                                                                     APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
NUMBER OF SEQ ID NOS: 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: White, Aaron P.
                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragmen
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragmer OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 151
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77.48;
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Pred. No. 6.3e-56;
Score 600;
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  DВ
  19;
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Length 151
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CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FABTSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 131
TYPE: PRT
ORGANISM: Salmonella enteritidis
US-09-543-407-31
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US-09-543-407-31
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                                CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 151
                                                                                                                                                                                                                                                                                         Sequence 16, Application US/09543407 GENERAL INFORMATION:
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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 116;
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APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
                                                                                                                                                  TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS FILE REFERENCE: 920043.406
                                                                                                                                                                                                        APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
ORGANISM: Artificial Sequence
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88.5%;
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    Mismatches

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Pred. No. 1.8e-55;
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APPLICANT: DOTAI, James L.
APPLICANT: COllinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PE
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                             RESULT 15
US-08-978-878-4
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Matches
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GENERAL INFORMATION:
APPLICANT: White, Aaron P.
                                                                                                                                          Sequence 4, Application US/08978878 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 103;
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              TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN FILE REFERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: SE 8801723-1
                                                                                                       APPLICANT: NORMARK, Staffan APPLICANT: OLSEN, Arne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 151
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Pred. No. 2.2e-52;
4; Mismatches 26;
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Pred. No. 5e-46;
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EARLIER APPLICATION NUMBER: US 07/347,189
EARLIER FILING DATE: 1989-05-04
EARLIER APPLICATION NUMBER: US 07/789,437
EARLIER FILING DATE: 1991-11-06
EARLIER APPLICATION NUMBER: US 07/970,846
EARLIER FILING DATE: 1992-11-03
EARLIER APPLICATION NUMBER: US 08/187,865
EARLIER APPLICATION NUMBER: US 08/187,865
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-00-5
EARLIER FILING DATE: 1994-00-5
EARLIER FILING DATE: 1994-00-05
EARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 4
LENGTH: 151
Search completed: March 11, 2004, 19:13:14
Job time: 172.3 secs
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; ORGANISM: Escherichia coli
US-08-978-878-4
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                                                                                               121 GNGAAVDOTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                              121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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US-10-767-701-43958

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US-10-296-085A-20

US-10-296-085A-27

US-10-296-085A-17

US-10-296-085A-18
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US-10-779-461-1
US-09-596-774-2
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US-10-045-674A-591
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US-10-767-701-45219
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US-10-620-246-6
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US-09-741-873C-2
US-10-767-701-45603
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Sequence 179, App	Sequence 158, App	Sequence 45857, A	Sequence 1755, Ap	Sequence 44940, A	Sequence 1466, Ap	Sequence 3, Appli	Sequence 1593, Ap	0	Sequence 41, Appl	Sequence 59, Appl	Sequence 43391, A	Sequence 429, App	Sequence 430, App	Sequence 6, Appli	Sequence 42696, A	Sequence 364, App	Sequence 71, Appl	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-09-741-873C-4
Sequence 4, Application US/09741873C
GENERAL INFORMATION:

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CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1989-05-04
PRIOR PRIOR PRIOR NUMBER: US 07/789,437
PRIOR PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR PRIOR DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR FILING DATE: 1992-11-03
PRIOR PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
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PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR PILING DATE: 1994-01-28
PRIOR PILING DATE: 1994-10-05
PRIOR PILING DATE: 1994-10-05
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Best Local S
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APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As
FILE REFERENCE: 012889-084
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 151
TYPE: PRT
ORGANISM: Escherichia coli
121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                61 TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
                                                                                                                   Similarity
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67.5%; Pred. No. 6e-39;
tive 16; Mismatches
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; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C82834_1.pep US-10-767-701-45603
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                                                                                                                                                             NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 45603
LENGTH: 234
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 45603, Appl GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                               APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR FILING DATE: 1992-11-03
PRIOR APPLICATION NUMBER: US 08/187,865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1989-05-04
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR FILING DATE: 1991-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/741,873C CURRENT FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Normark, APPLICANT: Olsen, 1
                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 08/978,878 PRIOR FILING DATE: 1997-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 012889-084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Fibronectin Binding Protein
                                                    FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(234)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Escherichia coli
                                                                                                                                    ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131
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                                                                                                                                                                                                                                                                                                                             Zhou, III.
Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                    Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
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Pred. No. 5.3e-32;
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US-10-603-150-2
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Best Local :
                                                                                                                                                                                                                                                                            Sequence 591,
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TITLE OF INVENTION: MAGED3-Like Gene Disruptions,
TITLE OF INVENTION: Compositions and Methods Related Thereto
APPLICANT: HOOGÉNBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMI
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-10-25
CURRENT FILING DATE: 2001-10-25
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PRIOR FILING DATE: 2002-06-24
NUMBER OF SEQ ID NOS: 4
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CURRENT APPLICATION NUMBER: US/10/603,150
CURRENT FILING DATE: 2003-06-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 9.9%;
Local Similarity 27.6%;
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                                                                                                                                                                             LADNER, ROBERT C.
COHEN, EDWARD H.
NASTRI, HORACIO G.
ROOKEY, KRISTIN L.
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PRIOR FILING DATE: 2000-04-17

PRIOR APPLICATION NUMBER: 09/837,306

PRIOR FILING DATE: 2001-04-17

NUMBER OF SEQ ID NOS: 635

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 527

LENGTH: 533
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US-10-045-674A-527
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                                                                                                                                                       Query Match
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SEQ ID NO 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 06/198,069
                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/045,674A CURRENT FILING DATE: 2001-10-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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NUMBER OF SEQ ID NOS: 635
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PRIOR APPLICATION NUMBER: 09/837,306
                                                                                                                                                                                                            OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                  TYPE: PRT
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ORGANISM: Unknown Organism
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64 R-KSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNN 122
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                                                                                                                                       Similarity
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COHEN, EDWARD H.
NASTRI, HORACIO G.
ROOKEY, KRISTIN L.
                                                   SGSALAGVVPQWGG--GGNHNGGGNSSGPDSTLSIYQ-YGSANAAL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGKLDSVAT-----DYGAAIDGFIGDVSGLANGNGAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                            Description of Artificial Sequence: Vector pCES5 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.7%; Score 75.5;
25.7%; Pred. No. 13;
                                                                                                                     9.7%; Score 75.5; I
25.7%; Pred. No. 17;
tive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVGDGDNS 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Mismatches
                                                                                                                                                         ВB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                      47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47;
                                                                                                                                                       6
                                                                                                                                                      Length 533;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
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                                                                                    -ALQSDA 63
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALOSDA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                              ; ORGANISM: E. US-10-771-241-299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-771-241-299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
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Best Local Similarity
Tatches 40; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C9039_1.pep US-10-767-701-45219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
US-10-767-701-45219
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                                                                                                                                        SOFTWARE: Fas
SEQ ID NO 299
LENGTH: 382
  Matches
                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 299, Application US/10771241 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 45219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/771,241
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
                                                                                                                                                                                                                                                                                                                                                APPLICANT: FORSYth, R. Allyn
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA.001C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zyskind, Judith APPLICANT: Forsyth, R. Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kovalic, Dav APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 38-21 (53535) B
                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 TPNPYEQAISIIGRTLSAFDEDNLIPCFGFGDASTHDQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 N-----AALVNQTAS--DSSVMVRQVGFGNNATANO 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 GDDYRSL--SQVTEALAQAGLESSNLIVGIDFTKSNEWTGKISFNRRCLHDI-----GN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 GADYDQLVTRVVTHEMAHAFRNNATI------DQWNAKNS------DITVGQYGGN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 PQWGGGGNHNGGGNSSGPDS----TLSIYQYGSANAALALQSDARKSETTITQSGYGN- 77
                                                                                                                                                                                  FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AALVNOTASDSSVMVROVGFGNNA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSYGYGYSYDYGSTSSGYNSRNTGNTSSGY---SARYAPSSENNVQPETTARLQRKYSRI 64
                                                                                                    Coli
Conservative
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                   25.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -QVGDGDNS 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -DYGAAIDGFIGDVSGLANGNGAT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
                   Score 73.5;
Pred. No. 17;
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Pred. No. 18;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                      DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
40;
                                      Length 382;
  Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
Gaps
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GNHNGGGNSSGPDSTLSI-YQ--YGSANAALALQSDARKSETTITQSGYGNGADYDQLVT 86

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                                                                                                    RESULT 10
US-10-767-701-56903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: 1
SEQ ID NO 6
                                                Sequence 56903, Application UGENERAL INFORMATION:
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 0376/97
PRIOR FILING DATE: 1997-04-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/620,246
CURRENT FILING DATE: 2003-07-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 1277/97
PRIOR FILING DATE: 1997-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ANDERSEN, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/044,624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1998-10-08
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules
                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 6 FILING DATE: 1999-01-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 10/138,473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1999-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2001-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/070,488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 1281/98
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                                                                                                                                                                       98 HAEFRLENNEFNVVDVGSLNGTYVNREPVDSAVLANGDEVQIG 140
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                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Ver.
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                                                                                                                                                                                                       NA----KNSDITVGQYGGNNAALVNQTASDSSVMVR----QVG 141
                                                                                                                                                                                                                                            OAGTESAVSGVEGLPPGSALLVVKRGPNAGSRFLLDQAITSAGRHPDSDIFLDDVTVSRR 97
                                                                                                                                                                                                                                                                              QYGSANAALALQSDARKSETTITQSGYGNGADY--DQLVTRVVTHEMAHAFRNNATIDQW 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROSENKRANDS, Ida
WELDINGH, Karin
FLORIO, Walter
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                                                                                                                                                                                                                                                                                                                9.4%;
ilarity 23.3%;
Conservative 2
                                                                                    Application US/10767701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1998-01-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09/415,884
                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                  Score 73;
Pred. No. (
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                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                    6.4;
                                                                                                                                                                                                                                                                                                                                                    DB 6; Length 162;
     and
                                                                                                                                                                                                                                                                                                                       47;
       Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                       Indels
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US-10-779-461-1
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CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 56903
LENGTH: 174
                                                                                                                                RESULT 12
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                                                                                                                  US-09-596-774-2
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LENGTH: 238
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application: GENERAL INFORMATION:
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                                                                                    Sequence 2, Applicat GENERAL INFORMATION:
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Best Local S
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                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/779,461
CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 60/447,073
PRIOR FILING DATE: 2003-02-13
NUMBER OF SEQ ID NOS: 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 00980/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Morton, Philip A
TITLE OF INVENTION: ANTIBODIES TO C-MET FOR THE TREATMENT OF CANCERS
APPLICANT: GRONER, BERND
APPLICANT: MORITZ, DIRK
TITLE OF INVENTION: BIFUNCTIONAL PROTEIN,
FILE REFERENCE: 24741-1521
CURRENT APPLICATION NUMBER: US/09/596,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                      FEATURE: OTHER INFORMATION: phage display generated human antibody
                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.4%;
Local Similarity 24.5%;
les 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113
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                                                                                                                                                                                  148
                                                                                                                                                                                                                                                 98 RWGQGTTVTVSSGGGGGGGGGGGG--
                                                                                                                                                                                                                                                                               25 QWG------GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD---ARKSETTITQ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LIKVAAFAAIVVSGSALAGVVPQWGGGGNHNG--GGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                  73 SGYGN--GADYD 82
                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATSITAVTVGNEVLSGTNAAML 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SDITVGQ--YGGNNAALV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MLAAAAAFAVLAPPAASSGPTPAPPALGINYGQVADNLPPPQAALLLLRALNATRVKLYD
                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/10779461
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                                                                                                   Application US/09596774
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Pred. No. 7
                                                                                                                                                                                                                                                                                                                  Score 73; DB Pred. No. 10; 5; Mismatches
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                                          PREPARATION AND
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                                                                                                                                                                                                                                                         -GSAQAVLTQPSSVSGAPGQRVTISC
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                                                                                                                                                                                                                                                                                                                                                       Length 238;
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; OTHER INFORMATION: chimeric amino acid sequence
US-09-596-774-2
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 635
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 594
                                                                                          Matches
                                                                                                                                    Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/837,306 PRIOR FILING DATE: 2001-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR FILING DATE: 2000-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 08/793,048
PRIOR FILING DATE: 1996-11-01
PRIOR APPLICATION NUMBER: PCT/EP95/01494
PRIOR FILING DATE: 1995-04-20
PRIOR PRIOR APPLICATION NUMBER: EP 94810244.7
PRIOR PILING DATE: 1994-05-02
                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: M13-III
OTHER INFORMATION: protein sequence
                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
HITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
HITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMI
HITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 3.2
                                                                                                                                                                                                                                                                                               TYPE: PRT
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                                         28 GGGNHNGG--GNSSGPDSTLSIYQY---GSANAAL-----ALQSDAR-KSETTITQS 73
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                                                                                                               Similarity
GGGSEGGGSEGGGSGGGGGGGGGGGTDYEKMANANKGAMTENADENALOSDAKGKLDSVAT-- 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----YQY--GSANAALALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAF 97
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21.2%; Pred. No. 12;
tive 14; Mismatches
                                                                                     Score 72.5; DI
Pred. No. 24;
14; Mismatches
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                                                                                     Indels 47;
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                                                CURRENT APPLICATION NUMBER: US/09/596,774
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 09/159,027
PRIOR FILLY DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 08/793,048
PRIOR FILLY DATE: 1996-11-01
PRIOR APPLICATION NUMBER: PCT/EP95/01494
PRIOR FILLY DATE: 1995-04-20
PRIOR APPLICATION NUMBER: EP 94810244.7
PRIOR FILLY DATE: 1994-05-02
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APPLICANT: GRONER, BERND
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                                 NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                      APPLICANT: GRONER, BERND
APPLICANT: MORITZ, DIRK
TITLE OF INVENTION: BIFUNCTIONAL PROTEIN, PREPARATION AND USE
FILE REFERENCE: 24741-1521
                                                                                                                                                                                                                                                                                                                                                                                     09-596-774-6
              SOFTWARE: PatentIn
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CURRENT APPLICATION NUMBER: US/09/596,774
CURRENT FILING DATE: 2000-06-19
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NUMBER OF SEQ ID NOS: 16
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PRIOR FILING DATE: 1996-11-01
PRIOR APPLICATION NUMBER: PCT/EP95/0
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PRIOR FILING DATE: 1998-09-23
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TYPE: PRT
ORGANISM: Artificial Sequence
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ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 YNAVAWYQQKPGQSPKLLIYSASSRYTGVPSRFTGSGSGPDFTFTISSVQAEDLAVYF 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Pred. No. 25;
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TYPE: PRT
CORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: chimeric amino acid sequence
US-09-596-774-6
Search completed: March 11, 2004, 19:14:20 Job time : 6.3 secs
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9.4%; Score 72.5; DB 5; Length 461;
Best Local Similarity 21.2%; Pred. No. 26;
Matches 25; Conservative 14; Mismatches 38; Indels 41
                                                                                                                                          182 YNAVAWYQOKPGQSPKLLIYSASSRYTGVPSRFTGSGSGPDFTFTISSVQAEDLAVYF 239
                                                                                                                                                                            48 ------YQY--GSANAALALQSDARKSETTITQSGYGNGADYDQLVTRYVTHEMAHAF 97
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Result
No.
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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     Score
Query
Match Length DB
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768
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n2_6/ptodata/2/paa/US997B_COMB.pep:*
n2_6/ptodata/2/paa/US99B_COMB.pep:*
n2_6/ptodata/2/paa/US99B_COMB.pep:*
n2_6/ptodata/2/paa/US99B_COMB.pep:*
n2_6/ptodata/2/paa/US109
COMB.pep:*
n2_6/ptodata/2/paa/US101_COMB.pep:*
n2_6/ptodata/2/paa/US101_COMB.pep:*
n2_6/ptodata/2/paa/US102_COMB.pep:*
n2_6/ptodata/2/paa/US103_COMB.pep:*
n2_6/ptodata/2/paa/US103_COMB.pep:*
n2_6/ptodata/2/paa/US104_COMB.pep:*
n2_6/ptodata/2/paa/US106_COMB.pep:*
n2_6/ptodata/2/paa/US107_COMB.pep:*
n2_6/ptodata/2/paa/US107_COMB.pep:*
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n2 6/ptodata/2/paa/US087 COMB.pep: *
n2 6/ptodata/2/paa/US087 COMB.pep: *
n2 6/ptodata/2/paa/US089 COMB.pep: *
n2 6/ptodata/2/paa/US090 COMB.pep: *
n2 6/ptodata/2/paa/US090 COMB.pep: *
n2 6/ptodata/2/paa/US092 COMB.pep: *
n2 6/ptodata/2/paa/US092 COMB.pep: *
n2 6/ptodata/2/paa/US093 COMB.pep: *
n2 6/ptodata/2/paa/US095 COMB.pep: *
n2 6/ptodata/2/paa/US096 COMB.pep: *
n2 6/ptodata/2/paa/US096 COMB.pep: *
n2 6/ptodata/2/paa/US096 COMB.pep: *
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_6/ptodata/2/paa/US084_COMB.pep:*
_6/ptodata/2/paa/US085_COMB.pep:*
                                                                                     SUMMARIES
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eductice 220,	250	equence 9129.	equence 235	equence 2353	equence 22325,	equence 22325,	equence 8854, A	e 8854,	equence 6, Appl	quence 21, Appl	equence 20638,	equence 20638,	nce 8, A	equence 5833,	equence 5833,	equence 5833,	equence 32, Ap	equence 39, Ap	equence 37, Ap	equence 35, Ap	equence 2, App	equence 2, App	equence 34, Ap	equence 5834,	equence 5834,	equence 5834,	quence 55, Appl	equence 2,	quence 2, Appl	equence 4,	equence 4,	quence 7,	equence 16	equence 31, App	equence 20	equence 18, App	equence 26	equence 12, App	equence 28, App	equence 22, App	equence 14,	quence 57, Appl	quence 5,	equence 24, App	equence 30,

ALIGNMENTS

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US-09-543-407-30

Sequence 30, Application US/09543407

Sequence 30, Application US/09543407

Sequence 30, Application US/09543407

Sequence 30, Application P.
APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406

CURRENT APPLICATION UNMERR: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 30

LENGTH: 151

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
FORTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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Sequence 5, Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER
FILE REFERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/09543407 GENERAL INFORMATION:
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APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: White, Aaron P. APPLICANT: Doran, James L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragmen
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                   HEMAHA-----NQTASDSSVMVRQVGFGNNATANQY 151
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Pred. No. 1.2e-65;
0; Mismatches 0;
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                                             PEPTIDE SEQUENCES
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; TYPE: PRT ; ORGANISM: Salmonella US-09-543-407-5
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US-08-233-642A-57
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NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for V
SEQ ID NO 5
LENGTH: 151
                                                                    US-08-233-642A-57
Query Match
Best Local Sim:
Matches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 57, Application US/08233642A GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION UNMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200
TELEPOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
                                                                                                                                                         TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kay, William W.
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: FLOOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5
NUMBER OF SEQUENCES: -
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP:
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 26-APF CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle STATE: Washington COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                        TOPOLOGY:
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                                                                                                                                       LENGTH:
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                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6300 Columbia Center,
                                                                                                                                           151 amino acids
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90.7%;
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                   88.0%;
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   Score 676; DB 6; Length 151; Pred. No. 4.2e-63; Mismatches 13; Indels
                                                                                                                                                                                                                                                                  920043.403C3
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Pred. No. 1.2e-63;
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Conservative

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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEF
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 151
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US-09-543-407-14
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 151
                                                                                                                                                                                                                                                                                Sequence 22, Application US/09543407 GENERAL INFORMATION:
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Best Local Similarity 81.9%;
Matches 136; Conservative
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
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Pred. No. 2.7e-61;
0; Mismatches 0
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RESULT 8
US-09-543-407-12
; Sequence 12, Application US/09543407
; GENERAL INFORMATION:
; APPLICANT: White, Aaron P.
; APPLICANT: Doran, James L.
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LENGTH: 151
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: White, Aaron P. APPLICANT: Doran, James I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragmen
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
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74.6%;
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Pred. No. 2e-56;
                                                                                                                                                                             -GGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Pred. No. 4.3e-61;
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US-09-543-407-26
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 151
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 151
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
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APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                             OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                       1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                           SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
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                                                                             MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60
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81.5%;
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                                                                                                                                                             Score 600; DB 19;
Pred. No. 4.9e-55;
4; Mismatches 24;
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Pred. No. 2.4e-55;
6; Mismatches 23;
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; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragmen; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major US-09-543-407-20
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US-09-543-407-20
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US-09-543-407-18
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                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version SEQ ID NO 20 LENGTH: 151
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/09543407 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                          APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
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APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
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                                                                                          ORGANISM: Artificial FEATURE:
                                                                                                                                      TYPE: PRT
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TYPE: PRT
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Pred. No. 6.3e-55;
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Query Match

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; SEQ ID NO 31
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-09-543-407-31
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; GENERAL INFORMATION:
; APPLICANT: White, Aaron P
; APPLICANT: Doran, James
; APPLICANT: Collinson, S.;
; APPLICANT: Kay, William
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                                            CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
                                                                                                                                                                                                                                                 Sequence 16, Application:
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                                                                                                                           APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
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   TYPE: PRT
ORGANISM: Artificial
                                   ENGTH: 151
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Local Similarity 89.3%;
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Collinson, S. K.
Kay, William W.
                                                                                                                                                                                                                                                                 Application US/09543407
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5; Mismatches
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Pred. No. 1.8e-54;
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RESULT 15
US-08-978-878-4
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                                                                                                                             Sequence 4, Application US/08978878
GENERAL INFORMATION:
APPLICANT: NORMARK, Staffan
APPLICANT: OLSEN, Arne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 122; Conserv
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Best Local Similarity
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TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN FILE REFERENCE: 012889-081 CURRENT APPLICATION NUMBER: US/08/978,878 CURRENT FILING DATE: 1997-11-26 EARLIER APPLICATION NUMBER: SE 8801723-1 EARLIER FILING DATE: 1988-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/543,407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: White, Aaron P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE: FEATURE: OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 151
                                                                                                                                                                                                                                                                                                                                    121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
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                                                                                                                                                                                                                                                                                                     GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
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Pred. No. 2e-51;
5; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 517; DB 19;
Pred. No. 3.2e-46;
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EARLIER APPLICATION NUMBER: US 07/347,189
EARLIER FILING DATE: 1989-05-04
EARLIER FILING DATE: 1991-11-06
EARLIER FILING DATE: 1991-11-06
EARLIER FILING DATE: 1991-11-03
EARLIER FILING DATE: 1992-11-03
EARLIER APPLICATION NUMBER: US 07/970,846
EARLIER FILING DATE: 1992-11-03
EARLIER APPLICATION NUMBER: US 08/187,865
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER APPLICATION NUMBER: US 08/318,519
EARLIER APPLICATION NUMBER: US 08/318,519
EARLIER APPLICATION NUMBER: US 08/495,959
EARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 151
TYPE: PAT
ORGANISM: Escherichia coli
US-08-978-878-4
Search completed: March 11, 2004, 19:13:14 Job time : 171.3 secs
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                                                                                                                            121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                               121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                                                                         1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
         protein search, using sw model
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1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
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                                                                       Pending_Patents_AA New:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
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         US-09-741-873C-4
US-09-741-873C-2
PCT-US04-02338-49
PCT-US04-05654-590
US-10-100-683-150-2
US-10-100-683-10326
US-10-100-683-10327
US-10-100-683-10327
US-10-771-241-299
US-10-771-241-299
US-10-767-701-45603
PCT-US04-05674A-557
US-10-045-674A-594
US-10-767-701-45603
PCT-US04-05674A-594
US-10-767-701-35046
US-10-767-701-35046
US-10-767-701-32417
US-10-627-556-392
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Sequence 4, Appli sequence 2, Appli Sequence 49, Appli Sequence 7608, App sequence 1755, App sequence 1755, App sequence 10326, A sequence 10326, A sequence 527, App sequence 527, App sequence 527, App sequence 41, Appl sequence 41, Appl sequence 5406, App sequence 5406, App sequence 5406, App sequence 541, Appl sequence 541, Appl sequence 541, Appl sequence 5724, App sequence 5724, App sequence 5724, App sequence 5724, App sequence 5724, App sequence 5724, App sequence 5724, App sequence 5724, App sequence 37217, A sequence 37217, A sequence 37217, A sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequence 3721, App sequen
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Query Match Best Local Similarity 68.9%; Pred. No. 2.1e-38; Matches 104; Conservative 18; Mismatches 29; Indels 0; Gaps Oy OY OY OY OY OY OY OSDARKGETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATALQ OSDARKGETTITQGGGNGADVGQGADNSTIELTQNGFRNNATALQ OSDARKGETTITQGGGNGADVGQGADNSTIELTQNGFRNNATALQ ON ON ON ON ON ON ON ON ON O	US-09-741-873C-4 Sequence 4, Application US/09741873C GENERAL IMFORMATION: APPLICANT: Normark, Staffan APPLICANT: Olsen, Arne FILLE OF INVENTION: Fibronectin Binding Protein As Well As Its Prepar FILE REFERENCE: 01289-084 CURRENT APPLICATION NUMBER: US/09/741,873C CURRENT APPLICATION NUMBER: US/09/741,873C CURRENT FILING DATE: 1998-05-06 PRIOR APPLICATION NUMBER: US 08/978,878 PRIOR APPLICATION NUMBER: US 08/978,878 PRIOR APPLICATION NUMBER: US 07/347,189 PRIOR APPLICATION NUMBER: US 07/347,189 PRIOR APPLICATION NUMBER: US 07/347,189 PRIOR APPLICATION NUMBER: US 07/789,437 PRIOR APPLICATION NUMBER: US 07/789,437 PRIOR APPLICATION NUMBER: US 07/789,437 PRIOR APPLICATION NUMBER: US 07/789,437 PRIOR APPLICATION NUMBER: US 07/790,846 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/318,519 PRIOR FILING DATE: 1994-01-28 PRIOR FILING DATE: 1994-10-05 NUMBER OF SEQ ID NOS: 11 SOFTWARE: Patentin version 3.0 SEQ ID NO 4 LENGTH: 151 TYPE: PRT ORGANISM: Escherichia coli US-09-741-873C-4	27 70.5 9.2 521 6 US-10-627-556-398 Sequence 399 28 70.5 9.2 1048 1 PCT-US04-05564-2086 Sequence 252 29 70 9.1 199 6 US-10-767-701-51583 Sequence 512 30 70 9.1 220 6 US-10-767-701-51583 Sequence 512 30 70 9.1 220 6 US-10-767-701-52948 Sequence 522 31 69.5 9.0 175 6 US-10-767-701-5965 Sequence 523 32 69.5 9.0 386 1 PCT-US04-05634-2526 Sequence 523 33 69.5 9.0 250 6 US-10-767-701-40104 Sequence 632 36 69 9.0 250 6 US-10-779-461-30 Sequence 643 37 69 9.0 391 1 PCT-US04-05634-336 Sequence 633 38 69 9.0 588 1 PCT-US04-05634-336 Sequence 332 39 69 9.0 588 1 PCT-US04-05634-336 Sequence 187 40 69 9.0 588 6 US-10-767-701-46258 Sequence 187 41 69 9.0 588 6 US-10-767-701-46258 Sequence 187 42 68.5 8.9 144 6 US-10-767-701-3246 Sequence 325 43 68.5 8.9 173 6 US-10-767-701-3246 Sequence 325 44 68.5 8.9 191 6 US-10-767-701-3246 Sequence 326 45 68.5 8.9 245 6 US-10-779-461-19 Sequence 327 45 68.5 8.9 245 6 US-10-779-461-19 Sequence 187
; Gaps 0; ANAALALQ 60 : GNSALALQ 60 HEMAHAGG 120 :: MTVKQFGG 120	Preparation	

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; ORGANISM: Escherichia coli
US-09-741-873C-2
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US-09-741-873C-2
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SEQ ID NO 2
LENGTH: 131
                                                                                                                                                                                                                                                                                                                                          Sequence 49, Application PC/TUS0402338
GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: MAPCAXS AS MODIFIERS OF THE
TITLE OF INVENTION: USE
                   SOFTWARE: P.
SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                          PRIOR APPLICATION NUMBER: US60/461,789
PRIOR FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US60/470,684
PRIOR FILING DATE: 2003-05-14
PRIOR APPLICATION NUMBER: US60/479,650
PRIOR FILING DATE: 2003-06-19
                                                             NUMBER OF SEQ ID NOS: 54
                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US60/443,484
PRIOR FILING DATE: 2003-01-29
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: PCT/US04/02338
CURRENT FILING DATE: 2004-01-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
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TITLE OF INVENTION: Fibronectin Binding Protein
FILE REFERENCE: 012889-084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Normark, Staffan APPLICANT: Olsen, Arne
                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: EX04-003C-PC
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                                                                                                                                                                                                 APPLICATION NUMBER: US60/447,358 FILING DATE: 2003-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/347,189
FILING DATE: 1989-05-04
APPLICATION NUMBER: US 07/789,437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/978,878 FILING DATE: 1997-11-26
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APPLICATION NUMBER: US 08/187,865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/970,846
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                                        PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.8%; Score 436; DB 5; 65.6%; Pred. No. 1.2e-31; rative 17; Mismatches 28
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PCT-US04-05654-590
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PCT-US04-05654-590
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                                                                                                                                                                                                                                                         SEQ ID NO 590
LENGTH: 321
TYPE: PRT
ORGANISM: Oryza sativa
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Best Local Similarity
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APPLICANT:
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TITLE OF I
                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
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PRIOR APPLICATION NUMBER: 10/675,852
PRIOR FILING DATE: 2003-09-30
                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374,780
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                                                                                                                                                                                                                     FEATURE: OTHER INFORMATION: G3384 Orthologous to G256
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Local Similarity 29.4%;
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                                                                                                                                     30;
                                67 ETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                   10 AAIVVSGSALAGVVPQW----GGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T: Kumimoto, Roderick W
T: Pilgrim, Marsha L
INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
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                                                                  AAYASSADNIARLLQGWMRPGGG----GGGNGKGPEAS-----GSTSTTATTQQQPQCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Broun,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yu, Guo-Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gutterson, Neal
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Century, Karen
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Haake, Volker
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Subell III, Arnold N
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                                                                                                                                     Conservative
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                                                                                                                                                      11.1%; Score 85; DB 26.3%; Pred. No. 1.8;
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GEGAASASASQSGAAAAATAQTPECSTETSKMATGGG
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Pred. No. 2
                                                                                                                                     Mismatches
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                                                                                                                                                                      DB 1;
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; ORGANISM: Homo sapiens
US-10-100-683-7608
                                                                                                                                                         Sequence 1755, Applications
Sequence 1755, Applications
GENERAL INFORMATION:
GRAPPLICANT: Sherman, Bradley K
APPLICANT: Shermann, Jose Luis
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Best Local 9
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SEQ ID NO 7608
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CURRENT FILING DATE: 2002-03-19
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                                                                                                                                                                                                                                               -US04-05654-1755
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APPLICATION NUMBER: US 60/047,601
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                                                                                                                                                                                                                                                                                                                                                                                                                                 76 GNGAD---VGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASD 132
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                                                                                                     Riechmann, Jose Luis
Jiang, Cai-Zhong
Heard, Jacqueline E
Haake, Volker
                                                                                                                                                                                                                                                                                                                      SS 288
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Reuber, T. Lyn
Keddie, James
Dubell III, Ar
                                  Adam, Luc J
Reuber, T. Lynne
                                                                     Ratcliffe,
                                                                                           Creelman, Robert A
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                                                                         Oliver
   Arnold N
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Pred. No. 4.8;
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                                                                                                                                                                                                                                                                                                                                                                                                -SSGGSGGSGGSRGDSGSE 286
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                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Applicat
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1755
                                                                                                                                                                                            Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374,780
PRIOR FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 10/675,852
PRIOR APPLICATION NUMBER: 10/675,852
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 2950
                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2002-06-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/603,150
CURRENT FILING DATE: 2003-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/391,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: R-1891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: MAGED3-Like Gene Disruptions, TITLE OF INVENTION: Compositions and Methods Re-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Robert G. Wisotzkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.2
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
FILE REFERENCE: MBI-0047 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 351
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
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                                                                                                                                                                                                                                                                                       ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                         LENGTH: 1160
TYPE: PRT
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                                                                                                                                                                                                            Local
     120 GNNAA 124
                                           939 VTSDGFAGNLGTNTGFGGTLGTGAGFSVSLNNGNGFGNGPNASFNRGLNTII----GFGS
                                                                                                                  879 GTSTDFSGGLNHNADFNGGLGNSAGFNGGLNTNTDFGGELGTSAGFGDGLGSSTSFGAGL
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                                                                            70 ITQSGY-----GNGADVGQGADNSTIELTQNGFRN--NATYDQLVTRVVTHEMAHAG 119
                                                                                                                                                     21 GVVPQWGGGGNHN-----GGGNSSGPDSTLSI-YQYGSANAALALQSDARKSETT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 SGYG-NGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 SALARVVAGGGGGGGGGDGDQWAWSSPSPSSS-----AAAAAARGVQERRREEQAMHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 SALAGVVPQWGGGGNHNGGG----NSSGPDSTLSIYQYGSANAALALQSDARKSETTITQ
                                                                                                                                                                                            33;
                                                                                                                                                                                                            n 10.1%;
Similarity 26.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kumimoto, Roderick W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Broun, Pierre E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gutterson, Neal
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                                                                                                                                                                                                                Score 77.5;
Pred. No. 3
                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                38,
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US-10-100-683-10326

Application US/10100683

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US-10-100-683-10327; Sequence 10327, Application US/10100683; GENERAL INFORMATION:
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US-10-100-683-10326
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Best Local Similarity
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GENERAL INFORMATION
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CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/040,162
                                                          PRIOR APPLICATION NUMBER: US 60/043,576
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: US 60/047,601
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: US 60/056,845
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-22
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                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1997-03-07
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                                                                                                                                                                                                   PRIOR FILING DATE: 1997-03-07
                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/040,162
                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Human Secreted Proteins
                                                                                                                                                                                                                                                                                            FILE REFERENCE: PS900
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ADDITICATION NUMBER: US 60/056,845
                                         APPLICATION NUMBER: US 60/043,580
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APPLICATION NUMBER: US 60/047,632
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APPLICATION NUMBER: US 60/047,599
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                                                                                                                                                                                                                                                                                                                                     Rosen, et al
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  NUMBER:
                       1997-04-11
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US 60/047,599
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Pred. No. 12;
13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34;
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; Sequence 299, Application US/
; GENERAL INFORMATION:
; APPLICANT: Zyskind, Judith
; APPLICANT: Forsyth, R. Ally
; TITLE OF INVENTION: GENES II
; TITLE OF INVENTION: ESCHERI
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                                                                                                               RESULT 11
US-10-771-241-299
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                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-779-461-40
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GENERAL INFORMATION:
APPLICANT: Morton, Philip A
TITLE OF INVENTION: ANTIBODIES TO C-MET FOR THE TREATMENT OF CANCERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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CURRENT APPLICATION NUMBER: US/10/779,461
CURRENT FILING DATE: 2004-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/447,073 PRIOR FILING DATE: 2003-02-13 NUMBER OF SEQ ID NOS: 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/056,892 PRIOR FILING DATE: 1997-08-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 386
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: phage display generated human antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 250
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FILING DATE: 1997-08-22
APPLICATION NUMBER: US 60/043,314
FILING DATE: 1997-04-11
APPLICATION NUMBER: US 60/047,632
FILING DATE: 1997-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 GGGSSNSGGGSGSGSGSGSNGDNNNGS 267
                                                                                                                                                                                         145 PASASGSPGQSITISCTGTSSDIGR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 GNGAD----VGQGADNSTIELTQNGFRNNAT 102
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                                                                                                                                                                                                                              60 QSDARKSE-TTITQSGYGNGADVGQ 83
                                                                                                                                                                                                                                                                   95 YCAISPLRGLTADVFDVWGQGTLVTVSSGGGGGGGGGGGGG
                                                                                                                                                                                                                                                                                                                                              26;
                                                                                                                                                                                                                                                                                                         9 FAAIVVSGSALAGVVPQWG------GGGNHNGGGNSSGPDSTLSIYQYGSANAALAL 59
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Similarity 31.1%;
28; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                 Similarity 30.6%;
                                                                                           Application US/10771241
                                                                                                                                                                                                                                                                                                                                              Conservative
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GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
ESCHERICHIA COLI
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Pred. No. 12;
13; Mismatches
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Pred. No. 7
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US-10-045-674A-527
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                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                          SOFTWARE: Pa
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SOFTWARE: FRATSEQ for Windows Version 3.0
SEQ ID NO 299
LENGTH: 382
                                                                                                                   Matches
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PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-10-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAM
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1999-01-27
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                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                          LENGTH: 533
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 64 R-KSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAG-GN 121
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                                   SGSALAGVVPQWGG--GGNHNGGGNSSGPDSTLSIYQ-YGSANAAL-----ALQSDA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COHEN, EDWARD H.
NASTRI, HORACIO G.
ROOKEY, KRISTIN L.
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Pred. No. 22;
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Pred. No. 15;
                                                                                                                 Mismatches
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LENGTH: 424
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
                                                                                                                                                                                                                       GENERAL INFORMATION:
             SEQ ID NO 45603
LENGTH: 234
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Best Local S
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                                                                                                   APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants and Uses Thereof Fo
FILE REFERENCE: 38-21(53535)8
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NUMBER OF SEQ ID NOS: 635
SOFTWARE: PatentIn Ver. 2.1
                                                    CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
                                                                                         CURRENT APPLICATION NUMBER: US/10/767,701
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CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 06/198,069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LADNER, ROBERT C. APPLICANT: COHEN, EDWARD H.
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PRIOR APPLICATION NUMBER: 09/837,306
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PRT
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                                                                                                                                                                                                                                                                                                                                                                                                            303 KGKLDSVATDYGAAIDGFIGDVSGLANGNGATGDFAGSNSQMAQVGDG-DNSPL---MNN 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 SGGGSEGGGSEGGGSEGGGSEGGGSGSGSGDFDYEKMANANKGAMTENADENALQSDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 R-KSETTITQ-----SGYGNG------ADVGQGADNSTIELTQNG
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INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAM.
INVENTION: OF ENTITIES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
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KRISTIN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description sequence
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Pred. No.
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                                                                                                                                             Other Molecules Associated With
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Query Match
Best Local Similarity
Matches 41; Conserva
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                                                      ; LENGTH: 624
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Orthologous to G1196
PCT-US04-05654-1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C82834_1.pep
US-10-767-701-45603
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Query Match
Best Local Similarity
                                                                                                                                                                       NUMBER OF SEQ ID NOS: 2950
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1466
                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374,780
PRIOR FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 10/675,852
PRIOR APPLICATION NUMBER: 10/675,852
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LOCATION: (1)..(234)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                   ICANT: Kumimoto, Roderick W
ICANT: Pilgrim, Marsha L
E OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
REFERENCE: MBI-0047 PCT
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INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GXYGEAGGSGXAYAQGGGQGGGGGGGQYGGSG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 SIY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MATTKLAALCFIVLLGIGGANAARVARYVSAGGGGGGGGGGGGRGRWRGGASRWGSGSGSGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLLKVAAFAAIVV--SGSALAGVVPQW---GGGGNHNGGGN-----SSGPDSTL 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sherman, Bradley K
Riechmann, Jose Luis
Jiang, Cai-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGF 142
                                                                                                                                                                                                                                                                                                                                                                                                                            Repetti, Peter
Century, Karen
Gutterson, Neal
Yu, Guo-Liang
Broun, Pierre E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dubell III, Arnold N
Pineda, Omaira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reuber, T. Lynne
Keddie, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.6%; Score 74; DB 6; Length 234; ilarity 21.8%; Pred. No. 11; Conservative 13; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reelman, Robert A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tcliffe, Oliver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Luc J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Volker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jacqueline E
                                                                                                                                                                                                                                    2003-09-30
9.6%;
26.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -NGGAYAQ-----GGAQGGGGGGGQYGGSGS----
Score 73.5; DB 1;
Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QYGSANAALALQSDARKSETTITQSGYGNGADVG 82
                  Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -SGYGSGSGYG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                            Matches
86 SDADV-----GREGORPVPVHRCILAARSTFFYNLFAAR------GREGOGAA 128
                                     66 SETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAA 124
                                                                              35 VAAQAAPVAAGE------ĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠSSVEVVŚLNRLSANLERLLLDSDLDC 85
                                                                                                                                                          31; Conservative
                                                                                                                   6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARK 65
                                                                                                                                                            11; Mismatches
                                                                                                                                                              52;
                                                                                                                                                              Indels
                                                                                                                                                              25;
                                                                                                                                                              Gaps
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Search completed: March 11, 2004, 19:14:20 Job time: 5.3 secs